

AOS 2024 Scientific Program Abstract Booklet

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Symposia

***Using passive acoustic monitoring and machine learning to assess landscapes of fear in response to goshawks (*Accipiter atricapillus*) in the Sierra Nevada**

M Pardo, L Gallagher, C Wood*Presenting author: Michael Pardo*, Cornell Lab of Ornithology, map385@cornell.edu

Predators create 'landscapes of fear' that affect the behavior of their prey, with consequences for the dynamics of entire ecosystems. Many birds adjust their vocal behavior in response to predator presence by producing alarm calls and mobbing calls or, conversely, by reducing vocal activity to avoid detection. However, few studies have investigated how predators affect the vocal activity of their prey at landscape scales. We monitored avian vocal activity with a landscape-scale grid of passive acoustic recorders covering the entire northern Sierra Nevada. We used the BirdNET algorithm, a machine learning model that can identify over 3000 species of birds by sound, to detect goshawk calls and assess the call rates of goshawk prey species. We tested two opposing hypotheses: 1) goshawks induce increased vocal activity by prey in the form of alarm calls and 2) goshawks induce decreased vocal activity by prey to avoid detection. We applied generalized linear mixed models to assess how goshawk presence affected avian call rates while accounting for temporal autocorrelation between detections. Analyses are currently ongoing but will be completed before AOS 2024.

***Nighthawk: A new tool for acoustic monitoring of nocturnal bird migration in the Americas**

B Van Doren, A Farnsworth, K Stone, D Osterhaus, J Drucker, G Van Horn*Presenting author: Benjamin Van Doren*, University of Illinois at Urbana-Champaign, vandoren@illinois.edu

Migratory birds are among the most well-studied animals on Earth, yet relatively little is known about in-flight behavior during nocturnal migration. Because many migrating bird species vocalize during flight, passive acoustic monitoring shows great promise for facilitating widespread monitoring of bird migration. Nighthawk is a deep learning model designed to detect and identify the vocalizations of nocturnally migrating birds. We trained Nighthawk on the in-flight vocalizations of migratory birds using a diverse dataset of recordings from across the Americas. Our results demonstrate that Nighthawk performs well as a nocturnal flight call detector and classifier for dozens of avian taxa, both at the species level and for broader taxonomic groups (e.g. orders and families). The model accurately quantified nightly nocturnal migration intensity (80% variation explained) and species phenology (78% variation explained) and performed well on data from across North America. Incorporating modest amounts of additional annotated audio (50–120 h) into model training yielded high performance on target datasets from both North and South America. By monitoring the vocalizations of actively migrating birds, Nighthawk provides a detailed window onto nocturnal bird migration that is not presently attainable by other means. This tool will empower diverse stakeholders to efficiently monitor migrating birds across the Western Hemisphere and collect data in aid of science and conservation.

***The Cockatiel Party Problem: Separating Sound Sources with an Acoustic Vector Sensor**

I Tolkova, H Klinck*Presenting author: Irina Tolkova*, Cornell Lab of Ornithology, itolkova@cornell.edu

In the last decade, integration of passive acoustic recorders with machine learning has facilitated large-scale, low-cost, non-invasive monitoring of birds and other vocal wildlife. While automated classification systems can now reach outstanding accuracy for individual focal recordings, their performance frequently declines when confronted with the dense overlapping vocalizations characteristic of biodiverse soundscapes. We aim to address this challenge by utilizing an acoustic vector sensor (AVS) in the form of a compact tetrahedral microphone array. An AVS measures both pressure and acoustic

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velocity, therefore enabling streamlined calculation of acoustic direction-of-arrival. By distinguishing directions of high intensity within a recording, we can decompose a soundscape into its constituent sources and numerically approximate their time- and frequency-domain signals. In this talk, we will demonstrate this analysis pipeline for dawn chorus recordings collected at North American wildlife refuges in late spring. To evaluate the utility of an AVS for ecosystem monitoring, we apply BirdNET, a deep-learning-based tool for bird song and call classification. A comparison of BirdNET performance with and without source separation shows a consistent improvement in species-level classification metrics. Furthermore, this approach opens additional opportunities for spatiotemporal analysis, including the tracking of moving sources, filtering of directional noise, and visualization of local species distributions within the surrounding environment.

Scaling up avian territory mapping and behavioral monitoring with automated acoustic localization

T Rhinehart, E Knight, E Bayne, S Lapp, J Kitzes

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A challenging but especially important application of passive acoustic monitoring (PAM) is estimating bird populations' abundance or density. Density estimation with PAM typically relies on ground-truth information about individual birds' behaviors, such as territory size, vocalization rate, and movement behavior. However, gathering this information at scale is often invasive and prohibitively time-consuming. To expand our ability to individually identify and monitor wild birds, we developed and tested a large-scale, non-invasive territory mapping method. In a field study in Alberta, Canada, we deployed 49 synchronized passive acoustic recorders. We estimated singing birds' positions using OpenSoundscape, an open-source Python package for bioacoustic analysis. We distinguished and mapped territories of individual birds using the localized songs' spatial density. These individually identified songs enabled us to estimate population density, individual vocalization rate, and movement behavior. Our automated pipeline localized over 23,000 songs from our four study species. We successfully mapped songs to individual birds' territories validated by in-person observation. Due to imperfect recall, the pipeline underestimated song rate by 15-90%, but manual song detection improved song rate estimates. Individual birds' distribution of movements matched the distribution of movements observed in-person. Notably, localization tracked longer-distance movements that in-person observers were unable to follow. The territory clusters enabled us to estimate these species' population density. In total, we created a detailed dataset that can be used as ground-truth for future studies of density estimation with PAM.

Extending, expanding, and integrating passive acoustic monitoring programs

C Wood

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Passive acoustic monitoring (PAM) has become a valuable and widespread tool in population monitoring. As resources accumulate and analytical techniques advance, there are increasing opportunities for the coverage of PAM efforts to grow. Yet the growth of PAM programs poses a variety of challenges, which we will discuss in increasing order of complexity: 1) extending existing monitoring efforts within an ecosystem, 2) expanding programs to new regions of species' ranges, and 3) integrating multiple monitoring efforts across an area of interest. Challenges range from standardizing metadata and recording equipment to making inferences across disparate ecoregions. Many potential problems have the roots in obscure technical aspects of audio processing and signal detection software but can substantially influence the inferences we might make about critical things like the status of at-risk species. Fortunately, careful planning and proactive coordination among stakeholders can avert many issues, opening up new and exciting possibilities for avian conservation and ecology.

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Novel ecosystem-scale passive acoustic monitoring to study cryptic avian species*K McGinn, B Zuckerberg, J Barry, S Kahl, G Jones, C Wood, S Whitmore, K Kelly, E Ng, M Peery***Presenting author: Kate McGinn, University of Wisconsin-Madison, mcginn4@wisc.edu*

Fire disturbance shapes the structure and composition of faunal communities in many forested ecosystems, but a new era of megafires that result from land use legacies and climate change has led to prolonged negative consequences for some forest specialists. Forest owls in the Sierra Nevada are presumably adapted to shorter-interval fires of mixed severity, but we have yet to quantify the distributions of this assemblage of species and their immediate and persistent responses to disturbance. In this study, we leveraged ecosystem-scale passive acoustic monitoring in the Sierra Nevada and occupancy models to 1) examine species-specific associations with burned habitat and fire legacies and 2) quantify the effect of novel fire disturbance on forest owl populations. Large areas of high-severity fire reduced site occupancy for most species in this assemblage of forest owls, including a mature-forest species for up to 20 years. Low- to moderate-severity fire benefited small cavity-nesting species, while patchy high-severity fire benefited one generalist species. As the climate continues to warm, fires that eliminate large, contiguous areas of live canopy cover could increasingly threaten some of these ecologically important species and the roles they play in ecosystems. Conversely, fires that resemble the region's historical disturbance events could promote the persistence of a diverse community of nocturnal avian predators. Management strategies that reduce fuel loads, restore historical low-moderate severity fire with small patches of high severity fire, and promote a mosaic of forest conditions will likely facilitate the conservation of these nocturnal avian predators.

Crowdsourced recordings reveal spatio-temporal variation in black-capped chickadee vocalization*C Branch, S Haley, M Walls, S Kahl, C Wood***Presenting author: Carrie Branch, University of Western Ontario, cbranch6@uwo.ca*

Temperate passerine ethos categorizes vocal types as either complex songs or simple calls. North American chickadees break this traditional classification by producing rather simple songs and complex calls. Black-capped chickadees are nonmigratory passerines that produce an array of vocal types, including fee-bee song, gargle calls, alarm calls, and their namesake chick-a-dee call, all with differing structure and function. Here we used crowdsourced recordings from BirdNET to assess spatio-temporal variation in black-capped chickadee vocalizations across their entire geographic range. Using >22,500 vocal exemplars, we found that fee-bee song and chickadee call production increased in the spring and summer, while gargle calls were produced significantly less, but consistently throughout the year. Furthermore, we found considerable geographic variation in song structure that deviates from the typical 2-note fee-bee song of black-capped chickadees. We were also able to identify the most common chick-a-dee call syntax. Taken together, these findings set the stage for future work aimed at understanding how environmental differences associated with geographic variation may shape vocal production of North American chickadees.

****Using bioacoustics to determine the outcomes of road closures on bird diversity at an urban-wildland interface****M Gaston, J Bennett, R Buxton***Presenting author: Millicent Gaston, Carleton University, millicentgaston@gmail.com*

Road networks and vehicle traffic pose a significant threat to wildlife and contribute to worldwide biodiversity loss. Roads and traffic threaten the long-term viability of bird populations by reducing landscape connectivity, increasing direct mortality, and reducing habitat quality (e.g., through noise disturbance). However, when the threat of traffic is removed, responses vary across species and context. We used passive acoustic monitoring techniques to explore the effects of traffic reduction on forest-obligate breeding birds in Gatineau Park, Québec, Canada, which has implemented road closures

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throughout the park for conservation purposes. To measure the effects of road closures on bird species richness, Shannon diversity, and community composition, we deployed 30 autonomous recording units at varying distances from roads across three treatment areas: temporarily closed roads (closed four days per week), permanently open roads, and permanently closed roads. Bioacoustic data were analyzed using manual identification of bird vocalizations and the machine-learning, multi-species identifier tool BirdNet. We found that treatment area was the strongest predictor of bird diversity metrics, with increased species richness and diversity in areas adjacent to permanently closed roads followed by temporarily closed roads, and decreased richness and diversity in areas adjacent to permanently open roads. Community composition also varied, with higher occupancy of disturbance-sensitive indicator species at sites with reduced traffic and at sites further from roads. Our findings highlight the potential value of road closures as a conservation tool to protect biodiversity at urban-wildland interfaces, along with the importance of evaluating conservation interventions to ensure effective outcomes. As bird populations decline globally, understanding the conservation benefits of road closures is important to balance human access to nature with conservation management actions.

***Bioacoustic assessment of surrogate species reveals an expansive conservation umbrella in California's Sierra Nevada**

K Brunk, H Kramer, M Peery, C Wood*Presenting author: Kristin Brunk, Cornell Lab of Ornithology, kristin.brunk@ibv.uio.no*

Preserving biodiversity is a central goal of conservation biology, but in practice, monitoring 'biodiversity' often centers on scrutinizing population trends for one or a handful of species that are presumed proxies for biodiversity. Despite the popularity of such surrogate species strategies, the links between biodiversity and surrogate species are rarely tested, especially across the broad spatial scales at which they are implemented. Here, we quantitatively evaluate a prominent surrogate species strategy using bioacoustics across 25,000 km² of California's Sierra Nevada, an ecosystem at risk of massive forest loss due to changing fire regimes and climate. We used multispecies occupancy models to quantify co-occurrence between six indicator species and the rest of the avian community (63 species). We found that 87% of the avian community had a positive association with at least one indicator species and that latitude played an important role in shaping co-occurrence for 16% of species pairs. Our work provides an important test of a well-worn conservation tool, and our results suggest that well-chosen surrogate species can indeed represent a large portion of the rest of the community.

***Acoustic monitoring reveals an increase in avian activity rates ten years after rat eradication on Pinzón Island, Galapagos**

J Tolchin, A Fleishman, K Dunleavy, M McKown, N Holmes, D Croll, C Wolf*Presenting author: Jaclyn Tolchin, jaclyntolchin@gmail.com*

Invasive rodent eradication from island ecosystems is a widespread and effective conservation action for protecting biodiversity. Monitoring the long-term outcomes of conservation actions like eradications is necessary to confirm that goals were achieved and to improve the efficacy of future efforts. Here, we present data from long-term surveys to monitor three avian species endemic to the Galapagos - brujo flycatcher (*Pyrocephalus nanus*), green warbler-finch (*Certhidea olivacea*) (both IUCN vulnerable), and Galapagos shearwater (*Puffinus subalaris*), during and after black rat (*Rattus rattus*) eradication from Pinzón Island. Automated recording units (ARUs) gathered data during (2012/13), two years after (2014/15), and ten years after (2022/23) eradication. We used custom-made convolutional neural networks (CNNs) to classify avian vocalizations on these recordings, and Bayesian hierarchical regression modeling to quantify changes in avian activity over time. We found inconsistent trends in call rates after two years, but after ten years we detected a significant increase in vocal activity for all three species (brujo flycatcher: 264% (31.8% - 967.2% HPDI), green warbler-finch: 421.3% (89.4% - 1426.1% HPDI), Galapagos shearwater: 476.8% (219.8% - 970.7% HPDI)), suggesting that rat removal may have been beneficial for these endemic birds. Our findings contribute to the growing body of literature on the effectiveness of invasive species eradications to aid in biodiversity conservation. Further, our use of ARUs and CNNs demonstrates the power of automated techniques for collecting and analyzing large datasets

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from isolated locations, highlighting their value as efficient tools for monitoring conservation outcomes.

How treating grassland conservation delivery as a supply chain can increase the effectiveness of our cross-boundary grassland bird conservation efforts

J Giocomo, K Ellison*Presenting author:* **James Giocomo**, American Bird Conservancy, jgiocomo@abcbirds.org

Conservation delivery can be defined as providing conservation practices and programs through technical assistance and financial incentives, mainly on private lands, to landowners, land managers, and other stakeholders to achieve shared conservation objectives. In the Great Plains, conservation delivery involves working with farmers and ranchers to implement sustainable agricultural practices that meets the objectives of the landowner while providing habitat for priority wildlife species and other ecosystem services, looking for win-win solutions. Getting the right conservation practices, in the right place, at the right time is impacted by many systems and decisions made at multiple scales and by multiple organizations, and can be treated as a supply chain. Our goal is to create a well-coordinated, collaborative, and adaptive system that maximizes the impact of conservation efforts on private lands in the central grasslands. We used the restoration of declining bird populations as a basis to build an understanding of the land management effort (acres) needed to meet bird population objectives. This understanding creates opportunities to plan for the kinds of programs (dollars) and the staffing (people) needed to ramp-up conservation delivery capacity. We'll show examples of how using a birds-acres-dollars-people framework can help implement strategies at various scales and address bottle-necks to help build and strengthen the cross-boundary conservation delivery supply chain.

Leveraging Multidisciplinary Data to Identify and Target Strategic Grassland Bird Conservation

B Ryder, C Latimer, Q Zhao, B Robinson*Presenting author:* **Brandt Ryder**, Bird Conservancy of the Rockies, brandt.ryder@birdconservancy.org

Grassland birds are among the most steeply declining guild of land birds with some species having lost 70-90% of their historic populations. Conservation planning and the subsequent recovery of these species, however, is challenged by grasslands being predominantly privately owned and used for food production. As such, transdisciplinary approaches that can understand how key threats facing grassland birds intersect with other key socio-ecological factors is essential for the successful recovery of grassland birds. Here, we develop an integrated dynamic full-annual cycle model using the best available bird count data to characterize spatial variation in abundance and contribution to population growth for a suite of steeply declining species. To identify the most cost-effective locations for investing in population recovery, we use the integrated model as a foundation for building spatial prioritization scenarios that account for key socio-ecological variables (vulnerability to key threats, landscape connectivity, climate, and human adaptive capacity to deliver voluntary conservation). We will highlight where the opportunities for conservation have the greatest likelihood of success for two scenarios that account for the risk of agricultural conversion and wood plant encroachment. Ultimately, outcomes will inform the strategic and targeted delivery of conservation to recover grassland birds.

Grasslands Outcomes Tool for Birds (GOT Birds) to provide decision support for conservation actions

A Haverland, A Bartuszevige, R Rylander, B Robinson*Presenting author:* **Amanda Haverland**, American Bird Conservancy, aa.haverland@gmail.com

Populations of grassland birds in North America have been declining for decades. Conversion of grassland to cropland is the most commonly mentioned cause for this decline, but the encroachment of woody plants is an important contributing factor as well. The Grasslands Outcomes Tool for Birds (GOT Birds) is a decision support tool that allows biologists to estimate the change in grassland bird abundance as a result of changes in tree cover. We used existing long-term bird monitoring data and geospatial

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products, including the Rangelands Analysis Platform (RAP), in boosted regression tree analyses to create species density models. We then projected changes in grassland bird populations using a woody transition risk model created with RAP data. The results will be incorporated into an online decision support tool where biologists can determine projected changes for a select suite of grassland and shrubland birds. We anticipate this decision support tool will be used by conservation planners and biologists who work with landowners to estimate wildlife outcomes within the areas of focus.

Using science and technology to drive conservation action that addresses the biome collapse in the Great Plains

S Cady, D Twidwell, C Roberts, D Fogarty, S Morford, D Naugle, D Uden

Presenting author: Samantha Cady, University of Nebraska-Lincoln, samantha.cady@unl.edu

Grasslands are an imperiled biome worldwide. In the North American Great Plains, large-scale woody plant encroachment is causing one ecological regime (woodlands) to become geographically larger at the expense of another (grasslands), ultimately driving grassland biome collapse. This phenomenon has direct and concerning consequences for grassland bird conservation (and biodiversity in general). Emerging technological advances, including the Rangeland Analysis Platform and its derivatives, have allowed for large scale tracking of these rapidly shifting biome boundaries. Combining these tools with ecological theory has yielded the capability to closely quantify and monitor these regime shifts, detect the scale at which they occur, describe their impacts on avian species, and develop proactive conservation strategies. Here, we describe these grassland conservation data products and their role in driving management action to address biome collapse. We then present case studies that illustrate how this technology can inform local grassland conservation efforts for three different iconic bird species. Our findings outline species-specific wildlife responses to these grassland collapse metrics including taxa experiencing profound losses as well as regions that have managed to positively bend the biodiversity curve in the face of woody encroachment.

Grassland Effectiveness Monitoring (GEM): Scalable monitoring to assess conservation program and treatment outcomes

A Matthews, R Rylander, D Bunting, M Duniway, J Giocomo, A Knight, A Leiva, R Perez, K Stonehouse, D Wiley, D Wilhelm

Presenting author: Anna M. Matthews, Oaks and Prairies Joint Venture, American Bird Conservancy, amatthews@abcbirds.org

Grasslands are an imperiled ecosystem in North America, with 2/3 of the historical distribution of this critical habitat lost. To counteract these declines, habitat restoration programs implement practices like brush management, prescribed fire, herbicide treatment, and prescribed grazing. About \$2.8 million/year is spent implementing these practices on private lands by U.S. Fish and Wildlife-Southwest Region's Partners for Fish and Wildlife program, and millions more is spent by other government and non-governmental programs. Monitoring data is scarcely available to assess habitat outcomes. The Grassland Effectiveness Monitoring (GEM) protocol was developed to fulfill this need and is designed to integrate with Bureau of Land Management and Natural Resources Conservation Service monitoring programs. It offers a simplified, tiered design that allows for differing observer plant identification skill levels while producing useful habitat assessment metrics. This protocol was tested on Grassland Restoration Incentive Program prescribed fire and brush management projects in the Blackland Prairie and Cross Timbers regions of Texas in 2021 and 2022. We tested the assumption that prescribed fire yields better quality early successional grassland habitat. Results from pilot data indicate that prescribed fire sites had significantly less woody cover than brush management sites. Prescribed fire sites had more grass and forb cover, and they produced higher cover of annual and perennial forbs. This case study provides an example of how monitoring can be used to assess effectiveness of treatments in restoring native habitat structure as well as how monitoring can be utilized to assess the outcomes of a habitat delivery program.

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(Re)connecting North Americans to their grasslands: Inspiring conservation through multimedia communications and partnerships**W Tong, I Liu, T Swartwout***Presenting author: Wenfei Tong*, Cornell Lab of Ornithology, wenfei.tong@cornell.edu

Visually stunning, scientifically informed media can catalyze conservation outcomes at scale for imperiled and underappreciated ecosystems like the grasslands of North America. The Center for Conservation Media at the Cornell Lab of Ornithology serves grassland conservation groups by co-designing tools targeted at the audiences most critical to helping our partners achieve their desired conservation goals. We will present a few examples to illustrate our process of making media that enables conservation partners to deliver solutions across the Great Plains and beyond. Our products range from data visualizations raising awareness about biome-wide declines in grasslands and grasslands wildlife, to more locally focused short films conveying the richness of grasslands, specific threats facing them, and the solutions local stewards are undertaking to protect these threatened ecosystems. We will conclude by highlighting takeaways from our experience so far and future plans to continue delivering tailored communications resources where they can make the biggest difference to grasslands and grasslands stewards.

Applying insights from human dimensions research to conserve grassland birds**D Bennett, C Berman***Presenting author: Drew Bennett*, University of Wyoming, drew.e.bennett@gmail.com

Bird populations have declined more in grasslands than in any other biome in North America. While ecological sciences are critical to understanding drivers of population declines, conservation is inherently a human process and the social landscape in the Great Plains, dominated by private land, presents significant challenges to sustaining species. Conservation programs are often implemented locally, yet are significantly impacted by policies and market dynamics operating at national and global scales that can drive conversion of grasslands to crops and other uses. Better understanding of the human dimensions can inform conservation efforts so they are better tailored to the social landscape such as by identifying conservation programs and practices that are likely to be adopted by private landowners in areas important for birds. This presentation highlight a research project in the Great Plains that aims to integrate social and ecological data and develop spatial models to inform conservation planning across the biome. We identify opportunities and challenges in integrating insights from human dimensions research with spatial models. The challenges underscore the need for increased social science research capacity to develop datasets at the necessary scale to integrate with ecological data. Successful integration, however, can be invaluable by identifying geographic areas with high 'conservation readiness' where the social and institutional contexts are conducive for implementing conservation at scale to stabilize declining grassland bird populations.

Keeping the moving parts moving: Using policy to build the full annual cycle conservation supply chain to leverage bird habitat needs**S Riley, J Riley***Presenting author: Steven Riley*, American Bird Conservancy, sriley@abcbirds.org

Applying the supply chain metaphor to bird conservation in the context of conservation policy is novel. We will explore how conservation policies, like the Farm Bill and the Endangered Species Act, help to shape the delivery and adoption of on-the-ground conservation. Policies can require actions (the creation of conservation programs, deployment of staff, or distribution of funds). They can also require a response to actions (mitigation, exclusion from programs, or legal actions). Policies and their applications do not happen in a vacuum, nor are they static. Applying old and new conservation and social science to old problems can help to leverage policy improvement. Applying influence can help to target and focus conservation actions to maximize impacts. There is complexity in creating, deploying and adapting conservation systems. By starting with desired outcomes, we can reverse engineer systems to achieve greater functionality.

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Species density models to inform grassland bird conservation in the Central Great Plains

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Grassland birds are among the steepest declining bird groups in North America, largely due to habitat loss associated with grassland conversion to cropland and shrub encroachment. To overcome this continent-wide conservation problem, science-based decision support tools are needed to allocate limited resources effectively. The Central Grassland Avian Modeling Project (CGAMP) was formed to begin filling knowledge gaps and developing spatially explicit models at scale that integrate data across various disciplines and geographies, with the central focus of advancing analytical models and subsequent spatial prioritization tools to address these urgent conservation needs. To date, CGAMP has leveraged diverse long-term continental scale bird-monitoring data from 2012-2020 (e.g., USGS Breeding Bird Survey, Bird Conservancy of the Rockies Integrated Monitoring of Bird Conservation Regions, State/Provincial Breeding Bird Atlas Data and Canadian Wildlife Service Survey data) and key environmental covariates (e.g., land cover, topography, climate, and vegetation) to develop annual, spatially explicit species density models for breeding grassland birds across the central grasslands from Canada to Mexico. Using a Boosted Regression Tree approach and species-specific detectability offsets, the models generate a spatially explicit density surface which can then be translated into trend. We will provide an overview of these models and some real-world examples of their utility for informing conservation of grasslands in the Central Great Plains.

*Creating a roadmap to conservation success in the Great Plains: The Central Grasslands Roadmap Initiative

M Hanna*Presenting author:* **Maggie Hanna**, Bird Conservancy of the Rockies, maggie.hanna@birdconservancy.org

The Central Grasslands Roadmap represents a diverse coalition striving to elevate and promote grassland conservation for future generations across 3 countries, Sovereign Indigenous Nations and 7 sectors. Beyond countries and Nations, the 7 sectors include; private land owners/producers, provincial and state agencies, industry, academia, non-governmental organizations, foundations, and federal governments. Spanning USA, Canada, and Mexico, this region represents 700 million acres, 60% of which has been converted to row-crop agriculture or has extensive invasion of woody trees and shrub species. Of the remaining 40% still in grass, half is vulnerable to conversion or degraded from woody species encroachment. Over the past four years, more than 750 people and 250 partners have contributed their perspectives on policy and funding needs, partnerships, communication, and science to address these biome challenges. The Central Grassland Roadmap operates under a constellation governance model to promote equity and inclusive engagement. Learn more at www.grasslandsroadmap.org. Together we want to conserve and enhance existing intact grasslands while strategically addressing threats that ultimately result in a net gain in healthy grasslands and more sustainable croplands. Our 10- year landscape goal is to restore and enhance 100 million acres. These actions will improve overall grassland condition, stabilize or reverse declining wildlife populations, improve water quality and quantity, enhance soil health, address economic challenges of the region, and help support diverse communities and cultures that have shaped our region for hundreds to thousands of years. The future of our grasslands depends upon elevating grasslands as a priority for investment, restoring ecological processes, reversing declines of threatened species and promoting healthy human communities.

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Ramping up grassland conservation through the JV8 Central Grasslands Initiative: horizontal and vertical integration of biological and social science with programmatic delivery systems

R Perez*Presenting author:* **Robert Perez**, Oaks and Prairies Joint Venture, chivato.perez@gmail.com

The Central Grasslands of North America primarily overlap eight Migratory Bird Joint Ventures representing over 72 federal, state, provincial, non-profit, academic and industry partners. These eight JV's have collaborated to form the JV8 Central Grasslands Conservation Initiative which seeks to stem the loss of grasslands and negative impacts to grassland birds. Through the JV8, JVs are working together across the breeding, migration, and wintering habitats occupied by grassland dependent birds throughout their annual cycle in Mexico, the USA, and Canada. JV8 is an ambitious initiative with the goal of conserving the iconic landscape and wildlife of the central grasslands of North America while supporting the ecosystem stewardship and livelihoods of the people who live there. Collectively, JV8 has identified conservation goals and associated costs needed to sustain priority bird populations. The strategies, funding, and partnerships required to achieve these goals are outlined in the JV8 Business Plan. The JV8 promotes shared experience and best practices between the 8 Joint Ventures and their partners to address conservation bottlenecks and expand effective grasslands conservation efforts. Further, the JV8 Central Grasslands Initiative directly supports goals of the Central Grasslands Roadmap by leveraging existing conservation delivery networks focused on voluntary conservation programs that sustain extant grasslands, restoring and enhancing degraded grasslands, and using the best available science to guide programs for meaningful grassland conservation. In this session we will highlight examples of JV partnerships and conservation delivery networks and also explore emerging challenges and opportunities for scaling up grassland conservation efforts and the power of partnerships to innovate.

Doing More Together: An Integrated, Hierarchical Monitoring Approach for Breeding Landbirds

M McLaren, J Timmer*Presenting author:* **Matthew McLaren**, Bird Conservancy of the Rockies, matthew.mclaren@birdconservancy.org

Recent reports indicate that many bird populations in North America are declining across a variety of habitats, highlighting a need for robust population information. Bird Conservancy of the Rockies and agency partners created the Integrated Monitoring in Bird Conservation Regions (IMBCR) program in 2008 in Colorado in response to national recommendations for improving avian monitoring. Today, the IMBCR program is the largest probabilistic, non-road-based breeding bird monitoring program in the country, spanning the Great Plains to the Great Basin. The strength of the IMBCR program lies in its partnership with numerous state and federal agencies and nonprofit organizations. We pool monitoring resources across the partnership and sampling occurs in a spatially balanced, nested framework. This creates efficiencies in both data collection and analysis and allows for inference to multiple scales, from a management unit up to state or region-wide. Each year, we provide several population metrics for 300+ species, and estimates of uncertainty, which are available at numerous scales for context. Biologists and land managers use these estimates for a variety of purposes, such as tracking and identifying species of concern and determining potential population impacts on migratory birds for environmental assessments. The estimates are publicly available on Bird Conservancy's new and improved data portal. Additionally, researchers conduct separate analyses with the monitoring data to answer specific questions or address hypotheses, and partners conduct targeted monitoring in project areas to evaluate management or conservation efforts. For these reasons, the IMBCR program provides critical information for breeding landbirds.

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Simulation-based power analysis to inform adaptive multi-species monitoring for state wildlife agencies**Z Wallace, Q Latif, D Pavlacky, C Kilner, C Latimer, M McLaren, B Nuse, J Reese, Q Zhao***Presenting author: Zachary Wallace*, Wyoming Game and Fish Department, zach.wallace1@wyo.gov

State wildlife agencies have statutory authority to manage most bird species in the United States. Given this broad responsibility and limited resources, multi-species avian monitoring programs provide crucial information for states to prioritize conservation and management efforts. The Integrated Monitoring in Bird Conservation Regions (IMBCR) is a partner-based breeding bird monitoring program that has been supported by the Wyoming Game and Fish Department since 2008. Annual statewide population estimates from IMBCR constitute the primary source of information to fulfill monitoring needs under the Wyoming State Wildlife Action Plan for multiple avian species of conservation concern. As with any broad-scale monitoring program, IMBCR must navigate tradeoffs in sampling allocation across space and time at multiple scales, while adapting to evolving programmatic objectives and fluctuating funding. Conventional power analyses typically assess the ability of alternative sampling designs to achieve objectives prior to data collection, rather than evaluating adaptive decisions for ongoing monitoring. We leveraged >10 years of monitoring data to conduct a simulation-based power analysis to inform optimal allocation of future sampling effort for IMBCR in Wyoming. Simulations incorporated existing data to test power to discern population trends for >70 priority bird species under realistic scenarios of the amount and spatial distribution of survey effort. Results of our analysis will inform decisions on allocation of limited resources to maximize benefits for avian monitoring and conservation in Wyoming, while establishing a framework for adaptive power analysis with applications to other geographies and monitoring programs.

Balancing wings and wanderers: Assessing the impact of nonmotorized recreation on avian communities on public lands**L Rossi, M McLaren, J Timmer, Q Latif, M Dressen, M Ditmer, H Abernathy***Presenting author: Liza Rossi*, Colorado Parks and Wildlife, liza.rossi@state.co.us

Nonmotorized recreation is one of the fastest growing uses of public lands, posing a constant challenge for land managers who must balance increased visitation with wildlife conservation. Many bird species are declining at alarming rates, highlighting the necessity for managers to fully understand the impacts of recreation on avian communities to inform conservation. Previous work has suggested that recreation may impact habitat specialists and migratory species more than habitat generalists and resident species. Yet, indicators of recreational intensity—such as trail counters and cameras—fail to capture off-trail usage and may mischaracterize recreational use patterns at larger scales relevant to managers (e.g., management units). Our study overcame these limitations by using anonymized and commercially available GPS smartphone locations to quantify recreational use in space and time. We leveraged the IMBCR program to monitor avian population and community metrics on public lands with trail networks. We conducted point counts at select recreation sampling units within 50 m of trails and at reference units representing the broader landscape. We related avian population and community metrics with recreation intensity and trail density, while accounting for relationships with habitat and environmental conditions. Our results provided novel information regarding potential impacts of recreation on avian population and community metrics to inform management of recreation on public lands. Moreover, our community-level analysis allowed for an evaluation of hypotheses concerning how life history traits (e.g., habitat specialization, migration behavior) modulates responses to recreation.

Leveraging modeling and sampling advancements in biodiversity monitoring using IMBCR data: case studies highlighting applications with USDA Forest Service focal species**J Sanderlin, V Stein Foster, S Sawyer, C Staab***Presenting author: Jamie Sanderlin*, jamie.l.sanderlin@usda.gov

With a high diversity of birds across the western United States and multiple stressors on these populations, there is a need for monitoring approaches that provide cost-effective information on

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population status across broad scales. One of the biggest monitoring challenges is the ability to efficiently allocate samples of species in space and time with limited budgets. This is less of a challenge with common species but becomes more problematic with rare species. Most broad-scale monitoring programs do well at tracking common species, yet many species have insufficient observations to detect trends with standard monitoring protocols. Under the USDA Forest Service 2012 Planning Rule, National Forests and Grasslands are mandated to select at least one focal species to track movement towards desired forest conditions through management actions. Birds are often selected as focal species based on habitat relationships aligned with desired resource conditions and monitoring efficiency but may be rarer on the landscape due to limited habitat, population size, or both. We will highlight case studies across National Forests in the western United States using IMBCR (Integrated Monitoring in Bird Conservation Regions) data to select and monitor focal species that leverage modeling and sampling advancements in biodiversity monitoring. We will illustrate how (1) modeling advancements in data integration for species' distribution models, and (2) sampling advancements using optimal sample designs (to maximize metric accuracy given a fixed budget) and additional sampling methods (i.e., passive acoustic surveys, participatory science) increase inference on trends of focal species in multi-species sampling frameworks.

Anticipating changes to grassland bird habitat from future climate across the Western Great Plains

A Monroe, N Van Lanen, C Duchardt, D Augustine, C Aldridge

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Over the last half-century, grassland bird populations declined more than any other bird group in North America. In addition to habitat loss and degradation of native grasslands, increasing greenhouse gas emissions will likely change temperatures and rainfall patterns across the Great Plains. This changing climate is expected to alter vegetation and their associated bird communities. To date, predictions of bird response to a changing climate have focused on temperature and precipitation, but vegetation changes (and associated bird habitat) also depend on factors such as vegetation type and soils. By studying how vegetation influences grassland bird species across the western Great Plains, we are developing models and maps of projected bird distribution under multiple future climate scenarios for grassland vegetation and land use change. These maps will help land managers and other decision makers understand how site-level projects fit within regional and climatic contexts. Training modules and a web-based application accompanying these maps will increase capacity among Federal, State, Tribal, and private partners in their conservation planning under a changing climate.

Quantifying the effectiveness of USDA private land conservation for grassland birds in the western Great Plains

D Pavlacky, A Bartuszevige, R Iovanna, C Kilner, Q Latif, C Latimer, D Naugle, J Timmer, D Twidwell, C Wightman

Presenting author: David C Pavlacky, Bird Conservancy of the Rockies, david.pavlacky@birdconservancy.org

Declining populations of grassland birds are one of the most pressing conservation problems in North America. Effective conservation requires quantifying species responses to threats and corresponding management actions. However, demonstrating species recovery in grassland ecosystems is complicated by extensive private land tenure and variable habitat requirements of species. Our objectives were to 1) determine ability of USDA practices to address primary threatening processes and 2) predict spatially explicit population responses to prioritize conservation action. We hypothesized the Conservation Reserve Program (CRP), Prescribed Grazing and Brush Management will counteract negative impacts of agricultural conversion, habitat homogenization and woody encroachment. We estimated community abundance and occupancy for 61 species of grassland birds using data from the Integrated Monitoring in Bird Conservation Regions program in the western Great Plains (2010 – 2020), and measured covariates from Rangeland Analysis Platform and USDA geospatial data. In Shortgrass Prairie of Colorado, the abundance of grassland birds increased with an interaction effect of restored CRP cover and

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high-productivity Ecological Sites ($\hat{I}^2 = 0.06$; $f > 0.99$). Community occupancy increased with an interaction between area enrolled in Prescribed Grazing and aboveground biomass ($\hat{I}^2 = 0.20$; $f = 0.98$). The abundance of grassland birds showed a quadratic effect of time since Brush Management ($\hat{I}^2 = -0.03$; $f > 0.99$). We predicted species diversity along covariate gradients, confirming agricultural conversion, habitat homogenization and woody encroachment are the primary drivers of biodiversity declines for grassland birds. Finally, we discovered CRP, Prescribed Grazing and Brush Management on private land recovered specific assemblages in distinct regions, suggesting spatial prioritization of USDA practices is an effective strategy for conserving avian biodiversity in the Great Plains.

Understanding conservation outcomes for grassland birds at multiple scales

A Bartuszevige, A Haverland, R Rylander, B Robinson, D Pavlacky

Presenting author: **Anne Bartuszevige**, Playa Lakes Joint Venture, anne.bartuszevige@pljv.org

The central grasslands in North America, extending from Canada into Mexico through the center of the continent, are among the most imperiled and least protected ecosystems in the world. Grasslands and associated wildlife are declining precipitously and have been for years with no end in sight. However, recent efforts to draw attention to this ecosystem collapse has drawn investment in conservation to the region. Agencies and funders of conservation work want to understand how well their investments achieve stated conservation goals beyond the amount of area conserved or money leveraged. The Grassland Outcomes Tool for Birds (GOT Birds) is meant to allow conservation planners and biologists estimate the effects of grassland improvement through woody plant removal on grassland and shrubland bird species abundance. We demonstrate how we are using long-term bird monitoring data and available geospatial data to develop models to estimate the effectiveness of conservation actions or lack thereof on grassland bird species abundance. We used boosted regression tree analysis to calculate density surface models and then reprojected future scenarios of grassland conservation and loss through tree encroachment. We use these models to understand changes in bird species abundance at broad, landscape spatial scales. Then we used hierarchical regression models to provide information to conservation delivery biologists and landowners on the relative benefit to birds at smaller, project-level scales. This information will be included on an online decision support tool platform accessible by biologists from agencies and nonprofits throughout the study region.

*What nomads can teach: Leveraging IMBCR data on Lark Buntings (*Calamospiza melanocorys*) to guide rangeland management

C Duchardt

Presenting author: **Courtney Duchardt**, Oklahoma State University, cduchardt@gmail.com

Recent research identifying steep declines in grassland songbird populations has led to increased calls for a better understanding of how birds use grassland landscapes throughout the annual cycle. Most grassland avifauna management is geared towards protecting and managing habitat for key species in focal areas, and this strategy works well for species with fairly high site fidelity. However, many grassland songbirds are notoriously nomadic, occurring in high numbers on a site in one year and rare or absent in the next. Managers may sometimes exclude these species from plans because they are rare, assuming that their absence in most years implies a lack of reliance on that landscape. However, the converse may be true - these nomadic species, which co-evolved with high spatiotemporal variability in resource availability, may in fact be using these landscapes only when ideal habitat conditions are lacking within their core range. This would change the role of a focal area from 'marginal' to 'critical' for a given species. We leveraged IMBCR data on an arguably charismatic nomad, the lark bunting (*Calamospiza melanocorys*), to determine if above-average abundance at a given site in a given year was a function of 1) ideal conditions (high precipitation and herbaceous vegetation production) in that location and 2) poor conditions (i.e., drought) within core range.

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An optimization approach to balance conifer removal outcomes for sagebrush and pinyon-juniper songbirds

N Van Lanen, J Shyvers, C Duchardt, C Aldridge*Presenting author: Nicholas Van Lanen, US Geological Survey, njvanlanen@gmail.com*

Prior research has demonstrated greater sage-grouse (*Centrocercus urophasianus*) and other sagebrush-obligate songbird populations likely benefit from conifer removal within sagebrush habitats. Unfortunately, growing evidence suggests pinyon-juniper associated species, including the declining pinyon jay, are likely to be negatively affected by conifer removal. Thus, managers require information regarding where conifer removal can be implemented to improve sagebrush habitat, while maintaining important pinyon-juniper habitat. To address this need, we first developed hierarchical songbird abundance-habitat relationship models in a Bayesian framework, using existing monitoring data and remotely sensed landcover data. The development of these models allowed us to map predicted songbird abundance given current conditions, and under a conifer removal scenario. We then calculated expected changes in abundance following conifer removal (hereafter, 'utility') for six species: Bewick's wren (*Thryomanes bewickii*), Brewer's sparrow (*Spizella breweri*), gray flycatcher (*Empidonax wrightii*), pinyon jay (*Gymnorhinus cyanocephalus*), sagebrush sparrow (*Artemisospiza nevadensis*), and sage thrasher (*Oreoscoptes montanus*). We incorporated these utility layers into a linear integer programming optimization framework using *priorizr* in Program R to identify locations for conifer removal based upon single species, single ecosystem, and multi-ecosystem management paradigms to compare conservation outcomes for our species of interest. Results from our analyses demonstrate the utility of a multi-species approach for balancing potential management trade-offs to non-target species. We identify locations for conifer removal treatments within greater sage-grouse habitat in the Utah portion of Bird Conservation Region 16 which maximize increased sagebrush songbird abundance and minimize decreases in pinyon-juniper associated songbird abundance, including the declining pinyon jay.

Leveraging broad-scale environmental and population monitoring to inform spatial prioritization and planning of forest management

Q Latif, J Timmer, J Cannon, B Nuse, C Kilner*Presenting author: Quresh Latif, Bird Conservancy of the Rockies, quresh.latif@birdconservancy.org*

Human land use and climate change have increased forest density and wildfire risk in western North American lower elevation conifer forests. Government policy supports active management to improve ecological function, including reduced wildfire hazard and improved habitat for wildlife. Managers need to discern where and how their efforts will further ecological priorities while assessing tradeoffs among competing objectives. We address this need by leveraging data from Integrated Monitoring in Bird Conservation Regions (IMBCR) and broad-scale remote environmental sensing for predictive modeling of avian and wildfire-related ecological responses to simulated forest management. We mapped predicted responses of wildfire behavior, wildfire-related soil erosion, and avian species occupancy and richness to simulated alternative management approaches along the Colorado Front Range. We represented 'fuels reduction' as a landscape-wide 30% reduction in canopy cover, 'restoration' as more nuanced reductions targeting historical conditions, and no change in canopy cover for reference. Model predictions projected widespread benefits for wildfire and avian habitat objectives with both management approaches, but with notable spatial variation in the magnitude of potential gains and potential for losses in bird species richness in some areas. Despite restoration explicitly targeting historically relevant ecological conditions, fuels reduction more consistently yielded moderate canopy cover conditions that optimized bird species richness. Regardless, predicted widespread ecological benefits suggest a wide range of management approaches would improve ecological function, and mapped predictions can help prioritize management.

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Actionable data science: quantifying the impact of Audubon's Conservation Ranching Initiative on grassland and aridland birds across the Great Plains**N Michel, T Meehan, C Wilsey***Presenting author: Nicole Michel*, National Audubon Society, nicole.l.michel1@gmail.com

The highest standard in conservation is the ability to quantify the beneficial impacts of conservation action. Over half of native grasslands in the US Great Plains have been lost to cropland, development, and tree encroachment. Without their native habitat, grassland bird populations have plummeted over the last 50 years. Audubon's Conservation Ranching Initiative was launched in 2016 to improve grassland quality on private lands to benefit birds and people. Through this market-based approach, Audubon partners with private landowners to develop and implement bird-friendly habitat management practices, including adaptive grazing regimes, woody plant control, and restoration of degraded grasslands. In that time, >100 ranches spanning ~3 million acres nationwide – including >70 ranches in the Great Plains – were certified for their bird-friendly management practices. During the first eight years (2016-2023), Audubon Conservation Ranches supported more diverse, abundant, and resilient grassland and aridland bird communities than other rangelands in the region, with consistent improvements over time. We measure these impacts with a Bird-Friendliness Index, which integrates bird abundance data from the Integrated Monitoring in Bird Conservation Regions (IMBCR) program, conservation scores from Partners in Flight, and functional diversity to evaluate management impact. Accountability metrics such as the Bird-Friendliness Index – particularly when calculated using robust datasets such as IMBCR – enable conservation organizations to communicate the benefits of their programs to partners, funders, and the general public, thereby building support to expand efforts to protect grassland habitats and the birds that rely on them.

Rocky Mountain Avian Data Center 2.0: An interactive, open-source Shiny app for visualizing & sharing avian monitoring data**J Reese, S Howland, J Timmer, M McLaren, C White, B Ryder***Presenting author: Jessie Reese*, Bird Conservancy of the Rockies, jessie.reese@birdconservancy.org

The Integrated Monitoring in Bird Conservation Regions (IMBCR) program is the second largest breeding bird monitoring program in U.S., spanning the Great Plains to the Great Basin. Bird Conservancy of the Rockies collaborates with state and federal agencies in order to produce population estimates (density, occupancy, trend) for 300+ avian species each year. Since 2008, we've amassed >3 million detection records. Our vision is that these data are used to guide conservation and management, not just in theory, but in practice. To that end, we maintain a high-quality, user-friendly online database that is accessible to all of our collaborators, as well as to the public, in the form of raw and summarized data. Recently, we re-developed the Rocky Mountain Avian Data Center (RMADC) 2.0 as a Shiny application. Shiny is an open-source tool for interactive data visualization which uses the R coding language. Using Shiny has brought key advantages to the RMADC, including more intuitive data filtering, a faster and more responsive user interface, and simplified web hosting. For ecologists with expertise in data visualization and mapping in R, Shiny offers an excellent pathway for people with no web development experience to build dashboards and apps for data dissemination. The RMADC allows us to make complex data accessible and actionable for land managers, policy makers, and other stakeholders, in order to translate data collection and analysis into conservation action.

Integrating IMBCR and semi-structured eBird data to improve distribution modeling for under-sampled species, and species of conservation concern**E Stuber, R Norvell, L Gruber***Presenting author: Erica Stuber*, erica.stuber@usu.edu

Structured surveys following specific sampling design are powerful tools for understanding species' distributions and trends, but (not surprisingly) are not well-suited for surveying all species. While any single survey method will have its particular limits, combining data collected under different protocols or sampling designs (or without design) has the potential to boost sample size, extend geographic and

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environmental coverage, and improve model estimates. Although eBird is one of the largest platforms collecting avian presence-absence data it isn't often used in analyses accounting for imperfect detection – observers don't typically conduct repeated site visits, or collect distance-sampling or time-of-detection information, which are most often used to estimate detectability. Here, we combine discrete time-removal and continuous failure-time models to jointly estimate detection rate from single-visit surveys that either record time-to-detection, or total survey duration without time-to-detection. We capitalize on the time-removal design of structured surveys (e.g., as in the Integrated Monitoring of Bird Conservation Regions program) coupled with eBird checklists of known duration to create a single hierarchical occupancy model accounting for imperfect detection. With a case study in Utah, we demonstrate the analytical improvements gained by coupling information gathered under these two survey designs. Augmenting ecological analyses through data integration can facilitate inference on increasingly rare species that may be data-deficient in any one dataset alone, and can improve the precision of ecological estimates. Improving population state estimates, and generating data-based estimates for rare species will both improve wildlife practitioners' ability to make evidence-based decisions regarding their species of interest.

Winter bird monitoring in the Chihuahuan grasslands

E Landi, C White, A Panjabi

Presenting author: **Edward Landi**, Bird Conservancy of the Rockies, edward.landi@birdconservancy.org

Grassland birds are among the most rapidly declining guild of birds in North America. To better understand these declines and their causes, numerous studies have investigated grassland bird demography, populations, and management effectiveness, however, most studies are conducted on the breeding grounds. Previous work suggests that conditions experienced by grassland birds on their wintering grounds may be a limiting factor for population growth, yet little research occurs during this part of the annual cycle. To expand the gaps in knowledge, Bird Conservancy of the Rockies (Bird Conservancy) developed a rigorous sampling protocol to estimate the density and abundance of wintering grassland birds in the Chihuahuan Desert region of Texas, New Mexico, and Mexico. These data will allow us to monitor bird populations during the winter season to give us a fuller picture of population growth or decline throughout the year. In addition, these data will inform managers about the habitat conditions wintering grassland birds prefer, allowing for informed decision making for grassland restoration projects. Finally, these data can be paired with demographic data and breeding bird data collected on projects such as Integrated Monitoring in Bird Conservation Regions to produce Integrated Population Models that provide information on population dynamics across the full annual cycle. We detected a total of 86 species and recorded 15,349 bird detections in 11 strata in grasslands and potential grasslands of the Trans-Pecos region of Texas. We had sufficient data to produce density estimates for 33 species like Chestnut-collared Longspurs (*Calcarius ornatus*) and Sprague's Pipit (*Anthus spragueii*) for regional and ranch strata.

Understanding Spatiotemporal Variation in Population Processes of Migratory Grassland Birds: A Novel Integrated Modeling Approach

Q Zhao, C Latimer

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Migratory birds experience vastly different environmental conditions throughout the annual cycle, imposing challenges for identifying conservation priorities in the face of habitat loss and climate change. Knowledge of the spatiotemporal variation in population processes and their drivers is essential for addressing such challenges, but requires modeling efforts at broad spatiotemporal scales that cannot be achieved by any single data set. Using a newly developed integrated distribution modeling approach that allows information fusion between distance sampling and opportunistic data, we evaluate how key environmental factors are affecting population growth rates for several steeply declining grassland bird species of conservation concern. In particular, our model allows decomposition of seasonal population changes in relation to local and cross-seasonal environmental drivers. Our results highlight the importance of different predictors affecting breeding and non-breeding populations. Based on these

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relationships, we projected locations with the greatest contributions to overall population growth. Lastly, we discuss how these data are being used to help identify strategic opportunities for conservation investments across the Great Plains biome.

A full-annual-cycle, integrated population model for two grassland sparrows of conservation concern

B Nuse, D Pavlacky, C Latimer, A Green, M Correll*Presenting author: Bryan Nuse, bryan.nuse@gmail.com*

Developing conservation strategies for long-distance migrant birds has been hampered by the difficulty in monitoring populations throughout the full annual cycle. We combined data from marked and unmarked individuals on both the breeding and wintering grounds within an integrated population model for two grassland birds of conservation concern, Baird's Sparrow (*Centronyx bairdii*) and Grasshopper Sparrow (*Ammodramus savannarum*). Because most of the data are from repeat count surveys, the basis for the model is a pair of linked Dail-Madsen models (aka dynamic N-mixture models) that connect the breeding ground sites (northern Great Plains in the US) to those in the wintering grounds (Chihuahuan Desert of northern Mexico and US southwest), to our knowledge a novel formulation. Vital rates are shared with model components informed by demographic studies on both the breeding and wintering grounds. Objectives for the study included: 1) explore performance of the model through simulations; 2) determine vital rates and seasons most limiting to the population; and 3) identify important covariate effects that can help inform management activities on both the breeding and wintering grounds. General results include higher estimates of breeding season survival compared to the wintering grounds; variable survival during migration; considerable annual variation in reproduction and population growth rates; and the importance of different landscape and climate conditions to various seasonal vital rates. Differences in the species' vital rates and covariate responses imply distinct life histories, with implications for full-annual-cycle conservation.

A range-wide hierarchical monitoring framework and web-application for targeted management of sage-grouse populations

C Weise, M O'Donnell, B Prochazka, L Wiechman, C Aldridge, P Coates*Presenting author: Cali Weise, croth@usgs.gov*

A range-wide hierarchical population monitoring framework, recently developed by the U.S. Geological Survey, improved the reliability of Greater Sage-Grouse (*Centrocercus urophasianus*) population estimates by accounting for temporal oscillations and spatial metapopulation structure. This framework also formed the basis for a Targeted Annual Warning System (TAWS) to assess when and where individual population trends are out of sync with temporal and regional trends. We developed secure and user-friendly decision support software that allows managers to interact with, query, and download spatial and temporal outputs from the range-wide hierarchical population modeling framework, for straightforward application to their management goals. The easy-to-navigate interface provides users with drop-down menus and interactive maps to define their timeframe and populations of interest. The software provides outputs including maps, figures, and tables displaying annual fluctuations in populations through time across relevant temporal and spatial scales. It also reports populations of concern, as defined by the TAWS, allowing managers to identify which populations may benefit from closer monitoring or management intervention within their management unit of interest. The centralization and accessibility of these data, through our software tool, promote an improved understanding of the threatening factors that impact local sage-grouse populations and promote informed management actions. Findings are preliminary and provided for timely best science.

Effectiveness of sagebrush conservation actions on Greater Sage-Grouse population performance: Did the birds get the memo?

P Coates, B Prochazka, S Webster, C Weise, C Aldridge, M Odonnell, K Doherty, J Tull*Presenting author: Peter Coates, U.S. Geological Survey, pcoates@usgs.gov*

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Developing effective conservation monitoring and analytical frameworks that incorporate robust assessments of actions in relation to target species' viability is critical for successful recovery efforts. However, quantifying conservation effectiveness is often difficult because of the complex nature of ecosystem processes and practical limitations associated with assessing target species' population dynamics. Here, we present an analytical framework that allows for quantification of conservation efficacy using Greater Sage-Grouse (*Centrocercus urophasianus*; hereafter, sage-grouse) as an example. Our approach utilized multiple web-based repositories of conservation actions within sagebrush ecosystems. State-space model estimates of abundance using data from lek count observations served as inputs to a progressive change before-after-control-impact paired series framework to evaluate efficacy of numerous unique conservation efforts. Model results provided evidence of substantial increases in population abundance associated with most conservation actions. Within the Bi-State Distinct Population Segment, which is currently under evaluation for federal protection under the Endangered Species Act, sage-grouse abundance at leks associated with conservation actions increased annually by 15.8%, on average, compared to controls, which amounted to a 57.0% cumulative increase since 2012. Although population gains varied substantially by the type of conservation effort and according to the number of lag years following its implementation, removal of conifers within sagebrush ecosystems generally resulted in the strongest positive effects compared to other actions. These findings are preliminary and provided for best timely science.

Range-wide patterns of Greater Sage-Grouse climate-associated adaptive divergence

S Zimmerman, C Aldridge, J Fike, S Oyler-McCance

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Species with distributions that span a broad range of environmental conditions may become locally adapted. With the changing climate, understanding the relationship between population structure and adaptation to the local climate will be crucial to effective conservation. The Greater Sage-Grouse (*Centrocercus urophasianus*) is an avian obligate of the sagebrush steppe, a climate-threatened plant community that spans six recognized ecoregions. Since the 1960s, the species has experienced a nearly 80% decline in population trend, leading to heightened conservation concern range-wide. There is a growing body of evidence indicating populations of Greater Sage-Grouse may be locally adapted. Conservation actions that involve facilitating gene flow across the species range (e.g., augmentation) can reduce the likelihood of genetic diversity loss and inbreeding depression, but risk displacement of locally adapted genetic variation and could result in outbreeding depression. Selecting source populations that are most similarly adapted to the local climate of the recipient site for conservation translocations would minimize the risk of maladaptation and provide the highest likelihood of persistence. We developed a range-wide Greater Sage-Grouse whole genome sequence data set and explored patterns of climate-associated adaptive divergence. We will present on genome-wide patterns of climate-associated adaptive divergence for the Greater Sage-Grouse with a focus on the conservation implications.

*Sage-grouse and climate change: Synthesis, analysis, and adaptation

C Lundblad, S O'Neil, B Brussee, J Bradford, G Wann, J Tull, M Casazza, S Espinosa, C Aldridge, P Coates

Presenting author: **Carl Lundblad**, carl.lundblad@oregonstate.edu

Greater Sage-Grouse (*Centrocercus urophasianus*) populations track wet-dry cycles in the sagebrush biome and are often described as vulnerable to climate change. However, the underlying direct and indirect mechanisms, their relative importance, and net effects on sage-grouse remain poorly understood. We reviewed the literature on the effects of weather and climate on sage-grouse population trends, demography, and behavior and used those results to guide and develop our own analyses of the effects of climate factors on sage-grouse population growth and vital rates (adult, brood, and nest survival) in the Great Basin of California, Nevada, Oregon, and Idaho. We used hierarchical models to explore the relative influences of concurrent and lagged (up to 1.5 years) indices of drought and precipitation on sage-grouse, dating back to 1985. Our results generally corroborate the paradigm that sage-grouse

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populations respond negatively to drought conditions through multiple mechanisms including those mediated by herbaceous plant productivity and intensifying interactions among invasive annual grasses and wildfire. Adult survival and population growth rates increased with increasing precipitation over the previous growing season, and nest survival declined with increasing nesting-season aridity. Brood survival decreased with increasing spring precipitation, though physiological exposure effects are not as well documented in sage-grouse as the habitat-mediated effects of climate. Our results help identify management strategies that may support sage-grouse's adaptive capacity and performance under intensifying wet-dry cycles and exacerbated ecological drought conditions. Findings are preliminary and provided for best timely science.

Modeling range-wide annual changes in Greater Sage-Grouse seasonal habitats over time (1995 to 2020)

G Wann, C Aldridge, M McLachlan, J Beck, B Timothy, P Coates, C Conway, D Dahlgren, J Dinkins, A Johnston, c hagen, P Makela, D Naugle, M Schroeder, J Sedinger, L Waldner, B Walker, P Williams, A Whipple

Presenting author: **Gregory Wann**, U.S. Geological Survey, wanng@usgs.gov

Wildlife populations commonly change their habitat associations temporally to meet resource needs. Identifying and protecting habitats associated with discrete seasonal periods is therefore an important conservation strategy to ensure populations have access to suitable conditions throughout their full annual cycle. We recently created predictive seasonal habitat models for Greater Sage-Grouse (*Centrocercus urophasianus*) across their U.S. distribution representing spring, summer, winter, nest, and brood habitats. We estimated resource selection functions (RSFs) from used-available locations using data from over 14,000 individual birds collected by multiple scientists, graduate students, state and federal agencies, and consulting companies. Importantly, our models included annually time-stamped predictor datasets representing landcover and other habitat conditions that changed over time, allowing us to make spatial predictions to different years back in time. We identified optimal thresholds to convert the continuous RSF predictions into discrete habitat categories, and estimate spatial changes in habitat from 1995 to 2020. We present these estimates using predictive maps to identify the regions and seasons where the largest changes have occurred, highlighting the seasonal periods where populations are likely to be most limited by habitat. Our study demonstrates the benefit of broad collaborative research to help inform management strategies for a wide-ranging species, but also highlights the critical importance of supporting local wildlife studies since conservation strategies are often needed at multiple scales.

Near or far: At what spatial scales does vehicular traffic affect sage-grouse populations in Wyoming

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Presenting author: **Richard Inman**, U.S. Geological Survey, rdinman@usgs.gov

Road networks and their associated vehicular traffic negatively impact populations of many terrestrial species by causing habitat degradation, functional habitat loss, and direct mortality. Inventories of roads used to assess these impacts often focus on the 'where' (e.g., spatial disturbance) but neglect the 'when' (e.g., temporal disturbance) or 'how much' (e.g., dynamic disturbance). Knowing these characteristics is critical for assessing the cumulative impact of roads and their associated vehicular traffic on ecosystems. We developed annual estimates of road age and vehicular traffic volume across the vast majority of roads in Wyoming (147,108 km) for the years 1986 to 2020. Declines and extirpation of Greater Sage-Grouse (*Centrocercus urophasianus*) have been documented at lek sites near major highways and other transportation infrastructure since the 1950s but are not well studied. Recent decades have also seen increased traffic volumes across most of the state, which can elevate stress hormones, change lekking behavior, and increase mortality. We use our estimates of yearly traffic volume in a multi-scale Bayesian hierarchical modeling framework to 1) assess how traffic has impacted Greater Sage-Grouse population growth rates, 2) identify the spatial scales at which these effects are most evident, and 3) identify what levels of traffic result in sage-grouse population declines. Our preliminary results indicate that effects of traffic volume tend to be detrimental to population growth rates, and that these effects are local.

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Indirect and direct influences of anthropogenic features on sage-grouse populations within sagebrush ecosystems**M Milligan, P Coates, B Prochazka, S Webster, S O'Neil, J Cupples, J Dinkins, S Abele, J Hill, S Szabo, J Tull, S Espinosa, M Ricca, S Mathews, M Casazza, D Delehanty, B Brussee, J Small***Presenting author:* **Megan C. Milligan**, US Geological Survey, mmilligan@usgs.gov

Sagebrush (*Artemisia* spp.) ecosystems are threatened by multiple forms of anthropogenic development, including increased telecommunication infrastructure, energy infrastructure, and surface mining activities. Infrastructure development can increase habitat fragmentation and increase the density of nesting and perching substrates for avian predators, while mining can fundamentally alter soil composition, topography, and vegetation communities. As a result, anthropogenic development could have both direct and indirect effects on sagebrush obligate species such as the Greater Sage-Grouse (*Centrocercus urophasianus*; hereafter sage-grouse), an indicator species for sagebrush ecosystems. We used sage-grouse lek counts and Bayesian hierarchical state-space models to evaluate population annual rates of change (λ) in relation to 1) telecommunication towers across a large portion of the sage-grouse range including Oregon, Wyoming, Nevada, California, and Idaho, 2) two geothermal development sites in Nevada, and 3) mining sites across Nevada. We found that telecommunication tower density and tower proximity to leks were negatively associated with sage-grouse population growth over time. Predicted apparent abundance declined ~24% within 5 km of geothermal sites and local extirpation increased by ~730% within 2 km. Sage-grouse annual rates of change also declined near mining sites, with substantive declines detected up to ~10 km from mining sites, even after active mining operations had ended. Together, our results help describe the individual and cumulative effects that multiple types of anthropogenic development can have on sage-grouse populations. These findings are preliminary and provided for best timely science.

Integrating sagebrush-obligate birds into a spatial conservation prioritization tool for guiding sagebrush ecosystem management and restoration**B Tarbox, N Van Lanen, A Monroe, J Shyvers, C Duchardt, C Aldridge***Presenting author:* **Bryan Tarbox**, USGS, btarbox@usgs.gov

Conservation of arid sagebrush-steppe ecosystems in western North America is largely guided by meeting habitat needs of Greater Sage-Grouse (*Centrocercus urophasianus*; hereafter, sage-grouse). While extensive and dynamic habitat requirements of sage-grouse may render it an effective umbrella species, evidence is mixed and some sagebrush-obligate and -associated bird species may require different management. Spatial conservation prioritization tools that optimize selection of where and how to efficiently and effectively allocate conservation resources have the flexibility to integrate management targets for multiple species, including those with unique habitat needs. We are developing a spatial conservation prioritization tool to support strategic ecosystem management planning efforts across multiple regions of the sagebrush biome. Our tool leverages emerging spatial data resources to produce maps representing optimal areas for sagebrush protection or restoration, based upon objectives. The flexibility in the tool's framework allows for customizing optimization scenarios that consider best-available species suitability metrics, favorable ecological indicators, key threats, and other important management considerations in the decision-making process. We demonstrate how such tools can be used to develop adaptable decision-support resources addressing the needs of multiple bird species while targeting ecosystem-oriented management objectives. We then compare and contrast expected species-specific outcomes of conservation action among spatial conservation planning efforts designed to manage for different combinations of sagebrush-associated songbird species.

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Using passive acoustic monitoring to inform multi-species management of sagebrush and aspen-associated songbirds across a gradient of juniper expansion**C Christensen, V Schroeder, S Wolfe, H Higgins, D Johnson, J Dinkins**Presenting author: **Cara Christensen**, carachristensen@gmail.com

Aspen (*Populus tremuloides*) plant communities generally represent less than 5% of western landscapes but support a high diversity of avian species despite their relatively small spatial footprint. In recent decades, western juniper (*Juniperus occidentalis*) has expanded into aspen plant communities which are found within the greater sagebrush (*Artemisia* spp.) ecosystem at higher elevations. As this expansion progresses, juniper infills the aspen canopy, causing changes in understory vegetation and, eventually, aspen mortality. While the impact of juniper expansion in aspen plant communities on specific avian species is understudied, we predict that it results in habitat loss and degradation for species that use aspen stands for food, cover, and nesting. Habitat loss may be greatest for primary and secondary cavity-nesting species that rely on aspen during the breeding season while tree-nesting species potentially use both aspen and juniper for nesting and may benefit from early stages of juniper expansion. We evaluated the impact of juniper expansion in aspen and sagebrush plant communities in the Steens Mountain area of southeast Oregon. From 2020 to 2023 during the breeding season, we remotely monitored avian species using autonomous recording units (ARUs). The placement of ARUs was stratified by sagebrush (n=22–39) and aspen (n=17–31) areas across a gradient of juniper expansion. We will present occupancy and abundance estimates for aspen, juniper, and sagebrush-associated avian species across a gradient of juniper expansion. These estimates will help inform and guide multi-species management, which is especially relevant since avian species may be responding differently to changes in vegetation over time.

Anthropogenic subsidies and wildfire affect density, occupancy, and interspecies interactions of three sympatric predators in a sagebrush ecosystem*T Owens, L Perry, J Dinkins**Presenting author: **Terrah Owens**, Idaho National Laboratories, terrah.owens@oregonstate.edu

Anthropogenic subsidization and disturbance can benefit generalist avian species by providing additional food, nesting, and perching resources. In the sagebrush biome, anthropogenic subsidization has led to population increases of Common Ravens (*Corvus corax*; hereafter ravens), Red-tailed Hawks (*Buteo jamaicensis*), and Swainson's Hawks (*Buteo swainsoni*). We used six years of count data to investigate how anthropogenic subsidies and wildfire affected these three sympatric predators' density, occupancy, and interspecific interactions in five sage-grouse Priority Areas for Conservation (PACs) in eastern Oregon. We used binomial N-mixture (abundance) and single- and multi-species occupancy models to account for imperfect detection and the effect of environmental variables on the densities and occupancy probabilities of each species. Our results indicated anthropogenic subsidies and recent wildfires (±10 years) were positively associated with the density and occupancy of ravens and Red-tailed Hawks and were indirectly associated with the density and occupancy of Swainson's Hawks. Estimated relative raven density and occupancy probability varied by year and ranged from 0.85–1.64 km⁻² and 0.66–0.94, respectively; estimated relative Red-tailed Hawk density and occupancy did not vary annually and was 0.52 km⁻² and 0.78, respectively; and estimated relative Swainson's Hawk density and occupancy varied by county and ranged between 0.11–0.28 km⁻² and 0.62–0.98, respectively. Multi-species occupancy models with anthropogenic and fire variables indicated that interspecies interactions were either independent or positively associated with the presence of one or both allospecifics. Our results provide evidence that anthropogenic subsidies create generalist predator hotspots in sagebrush ecosystems fragmented by wildfire, which may lead to greater risks of predation to prey species of conservation concern.

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****Cause-specific mortality of sagebrush songbirds during the post-fledging period****E Shertzer, A Chalfoun***Presenting author: Emily Shertzer*, University of Wyoming, eshertze@uwyo.edu

Juvenile periods often are characterized by high mortality rates, yet the factors influencing juvenile mortality remain unclear for many species. In particular, mortality during the vulnerable post-fledging period and potential carryover effects of nestling development on subsequent survival remain unknown for most birds. For example, wing or tarsal development may influence predation avoidance post-fledging, whereas body condition may influence exposure risk. Finally, these processes have rarely been studied in the context of human-impacted landscapes. We quantified post-fledging mortality and carryover effects of nestling traits on cause-specific fledgling mortality in a suite of declining sagebrush-obligate songbirds that breed within natural gas fields. We tracked 139 Brewer's Sparrow (*Spizella breweri*), 60 Sagebrush Sparrow (*Artemisiospiza nevadensis*), and 68 Sage Thrasher (*Oreoscoptes montanus*) fledglings in western Wyoming during June – August, 2021 – 2023, until mortality or dispersal. We identified the causes of mortality as predation or weather-related exposure when possible. Mortality varied annually and across species (e.g., 21% to 42%), as did the influence of nestling morphological traits. For example, wing and tarsus length predicted predation risk in Brewer's Sparrow fledglings, whereas body condition was associated with exposure risk. Mortality did not vary across the energy development gradient. Our results suggest that post-fledging comprises a vulnerable period for declining sagebrush songbirds, although to different extents across species and contexts, and that carryover effects influence cause-specific mortality risk.

****Prevalence and fitness effects of parasitic bird blow flies on sagebrush songbirds****D Jones, A Chalfoun***Presenting author: Donald Jones*, University of Wyoming, djones46@uwyo.edu

Parasites play an integral but often poorly understood role in ecosystems worldwide. As environmental disturbances such as changing climatic regimes cause shifts in the distribution and abundance of parasites, understanding the factors governing parasite-host interactions and the fitness consequences of parasitism will be critical for management and conservation of many taxa. We examined the prevalence and fitness effects of a common and widespread parasite of nestling birds, the bird blow fly (Diptera: Calliphoridae), in a population of declining sagebrush-obligate songbirds nesting in western Wyoming during 2017–2023. We counted the number of parasites on each nestling, recorded standard morphological measurements, and tracked a subset of individuals after fledging using radio telemetry. Higher parasite loads were associated with a reduction in wing cord length and tarsus length for Brewer's Sparrow (*Spizella brewerii*) but not Sage Thrasher (*Oreoscoptes montanus*) nestlings. For both host species, nestlings with higher parasite loads were at a higher risk of mortality during the post-fledging period. Causes of mortality included both predation and exposure to weather extremes. Our results demonstrate that although bird blow flies rarely kill host birds directly, they can reduce fitness and recruitment by increasing vulnerability to other sources of mortality during the post-fledging period. More broadly, we highlight the importance of considering how changes to host-parasite systems may interact with other stressors to influence the fitness of host species.

Using genetic, morphological, and ecological evidence to identify the subspecies of Sharp-tailed Grouse in south-central Wyoming**J Lautenbach, J Beck, A Pratt, A Gregory***Presenting author: Jonathan Lautenbach*, University of Wyoming, jonathan.lautenbach@gmail.com

Within Wyoming, there are three populations of Sharp-tailed Grouse (*Tympanuchus phasianellus*; hereafter STGR): Columbian STGR in western Wyoming, plains STGR in eastern Wyoming, and a population in southcentral Wyoming (hereafter SCWY population) that were historically considered Columbian STGR, but previous genetic work suggests otherwise. Our study used genetic, morphological,

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and ecological data collected from known Columbian STGR in eastern Idaho, known plains STGR in eastern Wyoming, and the SCWY population to better understand the subspecies status of the SCWY population. Using 2,500 SNPs, we found that Columbian STGR formed a distinct group, while plains and the SCWY population demonstrated considerable admixture between the populations. Using nine microsatellite loci, we found that the three populations of interest formed three distinct groups with little overlap in genotypes. Morphological and ecological data showed some differentiation between the three populations, however, there was overlap in morphological and ecological characteristics between the populations. Our results indicate that the SCWY population is most likely descended from plains STGR and through drift and isolation there may be recent genetic differentiation. These results considerably alter our understanding of the range-wide distribution of Columbian STGR and will affect consideration of conservation and management options for STGR in southcentral Wyoming.

Differences in sagebrush-obligate songbird nest survival in grazed landscapes in southeast Oregon

V Schroeder, D Johnson, W Robinson, D Bohnert, J Dinkins

Presenting author: Vanessa Schroeder, Oregon State University, vanessa.schroeder@oregonstate.edu

Precipitous population decline in some sagebrush-obligate species has generated an intense focus on the management of remaining habitat for sagebrush-obligate species in the Great Basin. As the predominant land use in the sagebrush ecosystem, livestock grazing is a central factor considered in most habitat conservation planning efforts. We have five years of data from a grazing experiment designed to assess the influence of two grazing regimes (dormant and spring-summer rotation; moderate utilization of native grasses, 30-40% by weight) and grazing exclusion using nine 15-20 acre sagebrush pastures on the reproductive success of sagebrush-obligate songbirds including Brewer's Sparrow (*Spizella breweri*) and Sagebrush Sparrow (*Artemisiospiza nevadensis*). We created an informed null model that incorporated temperature, precipitation, and vegetation variables which we used to assess the added influence of grazing regime on nest survival. Preliminary results from the informed null model suggest that effects of temperature and precipitation on daily nest survival rate varied by timing within the nesting season for both species, and Brewer's Sparrows that nested higher in shrubs had higher daily survival rates. We found limited evidence of an interactive effect of the pre-/post-treatment timeframe and cattle grazing treatment, suggesting a potential positive grazing effect on Sagebrush Sparrow and a neutral effect on Brewer's Sparrow nest survival. Our results indicate that variable weather and nest placement within shrubs, factors outside of management control, may have larger effects on nest survival than reductions in herbaceous cover caused by moderate grazing under the studied conditions

Estimating songbird response to cattle and wild horse grazing across the sagebrush biome

N Van Lanen, A Monroe, S O'Neil, A Nash, P Coates, K Schoenecker, C Aldridge

Presenting author: Nicholas Van Lanen, US Geological Survey, njvanlanen@gmail.com

Bureau of Land Management staff across the western United States are tasked with determining and setting appropriate grazing intensities of livestock and wild horses to concurrently manage for multiple uses and ecological integrity. However, wildlife responses to variable grazing intensities across the sagebrush biome are currently poorly understood. Thus, an improved understanding of wildlife responses to grazing can lead to more informed grazing management practices and facilitate multi-species management in the future. To address this, we are leveraging avian point count data from the Integrated Monitoring in Bird Conservation Regions (IMBCR) program collected across the western United States (2008 – 2023), wild horse and livestock grazing indices from public records, and remotely sensed vegetation data to evaluate avian sagebrush community response to livestock and wild horse grazing practices across the landscape. We are employing a hierarchical Bayesian community modeling approach, which accounts for incomplete detection of birds across the landscape, to model species-specific density responses to grazing and vegetation characteristics. In this talk, we'll share results regarding species' density responses to livestock and horse grazing timing and intensity. Our efforts will assist land managers in assessing whether current grazing practices are compatible with

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management of sensitive sagebrush-associated bird populations, including Brewer's Sparrow (*Spizella breweri*), Sagebrush Sparrow (*Artemisiospiza nevadensis*), and Sage Thrasher (*Oreoscoptes montanus*).

Free-roaming horses exceeding appropriate management levels affect multiple vital rates in Greater Sage-Grouse

J Beck, M Milligan, K Smith, P Street, A Pratt, C Kirol, C Wanner, J Hennig, J Dinkins, J Scasta, P Coates

Presenting author: **Jeffrey Beck**, jlbeck@uwyo.edu

Free-roaming horses (*Equus ferus caballus*) and burros (*E. asinus*) have increased to >3 times the Appropriate Management Levels (AML) of 26,785 for all 177 BLM Herd Management Areas (HMA). Recent research has implicated increasing horse populations as a driver of Greater Sage-Grouse (*Centrocercus urophasianus*) population declines. To evaluate potential demographic mechanisms driving declines, we compiled sage-grouse survival data from 4 studies in central Wyoming including 995 females, 1,075 nests, 372 broods, and 136 juveniles, across 15-years (2008–2022). Population estimates of horses for 9 HMAs in our study ranged from 59–700% of the maximum appropriate management level (AMLmax). Sage-grouse monitored outside HMAs represented control populations. To evaluate whether free-roaming horses were negatively impacting sage-grouse, we modeled daily survival of females, nest, broods, and juveniles. We found strong or moderate evidence that overabundant free-roaming horses negatively impacted nest, brood, and juvenile survival. When horse abundance increased to 300% from 100% of AMLmax, survival was reduced 8.1%, 24.9%, 24.3%, and 24.7% for nests, early broods, late broods, and juveniles, respectively. Our results indicate increasing free-roaming horses affected vital rates for critical life stages of sage-grouse, suggesting the need to maintain horse numbers below AMLmax to minimize impacts to sage-grouse populations.

Wild horse and livestock influences on Greater Sage-Grouse (*Centrocercus urophasianus*) populations across the sagebrush biome

S O'Neil, A Monroe, C Weise, N Van Lanen, A Nash, D Friend, K Schoenecker, P Coates, C Aldridge

Presenting author: **Shawn O'Neil**, U.S. Geological Survey, Western Ecological Research Center, soneil@usgs.gov

Livestock grazing is a widespread land use across the western United States, overlapping much of the Greater Sage-Grouse (hereafter, sage-grouse; *Centrocercus urophasianus*) range. During recent decades, populations of wild free-roaming horses (*Equus caballus*) have increased substantially within Bureau of Land Management (BLM) Herd Management Areas; these areas are also typically grazed by livestock. A recent study indicated sage-grouse populations often declined when horse populations exceeded appropriate management levels, identified by the BLM, in the Great Basin. Further, sage-grouse population trends were affected by the timing and level of livestock grazing based on allotment records across Wyoming, accounting for local vegetation productivity. However, a comprehensive study of both horses and livestock influences on sage-grouse populations has yet to be conducted across the sagebrush biome. To address this information gap, we are studying effects of horse population size, relative to BLM appropriate management levels, and livestock grazing indices to assess influences horses may have on multiple ecosystem health components, including population responses of sage-grouse. We will describe preliminary results assessing relationships between sage-grouse, horse, and livestock grazing indices across the sagebrush biome and compare results with previous studies. This study provides broad-based ecological information for decision-makers to balance multiple land uses in this complex system.

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Impacts of a native subsidized predator, Common Raven (*Corvus corax*), on sensitive avian species including a case study on Greater Sage-Grouse (*Centrocercus urophasianus*)**S Mathews, C Sanchez, S O'Neil, D Delehanty, P Coates***Presenting author: Steven Mathews*, U.S. Geological Survey, Western Ecological Research Center, smathews@usgs.gov

Common Raven (*Corvus corax*; raven) populations have increased across nearly all regions of their geographic range in North America. Concomitantly, numerous native species have experienced elevated rates of predation from ravens. Increased raven predation of many threatened and endangered avian species in the U.S. and Canada during nesting periods may be hampering species recovery. We explored the literature to aggregate existing knowledge and evaluate the impacts of raven predation on nests and young of sensitive avian species. We found evidence of nest predation on 8 sensitive avian species, and suspected nest predation on 1 additional species. All species shared aspects of nesting biology that suggested they would likely be susceptible to raven nest predation. The species experiencing highest impacts were Greater (*Centrocercus urophasianus*) and Gunnison (*C. minimus*) Sage-Grouse, Western Snowy Plover (*Charadrius nivosus nivosus*), Marbled Murrelet (*Brachyramphus marmoratus*). Additionally, we experimentally manipulated raven reproductive success via egg-oiling and measured population-level responses by sympatric populations of Greater Sage-Grouse. Egg-oiling successfully reduced raven breeding success, reduced raven densities at treated sites, led to an increase in nest-survival probabilities of nearby Greater Sage-Grouse, and Greater Sage-Grouse leks near oiled raven nests increased in abundance by about 5% compared to control leks. While questions regarding long term effects of raven control measures remain, egg-oiling can help wildlife managers reduce negative effects of ravens on Greater Sage-Grouse and potentially other sensitive prey. This information is preliminary, subject to change, and provided for best timely science.

Comparison of corvids and raptors in sage-grouse core and non-core areas: Assessing predator densities related to anthropogenic features**J Dinkins, C Revekant***Presenting author: Jonathan B Dinkins*, Oregon State University, jonathan.dinkins@oregonstate.edu

Many factors have contributed to declines in Greater Sage-Grouse (*Centrocercus urophasianus*; hereafter sage-grouse), including habitat loss and fragmentation from human development. While human development has been connected to lower sage-grouse demographic rates and their avoidance of anthropogenic features, it also provides an increased number of perch and nesting structures used by avian predators. Wyoming's sage-grouse Core Areas were designed to help conserve important sage-grouse habitat by reducing development within these Core Areas. Core Areas have maintained higher sage-grouse trends compared to Non-Core Areas, which could be partially explained by reduced predation rates. During 2017–2018, we performed 2,157 avian point counts along 380 8.05-km transects throughout the Wyoming Basin in western Wyoming, USA. We used distance sampling analyses to evaluate what anthropogenic features were connected to higher corvid and raptor densities and compared those densities among existing Core and Non-Core Areas with sub-stratification among areas of varying relative sage-grouse abundance. Our results indicated that agricultural lands, communication towers, roads, landfills and developed Non-Core Areas were positively related to corvid and raptor densities but specific effects depended on species. Core Area protections in the Wyoming Basin appear to reduce predation risk on sage-grouse, thereby functioning as predator management.

Wildfire, climate, and invasive grass interact to adversely affect Greater Sage-Grouse populations: Past, present, and solutions for the future**P Coates, B Prochazka, C Weise, M Chenaille, C Aldridge, A Monroe, M Rigge, D Pilliod***Presenting author: Peter Coates*, U.S. Geological Survey, pcoates@usgs.gov

Long-term negative effects of wildfire on Greater Sage-Grouse (*Centrocercus urophasianus*) within the Great Basin are self-perpetuated by an invasive grass-fire cycle. Conversion of sagebrush (*Artemisia*

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spp.) to annual exotic grassland following wildfire reduces functional habitat for Greater Sage-Grouse and jeopardizes population persistence. However, chronic effects of wildfire may vary across the distributional range of Greater Sage-Grouse based on regional variation in climate, ecosystem resilience, and resistance to invasive annual grasses. To understand effects of wildfire on Greater Sage-Grouse populations, we employed a Bayesian state-space model, which relates annual rate of change ($\hat{\lambda}_t$) in Greater Sage-Grouse population abundance to net loss of sagebrush to wildfire, while accounting for other environmental covariates. Across the range of Greater Sage-Grouse, we found support for an interaction between sagebrush loss and a one-year lag effect on summer precipitation. Although the strength of the effect varied among regions, the positive influence of precipitation decreased as sagebrush loss around leks increased. We also carried out multiple before-after-control-impact-paired-series studies to evaluate effects to different population vital rates (e.g., nest survival). We developed a stage-based, stochastic population growth model that integrated our estimated parameters from wildfire impacts to understand cumulative impacts to overall rate of change in population abundance. Our results suggest wildfire has both immediate and chronic effects on key life stages. Lastly, we used models to project $\hat{\lambda}_t$ over the course of 35-years under different management scenarios that reduce and mitigate negative impacts of sagebrush loss from wildfire. Findings are preliminary and provided for timely science.

Habitat selection strategies of Loggerhead Shrikes (*Lanius ludovicianus*) in novel risk-reward landscapes

E Schoenborn, A Chalfoun

Presenting author: Erik Schoenborn, eschoenb@uwyo.edu

Habitat choices are tuned by natural selection over evolutionary time, yet human-induced habitat alterations occur swiftly and alter risk-reward landscapes. Habitat modifications might therefore reduce the fitness outcomes of historically successful nest site and territory selection decisions. We tested the extent to which Loggerhead Shrikes (*Lanius ludovicianus*) navigated the novel risks and rewards induced by habitat alterations to optimize fitness outcomes, such as nest survival rates, clutch size, and nestling condition. Loggerhead Shrikes nesting in sagebrush habitats altered by natural gas extraction are uniquely suited to investigating habitat selection in an altered risk-reward landscape because they stand to benefit from the improved food acquisition offered by increased perch availability and more open foraging areas around well pads, yet are likely to experience increased nest predation rates from subsidized predator populations. We found that Loggerhead Shrikes selected territories closer to energy infrastructure yet experienced decreased nest survival in those areas. The main nest predator captured on video was the synanthropic Common Raven (*Corvus corax*). Contrary to our predictions, proximity to disturbance did not influence clutch size or nestling condition, thereby failing to compensate for the negative consequences of disturbance. Within our landscape context, natural gas fields were therefore functioning as ecological traps for a songbird already experiencing steep population declines in many parts of its range.

Investigating variation in spatial scales of effect across a species range: Insights from the Greater Sage-Grouse

A Monroe, M O'Donnell, M Rigge, J Heinrichs, A Whipple, P Coates, C Aldridge

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Greater Sage-Grouse (hereafter, sage-grouse; *Centrocercus urophasianus*) respond to landscape components at different spatial scales, and identifying relevant scales of effect is needed to plan for multiple land uses and avoid scale-dependent population responses. However, scales of effect may vary with study location, response type, and environmental variable, and therefore generalizing from previous, localized studies to other locations is uncertain. Previously, we applied a scale selection approach to estimate relevant spatial scales of effect for sagebrush cover around sage-grouse leks in southwestern Wyoming. We are extending this approach across the sage-grouse range using a standardized database of lek counts, testing for variation with geographic location (longitude and latitude), topography, and sagebrush connectivity. We then summarize scales of effect within spatial units (clusters) defined across

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the sage-grouse range and relevant to management. These analyses will allow managers to anticipate how spatial scales of effect may vary across these vast landscapes, anticipate scale-dependent population effects, and inform multiple land-use planning, particularly as they relate to changes in sagebrush cover. This approach also can be applied to other landscape components and help project population trends with scenarios for future sagebrush cover under a changing climate.

Population trends in non-core Greater Sage-Grouse relative to wind-energy development in Wyoming

J Beck, K Smith, C LeBeau, L Hoskovec*Presenting author: Jeffrey Beck, jlbeck@uwyo.edu*

Greater Sage-Grouse (*Centrocercus urophasianus*; hereafter 'sage-grouse') have declined range-wide, primarily due to habitat loss and degradation. The effects of wind energy on sage-grouse populations have not been adequately addressed. We investigated wind-energy infrastructure and changes in male sage-grouse counted on leks in central and southwest Wyoming, USA using Bayesian state-space models from 2000–2020. We conducted our study near 10 wind-energy facilities in proximity to sage-grouse leks outside of Core populations and dominated by big sagebrush (*Artemisia* spp.). Facilities became operational between 1998–2010 and had an average of 67 turbines. We considered several covariates describing wind-energy infrastructure including distance to the nearest wind turbine, number of turbines, and distribution (clustering) within 1.0, 2.0, 4.0, 6.0, 8.0, and 10.0 km. We also explored whether males attending leks exhibited lagged responses of 1–7 years following development. We used counts from 78 leks located within 15 km of wind-energy facilities, consisting of 288 counts before and 845 counts after development, respectively. Our findings were based on the average lek being 6.5 km from a wind turbine and most turbines were clustered such that undisturbed habitat remained surrounding leks. We expected wind-energy development would negatively influence trends in male sage-grouse lek attendance. However, we failed to detect a relationship between male sage-grouse lek attendance and proximity, density, or distribution of wind turbines following development in all models. Nonetheless, direct habitat removal and fragmentation from energy development does not provide benefits to sage-grouse populations.

Greater Sage-Grouse response to combined pinyon-juniper and mountain shrub removal in a mountain big sagebrush ecosystem in western Colorado

B Walker, K Stone, K Pauling, T Balzer*Presenting author: Brett Walker, Colorado Parks and Wildlife, brett.walker@state.co.us*

Expansion of pinyon-juniper woodlands into sagebrush (*Artemisia* spp.) ecosystems has reduced habitat for numerous sagebrush-obligate wildlife species in western North America and led to widespread habitat restoration efforts via pinyon-juniper removal. However, variation in the response of Greater Sage-Grouse (*Centrocercus urophasianus*) to pinyon-juniper removal and other types of vegetation treatments remains poorly documented. As part of a cooperative project to benefit mule deer, elk, and livestock, we mechanically removed pinyon-juniper saplings and tall, dense mountain shrubs (esp. Utah serviceberry, mountain mahogany, and antelope bitterbrush) from five adjacent plots totaling 227 ha in a mountain big sagebrush (*A. tridentata* vaseyana) ecosystem in western Colorado. To document Greater Sage-Grouse response to the treatment, we conducted a before-after, control-impact experiment using fecal pellet and vegetation surveys to quantify Greater Sage-Grouse and shrub responses to treatments. We augmented experimental data with information obtained from telemetry on VHF-marked females and GPS-marked males from 2007–2014. Mechanical treatments more closely aligned sagebrush and non-sagebrush shrub composition, height, and cover with vegetation measured around breeding and winter use locations of marked Greater Sage-Grouse. We documented a large and sustained increase in Greater Sage-Grouse pellet counts over 9 years following treatment concurrently with a decrease in pellet counts on nearby control plots. This project represents an example of how cooperative management projects can at least partially compensate for lost ecological processes while benefitting multiple stakeholders and sensitive wildlife in western sagebrush ecosystems.

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Spatiotemporal variation in sagebrush songbird demography across habitat and disturbance gradients**A Chalfoun, M Hethcoat, L Sanders***Presenting author: Anna Chalfoun*, U.S. Geological Survey and the University of Wyoming, achalfou@uwyo.edu

Understanding the fitness outcomes of habitat use and the underlying mechanisms is critical for assessments of habitat quality, population trajectories, and effective management prioritization. Given on-going and extensive habitat changes world-wide, and increased variation in environmental conditions such as weather, long-term datasets can be particularly valuable for characterizing spatiotemporal variation in trends, and identifying patterns that may not emerge without large sample sizes. We have been investigating patterns of reproductive success of sagebrush songbirds in western WY, USA since 2008 in relation to habitat structure and gradients of natural gas development. Areas with more surface disturbance associated with natural gas functioned as ecological traps for all three species of sagebrush-obligates (Brewer's Sparrow, Sagebrush Sparrow, and Sage Thrasher), albeit with variation in the strength of the trap across years. The mechanism underlying the trap included increased abundance of rodent nest predators in association with the re-seeded areas around well pads and other infrastructure that increased rates of nest predation. Yet, birds settled across the development gradients with equal preference. Within landscapes, the three species preferred different microhabitats, and the presence of microhabitat diversity was necessary for re-nesting strategies, nest-site partitioning among species, and the probability of nest survival. Together, our results suggest that large, undisturbed tracts of sagebrush steppe that contain variation in microhabitat structure will best support remaining populations of migratory sagebrush songbirds.

Songbird responses to fuel treatments and implications for threatened species**S Hanser, V Schroeder, J Pletcher, J Dinkins, P Cryan, L Ellsworth, B Newingham***Presenting author: Steve Hanser*, USGS Fort Collins Science Center, shanser@usgs.gov

Prescribed fire and mechanical tree removal treatments are used by land managers across the Intermountain West to reduce fuel loads and achieve ecological restoration goals. In sagebrush ecosystems, pinyon-juniper treatments have been implemented to help address long-term declines in populations of sagebrush-obligate bird species (e.g., Greater Sage-Grouse). Between 2006 and 2008, prescribed fire and mechanical tree removal treatments were implemented at 14 sites with pinyon-juniper expansion as part of a regional experiment, the Sagebrush Steppe Treatment Evaluation Project (SageSTEP). We conducted point count surveys and nest monitoring pre- and post-treatment to assess songbird community and species-specific responses. Recently, concerns about woodland-associated species (e.g., Pinyon Jay) have renewed interest in understanding the long-term changes due to these woodland removal treatments. We provide an overview of songbird community-level responses and present preliminary results from analyses of species-specific habitat selection and nest success. We will also preview ongoing efforts to elucidate long-term change in the songbird community and investigate daily, seasonal, and annual change in habitat use across this network of treatments.

Assessing songbird and vegetation response to conifer removal treatments in mountain big sagebrush communities of southwestern Montana**A Noson, N Van Lanen, C Aldridge***Presenting author: Anna Noson*, University of Montana Bird Ecology Lab, anna.noson@umontana.edu

Information regarding population-level responses of songbirds to sagebrush management is critical due to widespread declines of sagebrush-associated bird species. Conifer expansion into sagebrush ecosystems represents one threat to the integrity of sagebrush ecosystems, with conifer expansion estimated to encroach upon more than 1% of the sagebrush footprint annually. Conifer removal is the primary restoration tool in conifer-encroached, sagebrush ecosystems. Prior research suggests conifer removal alters songbird abundance and vegetation, however, little experimental evidence regarding songbird density and long-term vegetation response exists. Additionally, ecological response to

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treatments may lack transferability across the sagebrush biome, indicating place-based studies are needed to inform local management. We assessed two methods of conifer removal, prescribed fire and mechanical cutting, in mountain big sagebrush communities in southwestern Montana using a Before-After-Control-Impact design. Preliminary analyses indicated sagebrush-associated songbirds did not increase in response to either treatment method; however, mechanical cutting maintained populations, a desirable outcome in the face of ongoing conifer encroachment. We lay out an approach for modeling in a Bayesian framework that incorporates broad-scale avian population trends and estimates the spatial scales at which landcover influences individual species. Our ongoing modeling effort improves statistical power and evaluates treatment effects over time to account for lag effects and the duration of vegetation response to treatments. Results from this work will enhance land management decision-making with regards to treatment objectives, including lasting and meaningful restoration of sagebrush to stabilize or increase sagebrush-associated wildlife species' populations.

Goldilocks effects of temperature and precipitation on sagebrush songbird reproductive success

A Chalfoun, L Sanders, E Hall

Presenting author: Anna Chalfoun, U.S. Geological Survey and the University of Wyoming, achalfou@uwyo.edu

On-going climatic shifts have the potential to influence fitness outcomes and exacerbate population declines of many avian species, albeit to an unknown extent. Sagebrush songbirds including the three species considered the sagebrush-obligates (Brewer's Sparrow, Sagebrush Sparrow, Sage Thrasher) inhabit open aridlands that are experiencing increased variation in temperature and precipitation regimes. Yet, how proximate weather patterns influence fitness parameters on breeding grounds remains unclear. We investigated relationships between temperature and precipitation on the number of young fledged per nest using a sample size of over 5000 nests from four study areas ($n = 45$ unique plots) in Wyoming and Montana spanning 2002 – 2016. Each nest was linked with temporally matched, gridded daily temperature and precipitation values. Reproductive output was quadratically related to temperature and precipitation at all four study areas. Moreover, from a subset of nests at which nestling morphometrics were assessed, nestlings developed longer wings, which can aid in predator evasion, during warmer than average conditions. Colder temperatures during development were associated with nestlings with greater size-adjusted mass (i.e., lower surface-to-volume ratios) which may buffer individuals against cold snaps. Together, our results suggest that weather can strongly influence the reproductive outcomes of songbirds, with implications for on-going climate change and population trajectories. Nestling development, moreover, appears somewhat flexible in terms of allocation to different traits during different ambient weather conditions.

***From solo studies to global insights: Unleashing the potential of collaborative migration research using Movebank**

A Lohr, S Davidson, R Kays, K Safi, T Mueller, G Bohrer, A Kölzsch, M Wikelski

Presenting author: Ashley Lohr, NC Museum of Natural Sciences / Movebank, ashleylohr93@gmail.com

While single-methodology studies have provided valuable insights into bird migration, understanding the full scope and complexity of these avian journeys often necessitates a broader perspective. Data discovery and integration continue to present challenges for many migration researchers. Movebank, the global database for animal-borne sensor data, presents a unique opportunity to overcome these challenges by supporting the import of animal tracking data collected by nearly any method (e.g., GPS, Argos Doppler, solar geolocator, etc.) along with measurements from other sensors (e.g., accelerometer, magnetometer, heart rate, etc.) and study-specific attributes of animals, tags, and deployments. Additionally, the database harmonizes data to a single data model and vocabulary, facilitating meta-analyses and data re-use. Finally, flexible data sharing and permissions options allow data owners to easily share data with collaborators while a public-facing study summary enables project discovery. Collaborative data integration projects use Movebank to host curated study collections that serve as archives and public outreach platforms, streamline participation and data integration for migration atlases,

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and automate data processing for software applications. We will demonstrate how Movebank is used in each of these ways to better understand the full annual cycles of migratory species. Finally, we will discuss challenges experienced by data integration efforts and recommend steps to shorten the gap between data collection and successful project outcomes.

Challenges and opportunities for data integration to improve estimation of migratory connectivity

J Hostetler, E Cohen, C Bossu, A Scarpignato, K Ruegg, A Contina, C Rushing, M Hallworth

Presenting author: **Jeffrey A. Hostetler**, U.S. Geological Survey, jhostetler@usgs.gov

Understanding migratory connectivity, or the linkage of populations between seasons, is critical for effective conservation and management of migratory wildlife. A growing number of tools are available for understanding where migratory individuals and populations occur throughout the annual cycle. Integration of the diverse measures of migratory movements can help elucidate migratory connectivity patterns. However, data integration requires methodology that accounts for differences in sampling design, effort, precision, bias, and directionality. The R package MigConnectivity was developed to provide tools for estimating pattern and strength of migratory connectivity. The package now places greater emphasis on patterns of connectivity by separating estimation of migratory connectivity into two new functions: *estTransition* (transition probabilities) and *estStrength* from those transition probabilities. We used simulation and bidirectional data from Yellow Warbler (*Setophaga petechia*) to explore the challenges and limitations of data integration. We found accurate estimates can be obtained from either breeding to nonbreeding or nonbreeding to breeding data. For bidirectional data, integration can lead to more accurate estimates when data are available from all regions in at least one season. The updates to the MigConnectivity R package will facilitate quantitative comparisons of migratory connectivity to better understand the causes and consequences of the seasonal distributions of migratory animals. Multiple data types on animal movements are becoming increasingly available and integration of these growing datasets will lead to a better understanding of the full annual cycle of migratory animals.

Closing the knowledge gap: tracking data integration helps inform full annual cycle conservation of a range-restricted songbird, the Bicknell's thrush

M Hallworth, D Narango, J Goetz, C Rimmer, K Tolan, K McFarland

Presenting author: **Michael Hallworth**, Vermont Center for Ecostudies, mhallworth@gmail.com

Over the past few decades, tracking technologies have revolutionized our understanding of songbird migration and allowed researchers to unravel complex annual movements. However, the tracking technologies available for small-bodied birds have limitations when used to reveal annual migrations and estimate migratory connectivity. Integrating data from several tracking technologies could help offset these limitations and improve estimates of migratory connectivity, and help conserve species across their annual cycle. Here, we integrate several commonly used tracking technologies, including light-level geolocators, archival GPS tags, coded radio tags and stable isotopes, to improve estimates of migratory connectivity and identify critical migratory stop-over locations of the Bicknell's Thrush. The Bicknell's Thrush is a rare, range-restricted migratory songbird that breeds in spruce-fir-dominated forests of southeastern Canada and the northeastern United States and overwinters in the Greater Antilles in wet and mesic broadleaf forests. Its small population and restricted range make it a high conservation priority in Canada, the USA, the Dominican Republic, Haiti, and Cuba. Integrating various tracking technologies improved estimates of migratory connectivity and identified critical stop-over locations, including the mid-Atlantic region of the United States. Combining available data sources such as tracking technologies, stable isotopes, and morphological data can lead to new migration insights, foster collaborations, and highlight new opportunities for conservation.

Integrating methods and tools to understand bird migration in the Neotropics

C Gomez, N Bayly

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Presenting author: **Camila Gomez**, SELVA, camila.gomez@selva.org.co

Since 2009, SELVA's Migratory Ecology research program has used a suite of tools and methods to generate knowledge about the ecology of migratory birds in the Neotropics, contributing to significant advances over the last decade in our knowledge of birds needs during the least studied periods of their annual cycle – migration and the stationary non-breeding period. Here, we present examples of past and ongoing studies showing how a broad array of tools including standardized surveys, capture-recapture studies, territory mapping, behavioral observations, genetics, stable isotopes, citizen science, GIS analyses, and automated telemetry all contribute complementary elements that have significantly improved our understanding of the non-breeding ecology of migratory landbirds in the Neotropics. Using examples from Gray-cheeked Thrushes and Blackpoll Warblers, Tennessee Warblers and more, we show how each complementary method contributes unique information and it is only by combining results across multiple spatial and temporal scales that we gain powerful insights into how, for example, birds use stopover or non-breeding sites and the impact these have on subsequent stages of the life cycle, such as migration, and in turn how these individual sites are linked to breeding and wintering populations. We conclude that while remote sensing and long-distance tracking can provide important insights, it is essential to combine it with research on-the-ground to provide complementary information key to understanding migratory bird ecology at different scales and for the design of effective conservation strategies.

***Ecologically and genetically distinct lineages of an Afro-Palearctic migratory bird of prey show contrasting vulnerability to future climate**

J Ferrer Obiol, A Bounas, M Brambilla, G Lombardo, S Secomandi, A Bonisoli-Alquati, G Ficitola, A Galimberti, J Cecere, M Morganti, A Torroni, D Rubolini

Presenting author: **Joan Ferrer Obiol**, University of Milan, joan.ferrer.obiol@gmail.com

Assessing the potential impacts of anthropogenic climate change on wild species is hampered by limited knowledge about ecological and evolutionary factors that shape population dynamics and by a dearth of historical context on environmental changes at broad spatial and temporal scales. We integrated landscape genomics, demographic reconstructions, and species distribution models to assess possible effects of climate change on the past, present, and future population and global range dynamics of an Afro-Palearctic migratory raptor, the lesser kestrel (*Falco naumanni*). This species has a broad breeding range - from North Africa to East Asia - and non-breeding range - from the Sahel to South Africa. Leveraging range-wide genetic sampling, we identified two genetically and ecologically differentiated groups corresponding to the western and eastern parts of the species' breeding range. Consistent with the species' preference for warm and dry environments, we inferred a population decline during the Last Glacial Period (LGP), followed by a subsequent increase under warming climate. Demographic decline coincided with the divergence between the two lineages and a large contraction in breeding range, while the subsequent increase coincided with admixture events and an expansion of non-breeding range for western populations. Future climate projections revealed that eastern populations, especially those near the contact zone between the two lineages, are at higher risk of maladaptation, range contraction, increased migratory distance, and thus heightened extinction risk. Our results highlight the challenges of biodiversity conservation in the Anthropocene in the face of a rapidly changing climate that is threatening evolutionary lineages, depleting genetic diversity, and jeopardising species adaptability and persistence.

Integrating theory and data to predict migratory connectivity

M Somveille, K Ruegg

Presenting author: **Marius Somveille**, University College London, msomveille@gmail.com

Birds exhibit a remarkable array of seasonal migrations. While much research has been conducted on describing avian migratory behavior, with the availability of migration data increasing exponentially, we still lack a data-driven, mechanistic understanding of how species' breeding and wintering populations redistribute each year, that is, migratory connectivity. In this talk, I will present a modelling framework for migratory connectivity based on optimal energy balancing theory – i.e. birds migrate in a way that minimises energy expenditure while considering intraspecific competition for energy acquisition. The

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model leverages range-wide occurrence data together with tracking, banding and genomic data in order to simulate the energetically optimal redistribution of individuals between the breeding and wintering grounds of species. Using 25 species across the Americas, we find that the model accurately predicts empirical migration patterns, and thus offers a general explanation for migratory connectivity based on first ecological and energetic principles. The model was also used to show that the variation in seasonal climate tracking across a suite of 27 populations at a continental scale is more likely a consequence, rather than a direct driver, of migratory connectivity. I will discuss how our model is being used to investigate the emergence of a migratory divide, how it can inform broad-scale conservation strategies, but also how it provides a strong basis for exploring additional processes underlying the ecology and evolution of migration.

***Using integrated models to estimate migratory species' dynamics during cryptic periods of the annual cycle**

S Saunders, B DeLuca, J Deppe, T Meehan, N Michel, N Seavy, K Davis, E Zipkin, C Wilsey

Presenting author: **Sarah Saunders**, National Audubon Society, sarah.saunders@audubon.org

Data for widespread and migratory species are often fragmented across multiple monitoring programs or consist of multiple data types that may provide information on only certain periods, locations, or processes of the annual cycle. Integrating across these sources of information can overcome spatiotemporal gaps and provide a more comprehensive understanding of population dynamics during cryptic periods of a migratory species' life cycle. Here, we highlight three case studies in which data integration was used to improve estimates of (1) the spatial patterns of avian migration across the Western Hemisphere; (2) multispecies migratory connectivity for 112 migratory bird species; and (3) population dynamics of a data-deficient migratory bird species in decline. Taken together, these studies demonstrate the utility of integrated models over traditional single-methodology approaches, and we discuss the broader implications of these analytical advancements for enhancing conservation action. In particular, we elaborate on how results are being used to identify collaboration opportunities between jurisdictions that can help safeguard critical areas for migratory birds across the hemisphere. We conclude with an overview of promising future directions for further method development that will continue to provide important insights on bird migration science.

Integrating tracking data to differentiate between active migration and stopover regions to inform conservation

B DeLuca, L Berrigan, B Stewart, E Geldart, T Meehan, S Saunders, S Mackenzie, C Wilsey

Presenting author: **Timothy D Meehan**, National Audubon Society, Tim.Meehan@audubon.org

Recent advances in integrating migration location data have improved our understanding of spatial patterns of bird migration and connectivity across the western hemisphere. While these Merged Migration Maps (Meehan et al. 2022) provide useful identification of high concentration regions for many species, they currently cannot differentiate between active migration and stopover regions. Conservation actions that target the migratory periods are limited if we only know there is relatively high use in a region but cannot determine if that use is for stopover or active migration. Conversely, even if we can determine that a particular region is likely used for stopovers, it is likely not worth significant conservation resources if we cannot also determine that it is used by many individuals, potentially across many species. To better inform conservation decisions during migratory periods of the annual cycle we made several advances to the Merged Migration Maps, including integrating Motus detections and improved the modeling framework. In a related effort, Birds Canada developed a method to use Motus detections to estimate

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stopover durations across the hemisphere for 30 species. We combined stopover duration estimates with the Merged Migration Maps to differentiate regions of concentrated space use as either active migration or stopover. The resulting integrated maps will be used to make science-informed decisions about conservation actions specifically tailored to active migration or stopovers.

****A multi-city comparison of urban migration stopover and the underlying social landscape that supports it****M Jimenez, M Belotti, H McCasslin, K Horton***Presenting author:* Mikko Jimenez, Colorado State University, Migfjimenez@gmail.com

As urbanization continues to expand, understanding the role that cities play within social-ecological systems becomes increasingly crucial for effective conservation action. Despite their prevalence along North American flyways, the extent to which migrating birds use stopover habitats within urban landscapes remains poorly understood. Moreover, historical inequities in urban planning have resulted in enduring legacy effects, disproportionately burdening communities of color and low-income socioeconomic classes with environmental pollutants while often depriving them of access to green spaces. Consequently, there is a burgeoning interest in examining how ecological and social dimensions intersect with urban conservation efforts. This study aims to quantify the intensity of migratory stopover activity within urban areas and compare these patterns across the largest cities in the continental United States, thereby elucidating both the relative contributions of urban cores to regional stopover habitats and the underlying social landscapes that support them. To achieve these objectives, we have integrated weather radar estimates of stopover activity with fine-scale socioeconomic data pertaining to publicly owned urban green spaces. From an ecological perspective, our findings serve to advance our understanding of the degree to which cities may serve as stopover habitats for migratory birds. Furthermore, the integration of our results with socioeconomic data holds the potential to inform urban conservation messaging and highlight areas where such efforts may be expanded. Collectively, our study contributes to a growing body of literature suggesting that cities may play a significant role within macroecosystems.

Bridging gaps in migration research by integrating citizen science, radar, acoustic, and tracking data*B Van Doren, M Fuentes, D Slager, A Dokter, D Fink, D Sheldon***Presenting author:* Benjamin Van Doren, University of Illinois at Urbana-Champaign, vandoren@illinois.edu

Bird migration research draws on a diverse toolkit of sensors, modalities, and statistical methods, each with its own advantages and disadvantages. Approaches that successfully integrate these tools can yield greater insight into migration systems than approaches reliant on only one tool. BirdFlow is a modeling framework that uses species distribution models derived from citizen science data to infer population movement across continental extents. It uses weekly spatial distributions produced by eBird Status & Trends to infer probability distributions of individual birds' movement trajectories across space and time. These products alone are informative, but integrating the flow model with other data modalities is key to maximizing biological insight. Here, we discuss examples of data integration with BirdFlow. For example, data from tracked individuals can be combined with citizen science inputs to improve the accuracy of BirdFlow's movement reconstructions. In addition, flow predictions can contextualize specific-specific movement data from nocturnal acoustic monitoring stations, improving the utility of acoustic data for tracking migrants in the aerosphere. Finally, migration traffic observed by Doppler weather radar stations can validate BirdFlow predictions and inform a hemisphere-level modeling approach comprising hundreds of migratory species. We discuss the insights and challenges of hemispheric data integration, and the next steps towards an integrative understanding of migration systems.

Key factors driving population-level vulnerability in neotropical migratory birds**K Ruegg, C Bossu, M DeSaix, M Somveille, C Taylor, J Saracco, J Hagelin, S Turbek, R**

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Harrigan*Presenting author:* **Kristen Ruegg**, Colorado State University, kristen.ruegg@gmail.com

An estimated 1 out of every 2 songbird populations are declining across the Western Hemisphere. Because migratory birds travel vast distances between breeding and wintering areas, understanding why populations are declining has been difficult. To help overcome this challenge we combine data collected as part of the Bird Genoscape Project – a collaborative effort to use genomic tools to map population-specific migratory pathways – with other sources of tracking data (banding and geolocator) to connect breeding and non-breeding areas in 8 neotropical migratory bird species. We use Breeding Bird survey data to estimate population trajectories within genetically distinct groups and follow the methods used by the Road to Recovery Effort to categorize each genetically distinct population into threat categories (Red Alert, Orange Alert, and Yellow Alert). To assess factors driving population-level declines we model the contribution of various potential stressors encountered across the annual cycle to population-level vulnerability (the degree of climatic niche overlap, strength of migratory connections, amount of human disturbance, climate niche size, and degree of past climate change within each genetically distinct group). Our results support the idea that population-level vulnerability is best explained by the degree of climatic niche overlap between breeding and non-breeding grounds, the size of the wintering climatic niche, and the strength of migratory connections. Overall, this work provides a comprehensive framework for combining information from vastly different sources to address the key factors underlying population declines in neotropical migratory birds.

The scale of supplementary bird feeding in the United States: What and how do people feed birds?**E Greig, D Bonter, A Dayer, V Martin, R Mady***Presenting author:* **Emma Greig**, blufinch@uchicago.edu

Millions of people feed birds every day, engaging in what has been described as a large-scale 'unplanned experiment' (Jones 2018). We are still in the early stages of understanding the economic, social, and biological impacts of this hobby. The current study sought to quantify what, when, and how people in the U.S. feed wild birds. We used an online survey of the public to explore bird feeding practices. We related respondents' answers (n = 1096 completed responses) to seasonality, geography, and demographic variables (age, education, gender, race, and ethnicity) using multivariate logistic regressions. We found that survey participants had fed birds around their homes for an average of 15 years, spending on average 5 hours a week watching birds. The most common types of food provided were an economy mix of seeds, followed by sugar water, sunflower seeds, and suet. The majority (92%) of participants provided food throughout the year, and most food types were provided similarly across seasons except for suet and sugar water which varied seasonally. Geography was a significant predictor of provisioning for oily seeds and suet, with those being offered more frequently at higher latitudes. The social and demographic predictors of provisioning varied depending on the food type, but in general, the likelihood of people providing food was positively associated with their years of experience feeding birds and if they described bird feeding as more central to their life. In summary, our findings suggest that feeding birds is a hobby that is engaged in to a high degree by people who value birds, and this survey provides thus far the most comprehensive look at those individuals' provisioning behaviors and patterns.

The ecological consequences of supplemental feeding for wild bird communities**R Hall, D Hawley***Presenting author:* **Richard Hall**, University of Georgia, dr.richard.hall@gmail.com

Providing food for birds can have profound effects on their ecology, behavior and health. Given the global popularity of bird-feeding, and pervasive declines in once-common species, it is critical to understand the wider ecological consequences of feeding on avian communities. While studies have provided detailed insights into the effects of bird-feeding on focal species and two-species interactions (particularly host-parasite interactions), we lack understanding of how bird-feeding effects scale up to influence multi-species interactions, avian community composition and contributions of these communities to ecosystem function and services. Here we synthesize findings from empirical studies and mathematical

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models on bird feeding and other forms of anthropogenic food subsidy to explore effects of recreational bird feeding in a multi-species context. We identify significant knowledge gaps relating to evolutionary implications of bird-feeding, the consequences of removing bird feeders on community composition, and whether anthropogenic diet leads to excess nutrient deposition into ecosystems through concentrations of bird feces. We highlight key priorities for future research and discuss guidelines for recreational feeding of birds that maintain avian community structure and function in urbanizing landscapes.

Human-bird interactions in backyards and beyond: Who engages in bird-related activities?

A Dietsch, D Bonter, A Dayer, D Fulton, E Greig, E Neidhardt Gutierrez, R HALL, D Hawley, W Hochachka, K Langhans, M Manfredo, T Phillips, P Pototsky, N Sexton, K Slagle, T Teel

Presenting author: Alia Dietsch, The Ohio State University, dietsch.29@osu.edu

Evidence shows that people experience mental health boosts when seeing or hearing birds. Thus, people may seek out bird watching opportunities, provide food/water to birds, and/or modify landscaping around the home as intended 'bird-friendly' conservation actions. Given the possible social, economic, and ecological benefits of engaging in such bird-related activities, we explored the demographics of who participates in bird watching, bird feeding, and participatory science related to birds across multiple studies. For example, a study conducted on United States (U.S.) public lands, specifically wildlife refuges, indicated that recreationists who engaged in bird watching as a primary activity more often identified as female, white, living without children at home, and with higher educational attainment than other recreationists. A different study of U.S. birdwatchers (registered as eBird members) demonstrated similar demographic results. A survey of Washington state residents across 39 counties indicated that people who fed birds were also more likely to identify as white, female, and without children living at home than residents who did not feed birds. Meanwhile, results from Project FeederWatch, a participatory science effort related to observing and collecting data on birds, reinforced such findings, e.g., participants more often identified as white and as a woman with higher education levels and more years of age than the general public. Though evidence suggests that millions of U.S. residents engage in bird-related activities each year, the cumulative findings of these studies demonstrate that any benefits of such engagement appear to be unequally distributed across demographic subgroups.

How does observing birds at feeders influence human emotions? Results of a continental-scale survey.

T Phillips, A Dayer, P Pototsky, A Dietsch, K Langhans, D Bonter, E Greig, W Hochachka

Presenting author: Tina Phillips, Cornell lab of Ornithology, tina.phillips@cornell.edu

For the past 37 years, Project FeederWatch (PFW) has been collecting biological data about the abundance and diversity of birds that visit feeders in winter in the US and Canada. Beginning in 2023, PFW began integrating emotional information tied to participants' weekly bird counts; their observations of diseased or dead birds, mammals or predators; and behavioral interactions between birds seen at feeders. According to positive psychology, both positive and negative emotions in response to a stimulus or observation lead to different types and intensities of behavioral responses. Thus, the PFW database is capturing emotional states such as excitement, surprise, happiness, sadness, anger, or fear, as well as information on the quality (negative to positive) and intensity (low to high) of emotions. In this session, we will summarize participants' emotional responses to specific events (e.g. seeing a hawk near their feeder) as well as general emotions associated with weekly observation counts. We highlight factors that may influence individual emotions such as value orientations, demographic characteristics, and level of engagement participation in PFW. To our knowledge, this is the first participatory science project to fully integrate emotional data with biological data. Given the emergent link between emotions and behaviors, understanding this relationship is important for decision making related to management action surrounding bird feeders as well as advancing our understanding of how bird feeding contributes to overall human well-being.

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Supplemental feeding beyond North America: Lessons and questions from Brazil*E Alexandrino***Presenting author: Eduardo Alexandrino, Cornell University, eduardoalexandrino@hotmail.com*

Interest in feeding birds has increased among Brazilians, leading to questions about the potential impacts that supplemental feeding may have on native free-living birds. Although there is substantial knowledge about supplemental feeding in North America, this subject is rarely studied in Brazil. The presentation will share experiences and main outcomes from two studies recently performed in Brazil and highlight challenges for the future. First, in 2021, a survey revealed that Brazilians prefer feeders made with natural materials rather than anthropogenic materials, and Brazilians tended to perceive positive impacts caused by bird feeders (e.g., useful for the promotion of tourism and environmental education) while negative impacts (e.g., pathogen spread, bird habituation to feeders) were not recognized. Second, during the pandemic lockdown, dozens of volunteers participated in opportunistic sampling at 42 bird feeders with fruits across Brazil that were part of a series of events of live online birding. This participatory science approach detected 104 species in total, with up to 24 species at urban feeders and up to 36 species at non-urban feeders. Although this low budget initiative demonstrated the potential of participatory science focused on Brazilian bird feeders, interest declined after the end of the lockdown. Because of the limited amount of data of supplemental feeding in Brazil, management decisions are not based on data, and divergent opinions regarding the use of feeders prevail. As the practice of bird feeding grows in Brazil, so too does the need for additional data on the effects of supplemental feeding on birds in the Neotropics, and particularly on frugivorous species.

Increasing inclusivity for BIPOC, disabled, and neurodiverse people in a participatory science program focused on bird feeding*K Langhans, C Blume, C Cooper, A Dietsch, F McGregor, T Phillips, P Pototsky, T Watts, A Dayer***Presenting author: Kelley Langhans, Virginia Tech, langhans@vt.edu*

Participatory science (also known as citizen or community science) allows for collection of scientific data across scales beyond what is achievable for professional researchers alone while enabling broad exposure to the process of scientific inquiry and discovery. Historically, projects have reflected data gathered by participants who identify mostly as white, highly-educated, and high income. Increasing inclusivity in participatory science projects is necessary to ensure the benefits of participation are accessible to all, and that research priorities more clearly represent the diversity of the United States. In this presentation, we share our experience with making Project FeederWatch (PFW), a participatory science project focused on people who feed and watch birds, more inclusive for people identifying as 1) Black, Indigenous, or a person of color (BIPOC) and/or 2) disabled and/or neurodiverse. We conducted focus groups with people with these identities who already feed birds but do not currently participate in PFW. We explored how participatory science programs could better align with people's existing interests, what barriers people perceive to their participation, and how programs can eliminate those barriers. We present insights from these discussions, along with recommendations for changes to PFW to increase inclusivity. Where findings are transferable, we also denote ways in which participatory science projects more broadly may increase inclusivity by honoring the interests and contributions of historically underrepresented groups.

The Urban Bird Project: Participatory science through backyard bird feeding and culturally responsive approaches**J Smith, L Granger, A King-Kostelac, K Walker***Presenting author: Jennifer Smith, jennifer.smith@utsa.edu*

Participatory science is a powerful method of informal science education that has expanded scientific literacy. At the same time, it can positively affect participants through increasing their knowledge of, and

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appreciation for, the natural world; this may be especially important in urban areas where people are increasingly disconnected from nature. Yet, members of underserved minoritized communities often face barriers to participation in such programs. Moreover, participatory science methods often fail to integrate culturally responsive approaches that are proven to positively influence learning in members of minoritized communities. The 'Urban Bird Project' (UBP) aims to minimize these challenges by transforming urban yards in underserved minoritized neighborhoods of San Antonio into living laboratories to assess the effects of backyard bird feeding on the space use of two culturally relevant species, the Northern Cardinal (*Cardinalis cardinalis*) and the Northern Mockingbird (*Mimus polyglottos*). Between 2022 and 2023 we successfully recruited 32 households and three middle schools to UBP. In collaboration with participants, we collected data via backyard bird feeding, mist-netting, and observations. We assessed the effects of UBP on community members using an approach centered on the Strands of Learning Framework. Specifically, we assessed the impact of our approach on (1) interest and motivation to learn about birds, (2) knowledge about birds, (3) connection with birds and the natural world, and (4) science identity. We will present the results from this study and use them to provide recommendations for future participatory science efforts that aim to address barriers to participation by underserved minoritized communities.

Focusing on birds at supplemental feeding stations informs ecological research

D Bonter, E Alexandrino, E Greig, W Hochachka, E Miller, K Wilcox

Presenting author: **David Bonter**, Cornell University, dnb23@cornell.edu

Supplemental feeding of birds, engaging millions of people, is one of most direct ways in which humans are affecting species ranges, population trends, disease dynamics, community ecology, and foraging ecology. The full extent and complexity of these impacts are still being discovered, and data-collection at supplemental feeders provides valuable information for answering a suite of novel questions. Further, supplemental feeders provide an ideal context in which scientists and the public can collaborate in the research process. We will illustrate the potential value of data collection at bird feeders using examples from a large-scale participatory science program, Project FeederWatch, that has focused the attention of more than 80,000 members of the public on birds using supplemental feeding stations across the United States and Canada. Highlighting examples from studies of Evening Grosbeaks, Anna's Hummingbirds, House Sparrows, Eurasian Collared-Doves, and a suite of 130 species of birds interacting near feeders, we demonstrate how scientific research focused on supplemental feeding stations can help the research community understand population dynamics, range changes, invasive species, and behavioral interactions, respectively. Further, we highlight how the research community can utilize this rich resource of > 12 million hours of protocol-driven observations through an open-access data portal.

Feeder surfaces as infection sources: what do we know, and how can effects be limited?

D Hawley, R Meyers, S Teemer, W Hochachka, P Pototsky, R HALL, A Dayer

Presenting author: **Dana Hawley**, <http://www.biol.vt.edu/faculty/hawley/>, hawleyd@vt.edu

Bird feeders augment the spread of several avian diseases by providing high-contact surfaces, termed fomites, that parasites and pathogens can survive on and transmit from. One such pathogen is the bacterium *Mycoplasma gallisepticum* (MG), which causes frequent outbreaks of conjunctivitis in house finches (*Haemorrhous mexicanus*) in North America. MG can spread directly to house finches from bird feeder surfaces, but we still have much to learn as to the extent to which feeders contribute to MG spread, and how such spread can be mitigated by management actions such as feeder cleaning. We will briefly summarize what is known about the role of feeders as fomites of avian pathogens and parasites, with a focus on MG in particular. We will then present results of two recent empirical studies that we performed. First, we examined how ambient temperature influences pathogen viability on bird feeder surfaces. We found that MG is only viable on feeder ports for up to 2 days at warmer ambient temperatures. In contrast, colder temperatures allow MG to remain viable on feeder ports, and still highly pathogenic to birds, for up to one week. Thus, feeder surfaces likely contribute most to MG spread during winter. Second, we examined whether a simple cleaning technique that could be done readily by the

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public (using disposable bleach wipes) reduces disease spread in an experimental setting. We will discuss whether such cleaning altered either the speed or extent of MG transmission to a healthy cagemate. Finally, we will highlight the need for evidence-based guidance for the large numbers of people feeding birds as to how they can reduce or minimize disease spread from feeder surfaces.

Public policy: Birds are not the only ones impacted by guidance to cease bird feeding

A Dayer, P Pototsky, R HALL, D Hawley, T Phillips, A Dietsch, E Greig, W Hochachka, K Langhans, S Living

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Humans connect strongly with birds, driving the enormous popularity of residential bird feeding. In the face of recent avian disease outbreaks in the US, state and federal government agencies increasingly respond by providing recommendations to cease bird feeding. These recommendations may not fully consider established mental well-being impacts on people who feed birds and possible consequences for conservation of a decreased human connection to nature. Further, recommendations to cease bird feeding to reduce the spread of avian disease largely lack supporting evidence from ecological research. In fact many aspects of wild bird feeding are poorly understood from an ecological standpoint. State wildlife agencies are tasked with addressing emerging wildlife health issues and must act regarding the wildlife resources under their trust often with the limited facts available to them at the time. Yet, through a systematic web search we found that 23 US state agencies made recommendations to cease feeding wild birds in 2021–2022 in response to various avian disease outbreaks. While the resulting public response to recommendations to cease feeding has not been studied, anecdotal evidence from social media and websites indicates human frustration, fear, and concern, resulting in mixed intentions to comply with the recommendations. We contend that ecological and social science need to be applied in tandem to ensure that well-intended guidance to cease feeding of birds does not have unintended consequences. We showcase the work of a leader in this area, the Virginia Department of Wildlife Resources, who have created an evidence-based bird feeding management plan for responding to avian disease.

What is pyrodiversity and why does it matter for birds?

G Jones

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Pyrodiversity is a concept that, generally speaking, can be described as the variation in fire characteristics within a given landscape. Its emergence as a concept in western science originated in the 1990s, when researchers hypothesized that increased pyrodiversity would generate increased biodiversity - that is, species richness. This 'pyrodiversity-biodiversity hypothesis' has been tested across numerous taxonomic groups and in systems around the world, with varying degrees of support; evidence for positive pyrodiversity-biodiversity relationships has been examined (and found) in birds more often than any other taxa. In this talk, I will review the conceptual foundations of the 'pyrodiversity' concept including points of confusion and its weaknesses, provide a broad overview of evidence for pyrodiversity-biodiversity relationships in birds, and discuss why such relationships are important from theoretical and applied perspectives.

Finding the shape of pyrodiversity: Insights from a fire-restored landscape into ecological memory, scale, and the multi-dimensional response of biodiversity to varied fire histories

Z Steel

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Pyrodiversity or the variation in spatiotemporal patterns of fire is predicted to support diversity of birds and other taxa in fire-prone ecosystems. However, fire suppression and immersing 'mega-fires' have reduced pyrodiversity in many areas. Departures from historic patterns challenge rigorous tests of the

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pyrodiversity-biodiversity hypothesis and our ability to optimize fire management for biological conservation. We leveraged a 50-year landscape-scale experiment in Yosemite National Park and a nascent effort in the Sierra National Forest where historic fire regimes are being restored through managed wildfire use. We surveyed the bird, bat, and plant communities to test responses to various spatial and temporal components of pyrodiversity at different scales and levels of landscape memory (i.e., the relative importance of older disturbances that precede the most recent fire). The bird community responded positively to variation in burn severity, but the highest species richness was concentrated in landscapes burned in the last two decades rather than areas with high variation in fire frequency. This differential response to the severity and frequency components of pyrodiversity helps explain why studies of the pyrodiversity-biodiversity relationship using different methods can come to contrasting conclusions. Further, the avian community most readily responded to pyrodiversity within 500m of survey sites and to only the most recent fire, suggesting beneficial pyrodiversity can be restored relatively quickly with the first 'good fire'. Beyond birds, our analysis revealed important differences among taxa that can inform fire and conservation management in an increasingly flammable world.

Fire responses vary across the ranges of North American birds*A Stillman, G Jones, M Strimas-Mackey, G Duran, C Andrews, S Ligocki, T Auer, V Ruiz-Gutierrez, S Sawyer, D Fink***Presenting author: Andrew Stillman, Cornell Lab of Ornithology, stillman.andrewn@gmail.com*

Fire regimes are context-dependent, and so are the ways that birds respond. However, most information on bird responses to fire is location-specific and therefore hard to extrapolate across space. To make better conservation decisions in a fiery world, we need to understand fire regime impacts on birds across large areas while also capturing variation at scales which are tractable for fire management. To address this challenge, we used a spatiotemporal ensemble modeling workflow using eBird data to measure nonstationary effects of fire on six bird species used to guide management decisions in the U.S.: red-cockaded woodpecker, Bachman's sparrow, greater sage-grouse, pinyon jay, American goshawk, and olive-sided flycatcher. We then summarized information across the model ensemble to investigate spatially explicit relationships between species abundance and fire frequency, time since fire, and fire severity. This approach allowed us to map the direction, magnitude, and importance of fire regime associations at 27-km resolution across the range of each focal species. Our findings revealed previously undocumented fine-scale variation in fire regime associations. All focal species except for greater sage-grouse displayed both positive and negative effects for at least one fire covariate, even after removing estimates with low confidence. Critically, fire regime associations varied widely in magnitude even when directions remained constant. Moving forward, this analytical workflow provides a flexible approach for assessing range-wide fire impacts while also providing information at a sufficiently fine grain for resource prioritization and decision-making.

Examining the influence of severity and pyrodiversity on bird communities following an oak woodland megafire**K Calhoun, P Parker-Shames, Z Steel, H Oyler, J Brashares***Presenting author: Kendall Calhoun, UCLA, kcalhoun@ucla.edu*

Anthropogenic pressures have altered fire regimes across the western United States. These altered fire regimes, and the megafires they often produce, threaten ecologically and economically critical ecosystems and biodiversity across this region. Oak woodland savannas, in particular, may be sensitive to altered fire regimes, but there remains a significant gap in our understanding of how different characteristics of wildfire impact these ecosystems and the wildlife species that reside within them. In this study, we use an occupancy modeling framework to investigate how fire severity and pyrodiversity of a major wildfire in northern California impact the distributions of bird and bat species assemblages. We use acoustic monitors deployed across the Hopland Research and Extension Center following the 2018 Mendocino Complex Fire to examine how patterns of fire severity and pyrodiversity influence habitat preferences across a diverse community of woodland bird and bat species. We find that both taxonomic groups were resilient to the impacts of this megafire over time. While local scale pyrodiversity had

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negligible effects on species distributions, we found that moderate severity fire increased occupancy of bats, insectivorous birds, and tree nesting birds, but high severity fire decreased occupancy of ground nesting birds and granivorous birds. Due to the variable effects of severity across different species groups, fire and land management that can produce a variety of fire severity patches (broader scale pyrodiversity) could help preserve landscape heterogeneity in woodland savannas and improve regional wildlife biodiversity.

Avian species richness in a frequently burned ecosystem: A link between pyrodiversity and biodiversity

M Jorge, M Conner, E Garrison, M Cherry

Presenting author: Marcelo Jorge, University of Georgia, Marcelo.jorge@uga.edu

Fire influences the distribution of ecosystems on Earth, but the link between pyrodiversity, the heterogeneity in post-fire conditions, and biodiversity is just emerging. We tested the pyrodiversity begets biodiversity theory, which was developed at broader scales, to a scale where land management decisions are commonly made. To assess the effects of landscape attributes on avian species richness, we deployed programmable acoustic recorders at 34 sites in a frequently burned longleaf pine (*Pinus palustris*) ecosystem which were set to record three, five-minute sessions per day for six days over two years. We identified avian species by their vocalizations and grouped them by nesting and foraging guilds to assess the effects of land cover type, soil productivity, forest structure, and fire history characteristics, including, pyrodiversity on species richness and occupancy at the community, guild, and species levels using hierarchical Bayesian multispecies occupancy models. We defined pyrodiversity as the richness in time since fire values around a site. We found support for the pyrodiversity begets biodiversity hypothesis at the community level, as avian species richness increased with pyrodiversity ($\beta = 0.136$, 95% CrI 0.009–0.260). Species richness of cavity-nesting species decreased with increasing time since fire, suggesting frequent fire increases diversity of this guild ($\beta = -0.334$, 95% CrI -0.713 to -0.003). Our work highlights the importance of pyrodiversity as a driver for biodiversity, and links theory to practices by examining this phenomenon at a scale readily translated into conservation action.

Breeding bird response to fire and other disturbances in eastern hardwood forests

C Greenberg

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Historically, natural and anthropogenic disturbances in eastern hardwood forests maintained a heterogeneous landscape, with variable levels of canopy cover. Today, prescribed fire is used to restore disturbance-adapted plant communities, and presumably the associated wildlife. However, little is known about wildlife response to prescribed fire or wildfire variability in eastern hardwood forest, especially over a relatively long time period (i.e., >10 years). In this talk I present overviews of multiple, multi-partner short- and long-term studies that together address breeding bird responses to single or repeated low- and high-severity prescribed fire, mixed-severity wildfires, season of burning, wind disturbance, shelterwood harvests, and other silvicultural treatments in the southern Appalachians. Together, study results indicate that bird abundance and species richness increases in response to forest canopy reduction, whether by high-severity burns, wind disturbance, or shelterwood harvests. Increases are due to an influx of disturbance-adapted species, with little change in the abundance of most species associated with mature forests. In general, breeding bird communities show little change in response to low-severity prescribed burns or wildfire, or silvicultural midstory reductions if canopy cover is left intact. In the short-term, substantial forest overstory reduction by timber harvests or high-severity burns may be required to create forest conditions suitable for disturbance-dependent species.

Interactions of fire and cattle grazing on wintering bird communities in California oak woodlands

F Fogarty, C Adlam

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Many California bird species have been studied extensively on their breeding ranges, but less is known about their ecology in winter. In particular, little is known about how potential disturbances such as fire and grazing affect winter resource use and community structure. We surveyed wintering bird communities from Dec-Mar in 2016-2017 and 2017-2018 at 47 sites across a gradient of oak woodland and grassland at Audubon's Bobcat Ranch in central California. The reserve provided a unique study opportunity as it contains both grazed and ungrazed parcels and partially burned in both 2016 and 2017. We tested whether alpha and beta diversity were correlated with low to medium intensity fire in the previous year, active grazing, and vegetation characteristics. We found substantial differences between the factors correlated with alpha and beta diversity. Alpha diversity had a strong negative correlation with fire, but those effects were partially mediated by associated changes in ground cover and vegetation. Grazing did not have a clear relationship with alpha diversity. Alpha diversity was also positively associated with oak (*Quercus*) foliage mass and heterogeneity in ground cover. Beta diversity was significantly correlated ($p < 0.05$) with both fire and grazing, as well as the diversity of deciduous trees present at a site and the percent cover of litter and forbs. Our results also showed substantial variation in community composition between sites, even within the same treatment, but that fire, grazing, and vegetation explained significant amounts of this variation. Given projections that the annual area burned in California will continue to increase in coming years, understanding the impact of fire on wildlife habitat is a priority for research. Our findings suggest that while low to medium severity fire may decrease species richness at the site level in this system, it may contribute to higher diversity at the landscape level when it increases the heterogeneity of grou

****Influence of post-fire habitat structure and connectivity on abundance of Lewis's woodpeckers (*Melanerpes lewis*) in Oregon****B Welch, H Wan, K Adkins, F Fogarty***Presenting author:* **Brittany Welch**, Cal Poly Humboldt, bw204@humboldt.edu

Lewis's woodpeckers (*Melanerpes lewis*) are described as 'burn specialists' due to their preference for breeding in recently burned pine forests in the western U.S.. However, despite increasing fire activity, this species experienced a 48% range-wide decline between 1968 and 2019, which raises questions about their adaptability to altered fire regimes in the region. We partnered with the Oregon Department of Fish & Wildlife to investigate how Lewis's woodpeckers in the Eastern Cascades, Oregon were influenced by post-fire habitat characteristics such as snag size, snag density, and fire severity across five wildfires that varied in fire age, size, and severity. We also examined how the spatial configuration of burn severity at varying spatial scales influenced Lewis's woodpeckers' distribution. We utilized point count data collected from May 2023 – June 2023 to create N-mixture models to estimate Lewis's woodpecker habitat associations. Our models showed that recent burns (3 – 6 years) with lower snag densities (~65 snags/hectare) and larger snags (< 40 cm diameter) had the highest abundance of Lewis's woodpecker. Our spatial models indicated that more connectivity between severely burned patches positively influenced Lewis's woodpecker abundance. Results from this work provide information for formulating more effective conservation and management strategies tailored to Lewis's woodpecker populations in the Eastern Cascades of Oregon in response to increasing wildfire activity in the region.

****Value of unburned forest for Black-backed Woodpeckers within a pyrodiverse landscape****M Kerstens, J Dinkins, J Rivers***Presenting author:* **Mark Kerstens**, Oregon State University, mark.kerstens@oregonstate.edu

Recently burned forests typically create ephemeral resource pulses for cavity nesters and other fire-associated bird species. However, burned areas can become unsuitable for breeding within 10 years as post-fire succession progresses and key nesting and foraging habitat features degrade. The Black-backed Woodpecker (*Picoides arcticus*) has often been described as a post-fire obligate, yet recent studies in its western range have found this species nesting in unburned (green) forest with similar

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measures of reproductive output and juvenile survival between green and burned forests. In this study, we investigated which factors influence habitat selection within green and burned forests of south-central Oregon to understand how this woodpecker selects nesting habitat at landscape scales during the 2018-2021 breeding seasons. To do this, we estimated second-order habitat selection by measuring vegetation data at nest sites in green (n = 35) and burned (n = 58) forest and compared this to randomly selected landscape scale plots (n = 196). We also used a geospatial analysis approach to produce a predictive habitat suitability map for green forest. Preliminary results suggest woodpeckers select sites that burned at high severity but are not selective of tree species in burned forest, whereas in green forest this species selects for live or recently dead mature lodgepole pine (*Pinus contorta*) nest trees and use nest sites with higher abundances of snags relative to landscape availability. Because green forests comprise most of the forested landscapes in the western United States, our results will provide information needed to maximize the conservation value of green forests for fire-associated birds within pyrodiverse landscapes.

***Fire and foraging: Pyrodiversity provides energetic advantages for spotted owls in burned landscapes**

K McGinn, C Zulla, M Wright, Z Wilkinson, B Dotters, K Roberts, J Keane, M Peery, G Jones

Presenting author: Kate McGinn, University of Wisconsin-Madison, mcginn4@wisc.edu

Fire-adapted species have evolved to exploit foraging opportunities in heterogeneous landscapes. However, the widespread disruption of historical fire regimes may threaten the ability of fire-adapted species to acquire sufficient energy to survive and reproduce. While fire disturbance may benefit California spotted owls by creating forest heterogeneity and facilitating individual hunting behavior, large fires that are homogeneously severe can have widespread and long lasting negative effects on spotted owl populations. Here, we used a combination of fine-scale GPS tagging and camera monitoring in the Sierra Nevada and San Bernardino Mountains, California, to examine the impact of fire on the foraging behaviors and energetic consumption of breeding spotted owls. We found that individuals spent more energy for no energetic benefits in severely burned landscapes. In landscapes with higher pyrodiversity, individuals spent more energy obtaining resources but delivered prey with higher energetic potential to nestlings. At a fine-scale, successful prey captures were less likely where there was more high-severity fire, while lower-severity fire and a moderate level of pyrodiversity facilitated prey capture for some individuals. Thus, fire-driven heterogeneity may create hunting opportunities that promote energetic investments towards reproduction. However, as the climate warms and fires become increasingly large and contiguously severe, the energy spotted owls spend to forage may offset any energetic benefits of fire-driven heterogeneity. Ultimately, identifying forest restoration strategies that limit high-severity fire while promoting structural heterogeneity will be necessary to conserve trophic interactions in this and other forested ecosystems.

****A case for female birds**

J Wu, M Harbison, S Beilke, P Saha, B Bateman

Presenting author: Joanna Wu, University of California, Los Angeles, moxk@gmail.com

As a field, ornithology has historically misunderstood, overlooked, or assumed female organisms are similar enough to males. The danger of those assumptions emerges when results and decisions based on those findings do not align with reality, particularly when female birds differ from males in key aspects of their biology. In most biological fields, the typical scale of study goes no finer than the species-level, but this coarseness can obscure important intraspecific differences, including differences by sex. For birds, which are widespread and can be identified to sex more readily than many other taxa, current ornithological knowledge is disproportionately based on male birds. We highlight some studies focused on the female perspective as well as research gaps. Across many species, reproductive roles defy 'traditional' assumptions: female birds sing, and social selection and balanced or 'reversed' sex roles are fairly common. Other characteristics are also more sex-specific than previously thought: females tend to be more dispersive than males, have lower survival, may be affected by climate change differently, and

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often use different habitats, which have implications for conservation. We advocate for ornithologists to study sexes separately in these fields and more to not obfuscate any sex-specific signals. Potential solutions include broadening the use of methods that increase the detection of female birds and recruiting a diverse group of generalist scientists who can help equalize the field of ornithological research.

Female competition in a jacana hybrid zone*S Lipshutz***Presenting author:* **Sara Lipshutz**, Duke University, sara.lipshutz@gmail.com

Mating phenotypes can promote or impede reproductive isolation between species. Historically, research on speciation and sexual selection has focused on competitive males and choosy females. We explore the influence of female competition on speciation in a hybrid zone between two socially polyandrous Jacana species, for which female competition determines reproductive success. We compare a suite of pre- and post-copulatory phenotypic traits, including territorial aggression, body size, weaponry, vocalizations, plumage coloration, and sperm morphology. We find patterns of both convergent and divergent character displacement, in which phenotypic differences in sympatry are distinct from those in allopatry, suggesting species interactions may facilitate morphological evolution. We find that female competition can promote hybridization, but gene flow between species is limited and hybrids are rare, suggesting that forces of sexual selection may be opposed by natural selection, thereby maintaining porous species barriers.

Neurogenomics of female competition and male parental care**T Patton, K Rosvall, S Lipshutz***Presenting author:* **Tessa Patton**, Loyola University Chicago, tmp1575@gmail.com

Why are males and females different? Despite sharing vastly similar genomes, females and males of the same species exhibit morphological, physiological, and behavioral differences. Socially polyandrous mating systems, in which females compete for multiple mates and males conduct the majority of parental duties, have been valuable for investigating sex differences in behavior. We examined the extent to which differences in competition and parental care are reflected in the neurogenomic profiles of females, courting males, and parenting males in the northern jacana (*Jacana spinosa*), a socially polyandrous shorebird. We conducted RNA-Seq in two brain regions within the social behavior network: the preoptic area of the hypothalamus and the nucleus taeniae. Several hundred genes were differentially expressed between females and males in both brain regions. These include androgen receptor (AR), which had higher expression in females, and prolactin receptor (PRLR), which had higher expression in parenting males. Additionally, we identified multiple gene networks associated with competitive traits including aggression, weaponry, and gonad size. These networks were enriched for biological processes such as central nervous system myelination, morphogenesis, and spermatogenesis. These comparative transcriptomic analyses suggest that molecular mechanisms associated with competition and parental care may be universal, regardless of which sex performs them.

The secret life of female hummingbirds*N Najar, C Clark***Presenting author:* **Nadje Najar**, University of California Riverside, nadjenajar@gmail.com

Hummingbirds are classic models of sexual selection, vertebrate metabolism, and a major source of bioinspiration. The ecology and morphology of males and females can be dramatically divergent, yet we know little about the consequences of these differences. Band recoveries suggest female mortality is much lower than males, with females much more likely to return year-over-year. Females of several species are reported to double-clutch, raising two nests simultaneously. While incubating, females do not use torpor, further increasing their daily energy demands. Hummingbirds forage by hovering, so females should be under greater selection for efficiency during hovering. Female Bee hummingbirds have larger bodies, smaller flight muscles but larger wings than males. Females are thus predicted to have lower top speeds but be more efficient at hovering. A comparative experiment on four species confirms this pattern.

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Path analysis indicates the size of the flight muscles are the primary drivers of this difference. However, a captive experiment of male and female *Selasphorus* hummingbirds revealed a phenological effect on forward speed: males and females overlap their top speeds in the non-breeding season, but in the breeding season males exhibit much faster top speeds, likely due to testosterone-induced muscle changes. Unexpectedly, females also flew faster during the breeding season, which suggests steroidal effects on flight performance may not be limited to male hummingbirds.

***Exploring physiological mechanisms of seasonal behaviors through the lens of the female**

A Kimmitt*Presenting author: Abigail Kimmitt, akimmitt@umich.edu*

Females have been historically understudied in avian reproductive physiology, despite comprising approximately half of all animal populations. Female physiology plays a vital role in driving consequential events in the annual cycle, including reproductive phenology and fitness. Female reproductive timing is also flexible, such that individual females tracked across years can adjust initiation of egg laying with respect to spring temperatures. However, our understanding of the mechanisms underlying this flexible phenology remains poorly understood. I will summarize my work on the Dark-eyed Junco (*Junco hyemalis*), which has served as an ideal system to explore the mechanisms underlying female reproductive timing. Seasonally co-distributed populations of juncos differ in migratory behavior (i.e., migrant vs. resident) also differ in reproductive timing despite experiencing the same environmental cues in early spring. In females, I found differences in gene expression that suggested that residents' ovaries were more sensitive to upstream hormonal signals that likely explain population differences in reproductive development. I will also explore future directions to further investigate reproductive physiology in migrant-resident comparisons at the species-level (e.g., Song Sparrows and Swamp Sparrows) to understand the degree to which gene regulation of reproductive timing based on migratory behavior is conserved across more evolutionarily diverged taxa. Comparing mechanisms of reproduction in free-living populations can reveal important mechanisms that determine the onset of reproductive development.

Sex ratios skew and female occupancy decline in a warming world - what conservation of the southern white-tailed ptarmigan in Colorado looks like in the face of climate change

A Seglund, J Runge, D Sapena*Presenting author: Dillon Sapena, Colorado Parks and Wildlife, dsapena@yahoo.com*

It has been suggested that climate change will have a greater negative impact on birds inhabiting colder, high elevation habitats than species associated with warmer, lower elevation sites. One alpine avian species identified as a species of greatest conservation need in Colorado is the southern white-tailed ptarmigan (*Lagopus leucura altipetens*). This species lives year-round in the alpine life zone and has developed numerous adaptive strategies for this harsh environment. We investigated occupancy rates for the bird in 2011, 2021, and 2022 in northern, central, and southern Colorado. Estimates of occupancy for males increased from 2011–2022. Conversely, female occupancy declined from 2011 to 2021. Female occupancy rates were not statistically different from 2021 to 2022. We also estimated sex ratios and found similar patterns with male to female adult sex ratios becoming more skewed in favor of males from 2011–2022. A posteriori analysis of weather variables for female-only analyses found that female occupancy decreased as minimum temperatures in the breeding season increased. Male occupancy appeared to be unaffected by weather conditions. Lower female occupancy associated with increased minimum breeding temperatures may be due to reproductive costs associated with uniparental care.

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Since the female is solely responsible for incubating and raising broods, she may encounter physiological challenges such as hyperthermia, reduced body condition, and dehydration with increases in temperatures as well as increased exposure to predation in an attempt to find cooler microclimates. The distortion of adult sex ratios in a monogamous species, may indicate potential negative effects to the population.

Evolution of elaborate female color and female song in New World orioles.

K Omland, M Moyer

Presenting author: **Kevin Omland**, UMBC, omland@umbc.edu

Geographical and gender biases in the history of ornithology have caused missed opportunities and, in some cases, a backward understanding of key evolutionary and behavioral processes. Female birds have historically been neglected in studies of elaborate coloration and song. The main framework for thinking about the evolution of elaborate traits has been sexual selection, whereby competition amongst males for mates has led to elaborate coloration and long, complex songs. Females have either been ignored or assumed not to change. Our work on plumage coloration in orioles highlights that most tropical songbirds likely have elaborate coloration in both sexes. The ancestral oriole was likely a tropical resident with year-round territoriality and elaborate female plumage. More recent work on song in orioles, other blackbirds and all songbirds indicates that female song is much more common than previously thought. Furthermore, the common ancestor of all songbirds likely had female song, suggesting that that social selection acting on both sexes throughout the year may have caused the original evolution of bird song. We have recently compared female song in temperate and tropical orioles to understand losses of elaborate female traits. Moving forward, ornithologists accounting for female display traits will lead to a clearer understanding of the evolution of coloration and song. It will also facilitate a broader understanding of the full scope of topics in avian ecology, evolution and behavior.

**Comparing the structure and function of female song in closely related temperate and tropical orioles

M Moyer, M Ocasio, N Nieves-Colón, E Osorio, E Bare, B Lohr, K Omland

Presenting author: **Michelle Moyer**, University of Maryland, Baltimore County, michelle.moyer8@gmail.com

The ancestor of New World orioles was most likely a tropical oriole who defended territories year-round, with both males and females displaying elaborate plumage coloration and producing song. Sexual dimorphism of singing behavior in extant orioles likely evolved as a result of a reduction or loss of female song. However, little research has investigated the functional significance of these reduced or infrequent female songs. We compared male and female singing behavior in the Puerto Rican Oriole (*Icterus portoricensis*), a tropical oriole which has retained ancestral natural history characteristics, and the closely related Orchard Oriole (*Icterus spurius*), a temperate-breeding, migratory oriole. In both species, female song was acoustically reduced compared to male song, but Puerto Rican Oriole females sang almost as frequently as males. However, Orchard Oriole females sang significantly less often than males, which supports the theory that temperate natural history characteristics may result in relaxed selection for female songs in orioles.

Habitat and morphology shape song evolution in female suboscine birds

R Beco, G Macedo, G Bravo, O Johnson, A Luo, E Derryberry

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Song is used for many communication purposes, such as attracting mates, defending territories, and avoiding predators. As such, song is often under multiple selective pressures, including natural, social, and sexual selection. The drivers of vocal evolution are well described for male animals; however, it is less well known which selective pressures shape female song, in part because of a dearth of sampling. Among taxonomic groups, female birds are increasingly better sampled for vocal signals. This is especially the case for the antbirds (Thamnophilidae) in which female song of most species have been

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recorded. Previous work showed that male antbird songs are constrained by ecology (i.e., acoustic adaptation hypothesis) and by morphology (i.e., morphological adaptation hypothesis). Here, we tested the acoustic and morphological adaptation hypotheses in female antbirds using modern phylogenetic comparative methods. For this, we used a recent antbird phylogeny, with extensive sampling of female song, habitat, and morphological data. We ran model comparisons using Phylogenetic Generalized Least Squares analysis. We found that female species restricted to unexposed habitat produced songs with fewer number of notes, slower pace, and lower vocal performance when compared to species in exposed habitat. In addition, bigger bill volume constrains song to have narrower bandwidth, lower peak frequency, and lower vocal performance. Our results suggest that female song is associated with morphology and habitat conditions, supporting both the acoustic and morphological adaptation hypotheses. Our findings indicate the types of selection pressures shaping the evolution of female communication, a historically neglected research area.

****Female Song in Red-winged Blackbirds is Multi-functional****C Barros, L Benedict***Presenting author: Cristina Barros, University of Northern Colorado, cristina.barros@unco.edu*

Red-winged blackbirds are unusual in the temperate zone in that both the males and females sing frequently (Searcy & Yasukawa, 2014). Despite the high song rate of female Red-winged blackbirds, studies performed on male Red-winged Blackbird song far outnumber those on female song. Female Red-winged Blackbirds produce two distinct songs during the breeding season (Yasukawa et al., 1987), known as the 'Rattle', and 'Cheer' songs (Pieplow, 2019). There is not a clear consensus in the literature about the contexts in which female Red-winged Blackbirds use both song types (Beletsky, 1983), making it evident that additional behavioral experiments are required to determine function. I conducted playback experiments to test whether female song in this species functions in intrasexual competition, mate choice, or in pair communication by exposing banded females to both song types from unfamiliar females, song from unfamiliar males, and songs from a neighboring male, most likely their pair-bonded mate. Preliminary results revealed that on average, females sang more in response to playbacks of unfamiliar males than they did when exposed to playbacks of familiar males. Additionally, female Red-winged Blackbirds showed higher responses when exposed to playbacks of unfamiliar 'Cheer' song playback compared to unfamiliar 'Rattle' song playbacks. The findings of this study suggest that females may find 'Cheer' songs from females particularly aggressive, possibly due to the high intrasexual competition for mates in a polygynous system. Females may show strong responses to unfamiliar males compared familiar males for territorial defense, or possibly to initiate extra-pair mating opportunities.

Transcriptomics reveal neurogenomic associations with female and male song in a temperate songbird**K Odom, T Liddle, N Prior, C Krieg, T Stevenson, G Ball***Presenting author: Karan Odom, University of the Pacific, kodom@pacific.edu*

Extensive research has addressed the neuroendocrine mechanisms regulating male birdsong in temperate songbirds. Research shows that transitions in singing behavior from the nonbreeding to breeding season and regrowth of song control regions in males is mediated by testosterone. We know very little about the neuroendocrine and even less about the genetic mechanisms that cause female songbirds to sing. We are finding that female house wrens (*Troglodytes aedon*) sing with very low concentrations of testosterone. We also investigated the neurogenomic associations in HVC and POM in male and female house wrens between early and late breeding season when males and females naturally sing more or less. We found increased expression in males compared to females for genes involved in cell signaling, transport, development and growth. Genes with similar functions were also upregulated in females that sang more compared to females that sang less. In addition, we found sex differences in expression of genes that appear to be involved in both neural circuit development and androgen receptor expression. This could be a link between the neuroendocrine and neurogenomic mechanisms that regulate seasonal or sex differences in song.

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U.S. Endangered Species Act status of the Western Yellow-billed Cuckoo.**J Davis, M Conway***Presenting author: Jennifer Davis*, U.S. Fish and Wildlife Service, jennifer_L_davis@fws.gov

The U.S. Fish and Wildlife Service (FWS) recognized the western yellow-billed cuckoo as a distinct population segment and listed it as federally Threatened under the Endangered Species Act (ESA) in 2014. Historically, breeding western yellow-billed cuckoos occurred west of the Rocky Mountains, from British Columbia south into northwest Mexico. They no longer occur in much of their historic breeding range and are now mainly restricted to breeding along rivers and drainages in Arizona, California, New Mexico, and northwest Mexico with potential breeding in Idaho, Colorado, Nevada, and Utah. In 2021, FWS finalized Critical Habitat across the range, including 298,845 acres of land in portions of Arizona, California, Colorado, Idaho, New Mexico, Texas, and Utah. A Species Status Assessment (SSA) is currently in progress involving FWS, state agencies, and academic experts, to deliver foundational science for informing the upcoming Recovery Plan. A Species Status Assessment evaluates species needs and the current and potential future conditions of the species using a focused, repeatable, and rigorous scientific assessment using Resiliency, Redundancy, and Representation to understand species viability. Our SSA describes habitat quality across the range that will inform development of recovery actions and criteria in the future Recovery Plan. We will discuss the current status of the yellow-billed cuckoo under the ESA and what actions FWS is working on.

Range-wide occupancy of the western Yellow-billed Cuckoo (*Coccyzus americanus*) in the U.S.**J Stanek, M Whitfield, E Juarez, R Norvell, N Clipperton, E Duvuvuei, N Beauregard***Presenting author: John R Stanek*, Southern Sierra Research Station, john.stanek@southernsierraresearch.org

Following the extensive loss of riparian forest over the last century, the western yellow-billed cuckoo population suffered significant range reductions and extirpations from large areas of its historical range and is now recognized as a species of greatest conservation need by most western states and listed as a federally threatened species. In 2022, eleven states (AZ, CA, CO, ID, NM, NV, OR, TX, UT, WA, and WY) coordinated to conduct surveys across the western United States with the aim to identify habitat and characteristics associated with habitat occupancy, and create a habitat distribution model across their western range. Standard cuckoo surveys were conducted at 403 randomly selected sites, three times each, across eleven states. We used dynamic multi-scale modeling to obtain estimates of detection probability, landscape and local occupancy, species emigration and immigration (habitat colonization and extinction) within our sites. Cuckoo detection varied per survey visit, increasing from June to July surveys. Northing (-) and habitat % cover at sites (riparian [+], riparian woodland[+], ruderal riparian[-] habitat) and the greater landscape (agriculture % cover within 5 km[-]) were identified as top covariates in modeling large-scale and local-scale occupancy, habitat colonization and extinction parameters. Range-wide occupancy results can be used to assist land managers, particularly regarding regional cuckoo habitat use and prioritizing habitat restoration areas.

Using the R2R Framework to Guide and Assess Yellow-billed Cuckoo Progress toward Recovery**T Will, P Schmidt, K Holland***Presenting author: Tom Will*, University of Minnesota, tomcharleswill@gmail.com

Road to Recovery: Saving Our Shared Birds (R2R) is an independently-funded movement built on a commitment to science co-production among social and biological scientists, conservation practitioners, and impacted communities focused on the recovery of the most rapidly declining birds in the United States and Canada. By working together throughout the process of identifying limiting factors, designing strategies to address causes of decline, implementing conservation actions, and monitoring success, the R2R community seeks to eliminate the research-to-implementation gap. R2R's Species Recovery Progress Wheel is a self-assessment tool designed to help species working groups think about the

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different spheres of conservation work. The progressive criteria in the Wheel tool comprise not only biological steps (e.g., identifying linked populations, demography, limiting factors, and habitat change strategies); in addition, of 90 criteria, 40 relate specifically to human dimensions, inclusivity, and social responsibility. The Wheel also provides a visually compelling, graphic self-assessment of progress. Over the five months preceding the AOS meeting, R2R met with the Yellow-billed Cuckoo Working Group to explore the Wheel assessment. In this talk, we report on how the R2R process, as outlined in the Wheel's progress criteria, facilitated insights and modifications in the Working Group's plan of action, especially with respect to social and biological co-production and the effort to conduct research and conservation action with more deliberate attention to issues of social justice and inclusivity.

Using structured decision-making for incorporating coproduction and determining priority information needs and management actions for the Western Yellow-billed Cuckoo

H Walker, J Stanek, P Wohner, C Stanley, C Wise

Presenting author: **Hira Walker**, US Army Corps of Engineers, hira.a.walker@usace.army.mil

The Yellow-billed Cuckoo (*Coccyzus americanus*) is a Neotropical migrant landbird that generally breeds in wet habitats from temperate North America south to Mexico and the Greater Antilles, and winters primarily in central South America east of the Andes. Over the past century, western (e.g., in the US west of the continental divide) breeding populations have been extirpated or have undergone catastrophic declines primarily due to loss, degradation, and fragmentation of required riparian and xero-riparian breeding habitats. These declines have led to the listing of the western population (Western Distinct Population Segment) as federally threatened under the US Endangered Species Act and its inclusion as one the Road to Recovery's (R2R) pilot species. Under the R2R framework and in support of US and international conservation and recovery efforts, the Western Yellow-billed Cuckoo Working Group is actively working to identify critical uncertainties and vital management actions needed to reverse population declines. In this talk, we discuss how the structured decision-making (SDM) process can be used by the Working Group, R2R, and others to support these efforts. Specifically, we examine how, across the western cuckoo's annual range and life-cycle, the SDM framework can be used to engage multiple diverse groups (researchers, managers, interest groups) in collaborative efforts to 1) identify and quantify conservation objectives, 2) examine the effects of management actions, and 3) prioritize research and monitoring efforts to fill critical information gaps.

***Estimating population specific annual survival from satellite transmitters while accounting for device failure**

C Stanley, P Marra, C Rushing

Presenting author: **Calandra Stanley**, Georgetown University, callie@umd.edu

Survivorship is a key driver of population dynamics and estimating survival rates is fundamental to the development of management plans for species at risk. Advancements in tracking technologies have enabled direct measurement of mortality but these methods are still restricted to larger species that can carry the weight of larger transmitting devices (e.g. GPS-enabled transmitters). As the miniaturization of transmitter technologies continues, newer generations of transmitters are able to reliably record bird movements but are limited to Doppler tracking or infrequent fix schedules which makes them less able to separate mortality events from device failure. Therefore, linking variation in survival rates to population dynamics remains challenging for smaller species and those not well sampled by mark-resighting methods (e.g. highly vagile species). To improve the use of smaller Argos-based transmitters for quantifying population-specific annual survival, we developed a modelling approach to probabilistically infer whether observed loss of transmissions are the result of mortality or transmitter failure. The approach uses spatial replication of transmitter deployments and models of both mortality and device failure rates. Using simulations and Argos tracking data from Yellow-billed Cuckoos (*Coccyzus americanus*), we show that this approach can produce reliable estimates of differences in annual survival across populations. A major challenge in generating estimates using this method is the lack of publicly

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available information on transmitter failure and we urge researchers to include this information when reporting on future tracking studies.

Planning a Yellow-billed Cuckoo Genoscape

K Ruegg*Presenting author: Kristen Ruegg, Colorado State University, kristen.ruegg@gmail.com*

The Yellow-billed Cuckoo is a long-distance migratory bird species that has experienced significant population declines in the last 35 years. In particular, the western group was listed as threatened under the U.S. Endangered Species Act in 2014, prompting the formation of conservation plans. One of the main challenges in developing conservation plans for this species has been the lack of an efficient and reliable method to measure the strength of migratory connections between different populations throughout the year. One of the most comprehensive methods for assessing these migratory connections is through the construction of a genoscape. A genoscape is a map of genetic variation across the range of the species and once constructed it can be used to link populations with their non-breeding areas. The Working Group and its members have recently recognized the importance of constructing a genoscape as a crucial step in reversing the population decline of Yellow-billed Cuckoos. In this presentation, I will discuss the current understanding of population structure in Yellow-billed Cuckoos and the necessary steps to complete a genoscape for this species.

*Using autonomous recording units to identify and monitor western Yellow-billed Cuckoos in southwestern xeroriparian habitat

N Beauregard, S Sferra, T Theimer, B Pasch*Presenting author: Nicholas Beauregard, nickbeauregard@gmail.com*

Autonomous recording units (ARUs) paired with signal classification software can be used to detect species-specific songs and calls, making them useful for evaluating patterns in avian activity and occupancy. Application of such methods may be challenging for rare and cryptic species that vocalize infrequently or that occur in low numbers, and by inaccurate classification of target signals by classifiers. We tested the use of ARUs to identify occupied habitat for a cryptic and federally threatened distinct population segment, the western Yellow-billed Cuckoo (*Coccyzus americanus*). Using Kaleidoscope Pro, we developed a call-classifier and processed acoustic data collected in sites also surveyed using traditional human-observer methods, applying the same spatial and temporal detection criteria to estimate site occupancy for each method. The classifier detected a total of 4061 calls in four sites, and had an overall precision score of 0.06, recall score of 0.33, and F-score (beta = 1) of 0.102, indicating many calls were not detected by the classifier. Our results were consistent with other ARU studies of rare and cryptic species, however, and ARUs estimated occupancy as effectively as human surveys with as little as two hours of daily recording. Total detections varied between sites, likely due to differences in cuckoo population densities and the interaction between topography and ARU detection space. Our results suggest that despite performance shortcomings of call classifiers, ARUs can be effective for monitoring cuckoos, with potential for providing higher resolution temporal and spatial information on activity and habitat use.

*Patterns of migratory connectivity across the species range of Yellow-billed cuckoos (*Coccyzus americanus*)

C Stanley, D Tracy, S McNeil, P Marra*Presenting author: Calandra Stanley, Georgetown University, callie@umd.edu*

Understanding the distribution of species is a basic component of the fundamental ecology and biology of the species, however, for migratory species this is complicated by seasonal movements between breeding and non-breeding regions. For species in decline, deciphering patterns of migratory connectivity is also a critical component needed to understand and quantify the drivers of population decline as different populations may be exposed to different threats across the annual cycle. Using 2-g satellite transmitters we quantified patterns of temporal and spatial migratory connectivity for Yellow-billed

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cuckoos (*Coccyzus americanus*) across 8 breeding populations and 1 wintering population. Yellow-billed cuckoos exhibited moderate levels of migratory connectivity during the early stages of fall migration as 4 distinct migration routes and divergent migration schedules between eastern and western populations were identified. Population-specific migratory routes and timing ceased in South America where tracked individuals exhibited low temporal and spatial migratory connectivity south of the equator until arrival to a common non-breeding region in the Gran Chaco region. Spring migration was characterized by overall low migratory connectivity with 2 major migration routes identified. Key migration staging areas were identified in northern South America, the Yucatan peninsula and western Mexico. Yellow-billed cuckoos exhibited extensive itinerant movements across both breeding and non-breeding periods. This information provides critical information identifying the spatial requirements and regions of conservation importance for Yellow-billed cuckoo and is critical for moving the species along the Road to Recovery framework.

No place to land: can habitat degradation at stopover sites limit Yellow-billed Cuckoo populations?

E Jacobo, N Jaime Escalante

Presenting author: **Edwin Jacobo**, Washington State University, edwin.jacobo@wsu.edu

The Yellow-billed Cuckoo (*Coccyzus americanus*) is a Neotropical migratory bird species of conservation concern, particularly breeding populations in western North America. In its annual migration between breeding grounds in North America to wintering areas in South America, the species relies heavily on stopover sites for refueling and rest. However, the integrity of these stopover habitats is increasingly threatened by deforestation, driven by agricultural expansion and land-use changes. This study uses citizen science data, museum specimens, and species distribution modeling methods to characterize stopover habitat preferences by Yellow-billed cuckoos. We used the results from our analysis to explore the deforestation trends in regions predicted to be occupied by cuckoos during migration using remote sensing data. We examine and discuss the potential implications of habitat fragmentation and loss on cuckoo movement patterns, stopover duration, and overall fitness. Understanding the consequences of deforestation on the stopover ecology of the Yellow-billed Cuckoo is vital for informing conservation strategies and management practices aimed at preserving migratory bird populations in the region. By identifying key habitat requirements and vulnerabilities, our research contributes to the development of targeted conservation initiatives focused on mitigating the impacts of deforestation and safeguarding stopover sites critical for the persistence of Neotropical migratory birds like the Yellow-billed Cuckoo.

Restoration success on the lower Colorado River: How's it going 15 years later?

J Stanek, S McNeil, D Tracy, C Ronning

Presenting author: **John R Stanek**, Southern Sierra Research Station, john.stanek@southernsierraresearch.org

The western Yellow-billed Cuckoo (*Coccyzus americanus*) is most often associated with riparian habitat dominated by cottonwood (*Populus* spp.) and willow (*Salix* spp.) trees. Prior to dam construction and other development, riparian forests within such a dynamic system as the lower Colorado River (LCR) would have been a mosaic of tree ages and sizes. These large, naturally established forests have disappeared on the LCR and largely replaced by crop agriculture and degraded tamarisk (*Tamarix* spp.) dominated shrublands. In 2006 the Lower Colorado River Multi-Species Conservation Program (LCR MSCP) began large-scale planting of cottonwood (*P. fremontii*), willow (*S. gooddingii*, *S. exigua*) and mesquite (*Prosopis glandulosa*), mainly through conversion of agricultural fields. Between 10-100 ha were planted each year at multiple sites. Cuckoos moved into newly planted phases within the first 1-3 years after planting and quickly established the largest population in California. As trees aged, detections of cuckoos declined in the older stands and increased in more recent plantings. We encourage others to look at stand age and structure during surveys and monitoring of cuckoos. Understanding this relationship can guide habitat management in systems where flooding and scouring processes are absent.

Community collaboration for Western Yellow-billed Cuckoo conservation

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C Wise, S PragerPresenting author: **Cathryn Wise**, Audubon Southwest, 1birdqueen@gmail.com

Audubon Southwest is the regional office of the National Audubon Society, a respected bird conservation organization well-known for a focus on community engagement. The southwest team coordinates bird and habitat conservation activities in Arizona and New Mexico—the epicenter of Yellow-billed Cuckoo (YBCU) breeding activity in the US. Together with partners including the BLM, AZ Game and Fish Department, local Audubon chapters and community colleges, Audubon Southwest began engaging volunteers and interns in YBCU survey efforts in 2012 and continues a multi-pronged approach to monitoring cuckoos and engaging diverse audiences in outreach efforts. In this talk, Audubon summarizes data collected over 10 years on the Agua Fria National Monument in Arizona, shares lessons learned in engaging interns and volunteers in this long-term project and provides successful community engagement strategies including collaborative beer releases, public events, and media ideas.

Breeding by western Yellow-billed Cuckoos in a novel and important habitat in southeastern Arizona*N Beauregard, T Theimer, S Sferra, C Drost**Presenting author: **Nicholas Beauregard**, nickbeauregard@gmail.com

The identification of occupied habitat is an important component of recovery efforts for threatened and endangered species. The western population of the Yellow-billed Cuckoo (*Coccyzus americanus*) is federally listed as a threatened distinct population segment and has long been considered riparian-obligate, yet recent survey efforts in southeastern Arizona have documented cuckoos occurring in xeroriparian habitat during the nesting season. If these cuckoos are breeding, birds in xeroriparian habitat could represent a substantial addition to the species' numbers in western North America. We investigated the distribution and breeding status of cuckoos in southeastern Arizona xeroriparian habitat by comparing the results of standardized call-playback surveys to the results of nest searching efforts in the same sites from 2018 to 2020. We then used this information to interpret more extensive survey data from 2013 to 2020 and develop an updated breeding distribution map for southern Arizona. We confirmed breeding in 94% of sites categorized as occupied according to survey results, confirming regular breeding in these xeroriparian habitats. Combining our data with previous survey data, we estimated a minimum of 100 occupied areas in southeastern Arizona xeroriparian habitat, representing a substantial increase in the known breeding population in Arizona. Occupied sites were concentrated in southern and western 'Sky Island' mountain and foothill drainages, from 600–1800 m, with xeroriparian vegetation variously surrounded by Madrean-evergreen woodland, semi-desert grassland, or desert scrub. Cuckoos breeding in southeast Arizona xeroriparian habitat may be important for conservation efforts, but face potential threats from grazing, climate change, and development.

Western yellow-billed cuckoo (*Coccyzus americanus occidentalis*) breeding habitat suitability within the Middle Rio Grande, New Mexico.**R Siegle, D Moore**Presenting author: **David Moore**, sdavidmoore@usbr.gov

The western yellow-billed cuckoo (*Coccyzus americanus occidentalis*; YBCU) is a neotropical migratory bird whose population has been in steep decline due primarily to habitat loss and degradation. This species nests in large, dense patches of riparian vegetation, particularly with a willow and cottonwood overstory. Populations of breeding YBCUs have historically occupied the Rio Grande riparian corridor in central New Mexico. The Bureau of Reclamation began formal surveys for the YBCU in the Middle Rio Grande in 2006 and has continued annual surveying and monitoring efforts since that time. The YBCU was listed as threatened under the Endangered Species Act in 2014 and critical habitat was formally designated in 2021. In order to determine breeding habitat availability for YBCUs within the Middle Rio Grande, Reclamation conducted field-based vegetation mapping and created a Geographic Information Systems (GIS)-based habitat model in 2021. Mapping methods employed a classification system created by the MRG Biological Survey in the mid-1980's with minor modifications for this modeling effort. Habitat

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modeling criteria were developed by evaluating the distribution and habitat use of cuckoos within the Middle Rio Grande based on 1) telemetry studies and 2) single detections and territory estimations identified in presence/absence surveys. Variables included plant species composition, stand structure and density, and patch size and width. During the summer of 2021, 19,860 hectares of riparian corridor were mapped, of which 2,966 were determined to be suitable YBCU breeding habitat.

Using LiDAR to model riparian bird habitat in Southern California

B Orr, I Pryor, P Baker, J Hatten, L Hall*Presenting author:* **Bruce Orr**, Stillwater Sciences, bruce@stillwatersci.com

Technological advances in airborne laser mapping (also referred to as light detection and ranging or LiDAR) and other types of remote sensing are providing new tools for environmental assessment. Our talk will draw on recent and ongoing studies of two rivers in southern California to provide examples of how LiDAR and other remote sensing tools can be used, in conjunction with focused field data collection, to conduct river floodplain and riparian assessments and restoration planning at multiple scales (e.g., river corridor, reach, and site scales). Our current vegetation classification and mapping efforts are directly benefiting from the use of LiDAR to estimate stand and even individual tree canopy height along with relative elevation (which can serve as a proxy for factors such as depth to groundwater). The results of these efforts can be incorporated into habitat suitability models for riparian bird species such as the Western Yellow-billed Cuckoo and Southwestern Willow Flycatcher. We will discuss the results of a pilot study to explore the use of LiDAR to provide more detailed estimates of vertical vegetation structure (from ground surface to top of canopy) that may be used in modeling habitat suitability for other riparian wildlife species, such as the Least Bell's Vireo, and then conclude with some recommendations regarding future use of LiDAR and geospatial cluster analysis for riparian wildlife habitat assessment, modeling, and long-term monitoring along rivers in Southern California and, potentially, throughout the breeding range of the Yellow-billed Cuckoo in the western United States.

Yellow-billed Cuckoo (*Coccyzus americanus*) Breeding Phenology and Use of Russian Olive for Nesting in Western Colorado

A Petry*Presenting author:* **Adam Petry**, Western Biology, LLC, info@westernbiology.com

Inventory and monitoring efforts for the elusive Yellow-billed Cuckoo (*Coccyzus americanus*, YBCU) have been historically limited and inconsistent in western Colorado and many questions persist about the species' population status, breeding phenology, and habitat use in the region despite a significant recent increase in habitat management and vegetation removal projects. Although YBCU are rare and exhibit low solicited and unsolicited vocalization rates, existing data show a direct correlation between increased YBCU survey efforts and increased YBCU detections. In 2022, we conducted the first comprehensive spatially-balanced inventory for the species in western Colorado, which identified two surprising breeding hotspots located in fallow agricultural habitat dominated by Russian Olive (*Elaeagnus angustifolia*) and disconnected from traditional riparian corridors long-associated with species presence. In 2023, we discovered the latest known YBCU nest (August 5-24 in a Russian Olive fencerow) and site occupancy (September 20) in state history and subsequently performed a historical records review of probable and confirmed YBCU breeding attempts in western Colorado. Preliminary data indicate that YBCU incubation in western Colorado may peak between August 1-15 and fledging between August 15-30 and that both nest phases may occur later than previously anticipated. Preliminary data also demonstrate that YBCU continue to select for and potentially prefer Russian Olive for nesting in both riparian as well as agricultural and xeroriparian land use types. We propose Russian Olive may provide increasingly important surrogate, successional, and edge habitat for a variety of avifauna, especially as the health of riparian cottonwood galleries continues to decline across much of the Colorado Plateau. We recommend additional surveys and research to improve the understanding of YBCU ecology in western Colorado and to inform habitat management planning and guidelines in the region.

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Western yellow-billed cuckoo movement and breeding habitat use on the Middle Rio Grande, New Mexico

K Dillon, D Moore, T BarronPresenting author: **Tori Barron**, Bureau of Reclamation, tbarron@usbr.gov

The western yellow-billed cuckoo (*Coccyzus americanus occidentalis*; YBCU) population is in steep decline due to habitat loss and degradation, and is considered a threatened Distinct Population Segment under the Endangered Species Act. Cuckoos are unique in that they are typically not defensive of their breeding territories and have unusually large, and often overlapping, home ranges. As a result, critical data on the species' breeding habitat requirements is often conflicting or lacking entirely. The Rio Grande supports one of the largest remaining YBCU populations. Bureau of Reclamation biologists delineated 96 territories, based on the locations of 429 detections, between Isleta Pueblo and El Paso in 2019. This population has more than tripled in size since monitoring began in 2006. A radio telemetry study was initiated in 2017 in order to determine home range and habitat requirements of the species, as well as to improve population estimates and model carrying capacity. Twenty-nine YBCUs were captured and instrumented during the first 3 years of the study. Analysis of movement data found that YBCUs breeding on the Middle Rio Grande had an average 50% Kernel Home Range of approximately 7 hectares and an average 95% Kernel Home Range of approximately 38 hectares. However, home range size was also clearly related to habitat availability, such that YBCUs used more habitat if it was available. The 95% Kernel Home Range averaged approximately 60 hectares in areas with large, continuous patches of habitat, compared to only 18 hectares in areas with smaller and more disjunct habitat patches. Nevertheless, overall territory sizes were similar, averaging approximately 180 hectares, and individuals were observed to travel over a kilometer in a day during the breeding season. Native overstory vegetation comprised a large percentage of breeding territories, disproportionate to its availability on the landscape.

Alpine bird diversity, adaptations and resilience to climate change

K Martin, D de Zwaan, T Altamirano, D ScridelPresenting author: **Kathy Martin**, University of British Columbia, kathy.martin@ubc.ca

As centres of biodiversity and endemism, mountains represent nearly half of global biodiversity hotspots while covering only a quarter of the earth's landbase. At least 1,310 species (12% of all birds) breed above the treeline, with particularly high species richness in the global south. In North America, mountain habitats are used extensively by birds during the breeding and post-breeding periods (2.5-6 months), and can support up to 40% of local species pools. About 25% of mountain breeding species are listed as special concern or a higher level of vulnerability or endangerment. Adaptations for life in alpine habitats include physiological and behavioural mechanisms for blood/tissue gas exchange and efficient movement, morphology and crypticity for coping with temperature extremes and avoiding predators, respectively and genetic adaptations to deal with hypoxia. Increasingly, mountains provide climate and habitat refugia for open-country birds that were formerly widespread, but are now declining in the lowlands. However, climate change is reducing alpine bird distributions because of upshifted treelines, with some local extinctions reported. Overall, alpine birds can be useful sentinels of environmental change as they are sensitive to the strong climate warming and habitat degradation experienced in mountain systems. A major issue is lack of data. We urgently need comprehensive ecological monitoring and conservation research to determine the full alpine bird biodiversity, status and trends. Continental and global research collaborations are required to address whether high mountain birds have the resilience to persist despite these rapid environmental changes and escalating threats

Unravelling the seasonal distribution of birds in mountains

M Somveille, B Freeman, M Tuanmu, F La SortePresenting author: **Marius Somveille**, University College London, msomveille@gmail.com

Altitudinal migration, the seasonal movement of species between breeding and non-breeding grounds that are at different elevation, is a widespread, yet understudied, behaviour undertaken by birds and other mobile organisms in mountain regions. While altitudinal migration has been reported in hundreds of avian

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species worldwide, it remains unknown how this phenomenon affects the distribution of bird diversity along elevational gradients, and the underlying ecological drivers remain poorly understood. In this study, we use data from eBird to estimate 8003 species' seasonal elevational ranges along 37 mountain gradients across the world. We found that the patterns of the seasonal distribution of birds in mountains are condensed versions of the equivalent latitudinal pattern with a change of 1 degree along the latitudinal gradient being equivalent to a change of ~54–70 metres along the elevational gradient. We also show that a mechanistic model based on energy efficiency – i.e. optimising the balance between energy acquisition from the environment and energy use on biological processes – is able to explain well how birds distribute seasonally along elevational gradients. These findings provide a general explanation of altitudinal migration as a mechanism that allows birds to optimize their energy budget in the face of seasonality and competition in mountain regions. Finally, our mechanistic model provides a tool to better understand and predict how mountain birds will respond to anthropogenic change.

****Co-existence mechanisms in a diverse tropical bird community****S Ayebare, J Doser, A Plumptre, I Owunji, H Mugabe, E Zipkin***Presenting author: Samuel Ayebare, Michigan State University, ayebares@msu.edu*

Niche theory predicts that ecologically similar species can coexist through multidimensional niche partitioning. However, owing to the challenges of accounting for both abiotic and biotic processes in ecological niche modelling, the underlying mechanisms that facilitate coexistence of competing species are poorly understood. In this study, we evaluated potential mechanisms underlying the coexistence of ecologically similar bird species in a biodiversity-rich transboundary montane forest in east-central Africa by computing niche overlap indices along an environmental elevation gradient, diet, forest strata, activity patterns and within-habitat segregation across horizontal space. We found strong support for abiotic environmental habitat niche partitioning, with 55% of species pairs having separate elevation niches. For the remaining species pairs that exhibited similar elevation niches, we found that within-habitat segregation across horizontal space and to a lesser extent vertical forest strata provided the most likely mechanisms of species coexistence. Coexistence of ecologically similar species within a highly diverse montane forest was determined primarily by abiotic factors (e.g. environmental elevation gradient) that characterize the Grinnellian niche and secondarily by biotic factors (e.g. vertical and horizontal segregation within habitats) that describe the Eltonian niche. Thus, partitioning across multiple levels of spatial organization is a key mechanism of coexistence in diverse communities.

Mountain bird interspecific colonization and extinction dynamics are mediated by microclimate**M Betts, S Frey, B Gerber***Presenting author: Matthew Betts, matthew.betts@oregonstate.edu*

It is generally accepted that competitive interactions drive the distributions of many species, but climate-envelope models generally ignore them. This may partly explain poor predictive performance of species distribution models (SDMs) in the face of climate change. The few existing efforts to model species interactions (e.g., joint SDMS) often suffer from the 'missing variable' problem resulting in spurious apparent interactions. We capitalized on a 14-year, landscape-scale dataset in a relatively stable old-growth forest to test the hypothesis that colonization by one species could affect either the local extinction or colonization by phylogenetically related species. Using multi-species dynamic occupancy models, we tested the long-held hypothesis that negative species interactions might be mediated by climatic conditions. The expectation was that competitive interactions should strengthen in warmer microclimates, and lower elevations. Species interactions were mediated by microclimate for some, but not all species pairs. Counter to our hypothesis, we found that related species pairs more often showed colonization dynamics indicative of attraction rather than repulsion. In some cases, competitive interactions at warmer climates flipped to become attractive interactions in colder microclimates – support for the 'stress gradient hypothesis, which has rarely been tested in birds.

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The biogeography of reproductive success along elevational and latitudinal gradients*P Gokhale, T Price, B Freeman**Presenting author: **Pranav Gokhale**, pranavgokhale1@gmail.com

Understanding why species occur where they do is a fundamental question in biogeography and macroecology. In my talk, I will present data on two studies investigating the macroecology of fitness along environmental gradients - one testing patterns along an elevational gradient in the Himalaya, and one testing patterns across the North American latitudinal gradient using NestWatch data. In both datasets I will test predictions of the Abundant Center and Biotic Interactions Hypothesis. The Abundant-Center Hypothesis predicts higher reproductive success at the center of their ranges, with a decline away from it, producing a hump-shaped distribution of reproductive success. The Biotic Interactions Hypothesis predicts that species should have lower reproductive success at low latitudes and low elevations, with increasing reproductive success towards higher latitudes and elevations, due to stronger biotic interactions such as nest predation in low latitudes and elevations. Overall, my projects will provide fundamental insights into how fitness (reproductive success) varies across space, offering valuable understanding of the ecological and evolutionary drivers that shape the geographic range limits of species.

Genomic insights into high-altitude adaptation: studies of avian species in the Himalayas and Tibetan Plateau.*S Lamichhaney, N Wang, C Palacios, P Ghimire, P Chettri, N Dahal**Presenting author: **Sangeet Lamichhaney**, Kent State University, slamichh@kent.edu

Altitudinal gradients, such as those in the Himalayas, offer a unique opportunity to study mechanisms of physiological adaptation due to the pronounced shifts in environmental conditions along the gradient. However, despite being a global biodiversity hotspot, the Himalayas are underrated due to limited molecular studies on biodiversity patterns and species adaptation. Recent advancements in genomics have revolutionized the studies of genetic diversity, population structure, and evolutionary history of organisms, and hence offer exciting prospects to examine mechanisms driving biodiversity patterns in mountainous regions like the Himalayas. Our research group uses birds residing across the altitudinal gradient in the Himalayas and Tibetan plateau to uncover differences in acclimation/adaptation strategies among species with diverse life-history strategies and characterize genetic mechanisms underlying acute and chronic hypoxia response. Current projects include the study of Tibetan Partridge (*Perdix hodgsoniae*) where we have conducted population and landscape genomics and transcriptomics analyses, to identify genomic regions under selection, key bioclimatic variables associated with these genetic variations, and predict climate-induced genomic vulnerabilities in diverse high-altitude environments. Over the next decade, our goal is to establish birds from the Tibetan plateau and the Himalayas as a study system by expanding research efforts to include a broader range of species, including both resident and migratory birds, to capture the full spectrum of biodiversity and adaptation strategies in these regions. We also aim to strengthen collaborations with local communities and stakeholders to ensure the translation of research findings into effective conservation actions, aimed at preserving the unique biodiversity of the Himalayas.

****Comparative patterns of genetic and morphological divergence along an Andean elevational gradient****A Lele, J Drucker, E Bonaccorso, J Bates**Presenting author: **Abhimanyu Lele**, University of Chicago, abhimanyu.lele@gmail.com

Patterns of genetic and phenotypic divergence along environmental gradients and heterogeneous habitats provide insights into the processes driving adaptive evolution at fine spatial and temporal scales. The tropical Andes famously host a megadiverse avifauna, and the contribution of microevolutionary processes to generating the region's biodiversity remain poorly understood. In particular, no broad comparative study has examined adaptive divergence along elevational gradients using genomic data.

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Using a comparative framework, I examine gene flow and morphological divergence in a suite of more than 30 non-migratory passerines inhabiting the western slope of the Ecuadorian Andes. I collected reduced-representation genomic data (5000-20,000 SNPs) from more than 1000 individuals, and nine morphometric measurements from approximately 1800 individuals, representing 28 genera and 14 families. I used standard measures of gene flow and population differentiation to quantify genetic variability for each species along its entire elevational range, and multivariate analyses to examine morphological variability. Using Bayesian selection scans, I find evidence suggesting local adaptation in multiple species, in addition to widespread morphological variation with elevation. Finally, I investigated the effect of species ecology, including diet, foraging stratum, and dispersal ability, on genetic and morphological variability with elevation using phylogenetic linear mixed models. These results demonstrate the power of comparative genomics to investigate longstanding questions about gene flow and adaptive divergence across heterogeneous environments.

****Evolution of Neotropical landbird elevation ranges****C Gadek, C Witt***Presenting author: Chauncey Gadek, cgadek@gmail.com*

To anticipate elevational range dynamics in a changing world, we need to understand how elevational ranges have evolved. Across the avian tree of life, what was the rate of elevational shifts? Have upward and downward shifts occurred at similar rates? And do upper and lower limit dynamics vary with elevation as predicted by the Dobzhansky-MacArthur Phenomenon? Here we addressed these questions and reappraised a previous claim that there was an excess of downward shifts. To do this, we modeled the evolution of elevational ranges as a boundary-crossing process across elevation contours. We employed two modeling approaches: (1) serial state-dependent speciation and extinction models, each of which modeled range evolution across a single elevational threshold; and (2) multistate biogeographic models that estimated the history of elevational range shifts as a sequential expansion-contraction process among adjacent elevational zones. The results were strongly affected by physical landforms, namely the declining land area with elevation and the limited connectivity of ranges with high mountains that provide opportunities to ascend. The reported excess of downward rates reflected the geometric bounds of ranges and was sensitive to the threshold selected. Multi-state biogeographic models revealed that rates varied with elevation in ways predicted, in part, by the Dobzhansky-MacArthur Phenomenon. Clades varied in their rates of elevational shift in ways that help to explain their relative success at altitude. Overall, the results show subtle signatures of eco-evolutionary constraints against a strong influence of physical landforms, the overwhelming drivers of elevational diversity gradients.

Intraspecific variation in diet and foraging behavior of Andean forest birds across an elevational gradient of exploitative competition**J Drucker, A Lele, M Arias, E Bonaccorso, J Bates***Presenting author: Jacob Drucker, University of Chicago, jrdrucker@uchicago.edu*

Competition is thought to have a profound effect on bird community structure in tropical mountains as species are packed into the narrow climatic zones that turn over with elevation. While many studies have asked how competition shapes the narrow elevational species distributions that characterize the Andean avifauna, few have examined the effects of competition on complex ecological traits such as diet and foraging behavior that underlie community assembly in this biodiversity hotspot. Furthermore, previous work has focused on interspecific territoriality, rather than measuring how birds exploit local resources such as food and habitat. We quantified intraspecific variation in dietary and foraging niche breadth as well as species richness and abundance at ten localities across a 3000-meter elevational gradient in northwestern Ecuador. We derived diet composition from DNA-metabarcoding of ~1200 fecal samples, foraging niche breadth from network analysis of ~3000 foraging observations, and species richness and abundance based on ~5000 occurrences from mist-netting and point counts. Using bayesian modeling, we asked whether species richness and the abundance of con- and heterospecifics was associated with 1) a change in dietary niche breadth at the elevational range-extremes of eight insectivore species and 2) the foraging niche breadth of 50+ species relative to the niche space occupied by the entire bird

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community at that locality. Our results address the plasticity of two key traits that mediate species richness and resilience to global change.

***The biogeography of avian abundance along elevational gradients**

M Arias, A Lele, J Drucker, E Bonaccorso*Presenting author: Maria Arias, mjaras999@gmail.com*

The 'abundant-centre hypothesis' predicts that species tend to be most common at the center of their distribution, and scarcer towards the edges, reflecting the distribution of optimal conditions and resources. We used data from mist-net and point count surveys to study the shape and the drivers of abundance of 25 passerine bird species along a 3000-m elevational gradient on the northwestern slope of the Ecuadorian Andes, where the Tropical Andes and Chocó biodiversity hotspots converge. We modeled the shape of the abundance distributions of species across the elevational gradient, and used N-mixture models to ask questions about the biotic and abiotic factors that shape abundance. We show that the elevational distribution of bird abundance in these tropical mountain forests varies among species, and that no single parameter predicts local spatial patterns throughout the gradient. Our results point towards the complex and multifaceted system of ecological factors that shape species' distributions in the Andes and reinforce the need to develop more effective conservation strategies that are imperative to preserve mountain habitats in the face of climate change and persistent anthropogenic pressure.

Vocal traits and community assembly in a speciose montane bird community

R Rumelt*Presenting author: Reid Rumelt, University of Miami, rumeltr@miami.edu*

The avian species diversity of the Andes-Amazon Gradient is due in part high rates of species turnover with increasing elevation. Partitioning of elevational gradients in the tropics has traditionally been viewed through the lens of Janzen's hypothesis; however, more recent work has indicated that competitive interactions are an important force determining species range limits on tropical montane gradients. There exist numerous sister species that occupy adjacent elevational bands on this gradient but overlap somewhat at their shared border, with species that defend breeding territories year-round occupying narrower overlap zones than those that do not. Therefore, it is plausible that such local-scale interactions prevent sister species from co-occurring at the same sites due to competitive exclusion, despite occurring at similar elevations. To assess the strength of local-scale interactions in structuring this montane bird community, I utilize acoustic monitoring and machine learning audio classification to test whether species overlap less at single sites than regional-scale summaries of their elevational ranges would suggest. I also test whether site co-occurrence is negatively correlated with vocal trait overlap, as might be hypothesized if vocal similarity leads to increased interspecific aggression. This work represents an extension of previous studies implicating competition in determining of elevational range widths of tropical birds and could have implications for the strength of novel interspecies interactions due to climate warming.

Mountain Bird Network; case examples and future directions

S Jones, B Freeman*Presenting author: Samuel Jones, Georgia Tech, samuel.ei.jones@gmail.com*

Absence of data remains a pervasive challenge inhibiting our ability to understand the patterns, processes, and make predictions of the impacts of climate change on montane bird communities. This is despite the well-established recognition of the importance of mountains for avian diversity globally. The 'Mountain Bird Network' bridges this gap – a compilation of >150 published, and unpublished point-level datasets along elevational gradients globally, that are at a granular scale sufficient to determine necessary species abundance patterns to interpret fine scale processes. Here, I present initial analyses from the Mountain Bird Network drawing on case examples of large elevational datasets in Cyprus, Bioko (Equatorial Guinea), and re-survey data from Costa Rica. Specifically, I display how we can leverage historic and contemporary data to test the 'lowland biotic attrition' hypothesis (that lowland communities

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lose species to higher elevations), and explore how global datasets can inform both the past, and the future of mountain bird communities. Finally, I discuss knowledge gaps that fieldworkers can actively contribute to to achieve greater coverage of the Mountain Bird Network as a sentinel project for mountain birds globally.

***A century of landscape changes has led to grassland bird species declines along a tropical montane gradient**

V Ramesh, A VA, A Rajan, C Das, P Rajan Gupta, A Mohan, R VV, M Tingley, R DeFries

Presenting author: Vijay Ramesh, Cornell Lab of Ornithology, vr292@cornell.edu

Habitat loss and landscape transformation are leading causes of species declines. Yet, we know little about the long-term impacts of landscape change on species in tropical mountain ecosystems. Using an integrative approach that combined colonial-era and modern datasets on land cover and species observations, we examined how a century of land cover changes across the Nilgiri hills of the Western Ghats biodiversity hotspot has impacted bird communities. We carried out a historical resurvey across locations where bird species were formerly reported and quantified changes in bird relative abundance across time periods. Next, we assessed if climate and land cover changes were significantly associated with changes in the relative abundance of bird species. We found that the mean annual temperature has increased by 1C to 1.5C across the Nilgiri hills (across elevations; Mann-Kendall test, $p < 0.05$). Over 75% of the landscape that was formerly grasslands in 1848 is currently occupied by exotic timber plantations and cash crops, such as tea. The relative abundance of grassland bird specialists was significantly lower in the modern time period compared to historical time periods and declined over time (beta regressions, pseudo $R^2 = 0.53$). Our study highlights how anthropogenically induced environmental changes impact bird communities today. Grasslands are a unique ecosystem, often mischaracterized and misunderstood, and warrant immediate attention if we are to stem potential biodiversity losses in this landscape.

Connecting elevational shifts in breeding distributions to non-breeding anthropogenic disturbances.

T Price

Presenting author: Trevor Price, University of Chicago, pricet@uchicago.edu

Most work on altitudinal responses to climate change in birds has correlated breeding distributions to climate on the breeding grounds (temperature and precipitation). I address two features that are likely to affect breeding distributions beyond breeding climate. First, population sizes of many species are changing, and species with declining populations may well contract in elevational range, as individuals settle in optimal locations. Second, body condition is known to affect timing of return, and timing may affect where species breed (late arrival, higher up the mountain). I investigate the elevational distributions of two migratory bird species in the west Himalaya and link them to studies of these same species in their winter quarters in the plains of India. In the breeding season the lower elevational range of both species has moved upslope between the 1990s and the present, with no clear indication of changes in density in the remaining part of the range, or movement of the upper range limit. I argue that population declines in the winter, and effects of condition on return timings have contributed to the range contractions. However, direct effects of climate in the breeding grounds are also important (for example, early season storms delay breeding, and later season storms cause nestling mortality of earlier breeders). The relative contribution of breeding and winter may differ between the species. In the winter quarters species declines are more easily attributed to land use change than any effect of climate.

***Impacts of climate change on nest predators and nest success of trailing-edge populations of songbirds in the southern Appalachian Mountains**

U Gupta, W Lewis, R Cooper, R Chandler

Presenting author: Urvi Gupta, University of Georgia, urvi.gupta@uga.edu

Trailing-edge populations at low-latitude range margins face high risk of extinction from climate change,

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but the extent to which increased contact with novel warm-adapted nest predators contributes to climate-induced population declines is unknown. The southern Appalachian Mountains harbor trailing-edge populations of several bird species, including the Black-throated Blue Warbler (*Setophaga caerulescens*), whose local distribution has shifted towards higher elevations. Our results indicate that nest survival at high elevation sites has decreased from 68% in 2003 to 35% in 2019, which is comparable to nest survival at lower elevations. The increased predation rate at high elevations suggests that the abundance and diversity of nest predators may have increased at high elevation sites. Recent camera trap data indicates that nest predators include the Barred Owl, Broad-winged Hawk, red squirrels, bears, coyotes, rat snakes and small rodents (mice and rat species). Studying the spatio-temporal dynamics of nest predators along the climate gradient, as well as bottom-up effects of trophic interactions involving arthropod prey can illustrate how trophic interactions play a role in range shifts.

Afro-montane understory birds increase in body size over four decades*M Neate-Clegg, M Tingley, W Newmark***Presenting author: Monte Neate-Clegg, University of California, Santa Cruz, monteneateclegg@gmail.com*

Of the myriad responses to climate change, an emerging trend is the widespread decrease in animal body size with warming temperatures. Birds, in particular, have been shown to be decreasing in body size in several areas – most notably the Amazon Basin and temperate North America – but trends in much of the world remain unexplored. Here, we analyze temporal trends and climatic associations of body mass for 42 resident bird species over 36 years in the Usambara Mountains of Tanzania, a tropical montane global biodiversity hotspot. In addition, we assess trends in wing length and mass:wing ratio over 21 years. Finally, we examine whether species-specific trends in body mass are related to average body size or to trends in apparent survival. We report significant long-term trends and temperature associations across the bird community. Although the drivers of morphological changes remain unclear – and climate change cannot be ruled out – such changes among Afrotropical montane birds provide an intriguing counterpoint to observed declines in body mass elsewhere and suggest that trends in body mass in tropical birds may be mediated by biogeography or other abiotic or biotic drivers.

The Mountain Bird Network: towards a global monitoring program for montane birds in the Anthropocene**B Freeman***Presenting author: Benjamin Freeman, Georgia Tech, benjamin.g.freeman@gmail.com*

Mountains are home to exceptionally diverse avifaunas that are exceptional study systems for studying community ecology, adaptation, and speciation. In this talk I will recap this symposium, weaving together the different perspectives of participants and moving towards synthesis. The goals of this symposium are twofold. First, to bring together researchers from around the globe studying montane birds from different angles, in order to share what we know about montane bird ecology, evolution and conservation. Second, to bring together expertise to identify crucial knowledge gaps and foster collaborative research networks.

Synthesizing the Impacts of On-Shore Renewable Energy on Birds and Summarizing Current Best Management Practices*C Setash***Presenting author: Casey Setash, Colorado Parks and Wildlife, casey.setash@state.co.us*

Energy infrastructure in the United States is rapidly transitioning from primarily oil and natural gas to wind and solar as a means to combat climate change. The US Energy Information Administration reports that net renewable energy generation has more than quadrupled since 2010 and that 21% of the United States' energy resulted from non-fossil-fuel sources in 2022. While expanded renewable energy infrastructure is necessary to prevent the most catastrophic results of climate change, its impacts, both direct and indirect, must be evaluated to prevent further losses of biodiversity. Birds are one taxon particularly susceptible to impacts resulting from renewable energy and have already undergone severe

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declines globally in the last several decades. I conducted a synthesis of the local impacts of renewable energy infrastructure on avian biodiversity and the taxon-specific nuances relevant to maintaining biodiversity can therefore assist ecologists as they face this paradoxical conservation challenge in the coming decades. This synthesis was meant to provide a resource to ecologists for making informed, science-based recommendations with regards to siting and mitigation of future renewable energy infrastructure when possible, present an exhaustive review of literature focused on indirect avian effects of renewable energy infrastructure and present a complete database of effect sizes and direction, and summarize best management practices and current research needs in light of previous studies. I identified 38 studies representing a total of 187 unique study variables that quantified indirect effects of renewable infrastructure on birds. Of these, the highest proportion detected neither positive nor negative effects of infrastructure on the response variable of interest, and the largest number of studies focused on prairie grouse, but waterbirds, diurnal raptors, Passerines, and other gamebirds were represented as well.

Vulnerability of golden eagles to renewable energy production

T Conkling, A Duerr, S Endyke, T Miller, B Millsap, D Nelson, H Vander Zanden, G Zimmerman, T Katzner

Presenting author: Tara Conkling, tاراconkling@gmail.com

As renewable energy production expands across North America, regulatory guidelines often call for estimates of population level impacts of renewable energy-derived fatalities on wildlife. We developed a framework to define the geographic origin of individuals killed at renewable facilities and then to use demographic models to estimate consequences of renewable energy development for those origin populations. Previous studies have used stable hydrogen isotope values ($\delta^2\text{H}$) to define the geographic origin, but there is substantial uncertainty associated with hydrogen-based origin assignment. To overcome these challenges, we used a multi-isotope approach to geolocation, considering isotopes of carbon ($\delta^{13}\text{C}$) and sulfur ($\delta^{34}\text{S}$) in addition to $\delta^2\text{H}$ values, to evaluate the subpopulation of origin for Golden Eagles found dead at wind energy facilities in Wyoming. We then used a Bayesian integrated population model to identify vulnerability of these subpopulations to fatalities from wind energy development. Preliminary data suggest that the multi-isotope assignment process using $\delta^2\text{H}$, $\delta^{13}\text{C}$, and $\delta^{34}\text{S}$ values resulted in substantially improved estimates of population of origin compared to those derived from a single isotope alone. Demographic models identified widely varying levels of vulnerability among subpopulations, with notable differences between migratory and resident populations. Our approach illustrates the relevance of multi-element isoscapes to further identify subpopulations of interest and assess vulnerability of species potentially affected by wind energy development for multiple distinct breeding and wintering subpopulations.

Wind Energy and Grouse Populations: Can grouse endure the increased demand for renewable energy?

C LeBeau, K Smith, S Howlin, A Tredennick, K Kosciuch

Presenting author: Melanie McCormack, Western EcoSystems Technology, Inc, mmccormack@west-inc.com

Grouse (Tetraonini spp.) are of particular interest worldwide because of their cultural importance and conservation concern due to population declines. Grouse are often considered indicators of overall ecosystem health and are sensitive to anthropogenic disturbances. Most grouse species benefit from large and intact habitats to satisfy their life history requirements; however, due to habitat loss and fragmentation, many grouse populations are declining. The extent of negative behavioral responses associated with anthropogenic features sited in grouse habitats, including wind energy facilities, likely varies by species, facility characteristics, and the surrounding landscape. Given the increased demand for renewable energy, and to better understand responses and management of grouse species relative to wind energy developments, our presentation summarizes the current science evaluating the effects of wind energy development on grouse through a qualitative and quantitative assessment. We qualitatively reviewed over 350 documents specific to wind energy and grouse. Fifteen (15) peer-reviewed studies evaluated grouse avoidance behavior, lek attendance, and/or survival relative to wind energy facilities for

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three grouse species in the Western US and were used in a meta-analysis to quantitatively evaluate effects. We found evidence that grouse were displaced from habitat in close proximity to wind turbines, but findings varied by species. We found no evidence that proximity of wind turbines impacted survival on the studied grouse species. Our findings highlight many research priorities, including a need to evaluate the potential long-term or cumulative effects of extensive development, which will require a coordinated effort among researchers, regulatory agencies, and developers to link research, monitoring, and management that treats each new wind-energy development as an opportunity to test hypotheses and refine mitigation approaches.

Evaluating Impact and Risk to Migratory Birds from Renewable Energy Development across the Continental U.S. using eBird

R Natale, P Howell, E Kershner, V Ruiz-Gutierrez, C Davis

Presenting author: Rossey Natale, Cornell Lab of Ornithology, rnn22@cornell.edu

As the renewable energy sector expands, consideration for the potential impacts of infrastructure development (e.g., the placement of wind turbines) on avian populations is needed. However, it can be difficult to accurately identify areas where the placement of infrastructure may be the most or least harmful to bird species. Potential impacts for many species will also vary depending on the time of year (e.g., migratory periods vs. breeding season). Assessments must therefore consider risk across the full annual life cycle. Here, we present a framework for using broad-scale, high-resolution data products derived from eBird – the world's largest biodiversity database generated via participatory science – to identify Bird Concentration Areas (BCAs) that can be used to inform risk assessment at multiple spatiotemporal scales. BCAs are areas that host an exceptionally high abundance and/or diversity of avian species and can be generated for different species groups of concern or combined across species groups to highlight areas of 'high' versus 'low' importance and therefore risk. We will present several applications demonstrating how BCAs can be used to evaluate risk for infrastructure development at a high spatial resolution (3km x 3km) across the continental United States and throughout the full annual life cycle. Additionally, we will highlight how this approach can be easily adapted to accommodate species- or site-specific factors (e.g., species conservation status, spatially-explicit population trends) to further refine BCAs based on project objectives.

Science to streamline renewable energy development: the Renewables-Wildlife Solutions Initiative

T Katzner, T Conkling, M Davis, A Hale

Presenting author: Tara Conkling, U.S. Geological Survey, todd.katzner@gmail.com

Regulatory agencies often are asked to make management and permitting decisions about consequences to wildlife populations from renewable energy. This is problematic because although there are good tools to estimate rates at which wildlife are killed at renewable facilities, there are not similar tools to estimate cumulative and population-level effects of these fatalities. Consequentially, managers often are constrained to make difficult policy and management decisions reactively and with inadequate information, causing delays in permitting and compliance management. The Renewables-Wildlife Solutions Initiative (RWSI) is designed to provide timely, data-intensive science to assist streamlining of renewable energy development by rapidly assessing relative vulnerability of potentially affected wildlife populations. We assess relative vulnerability by (1) developing frameworks and infrastructure for collection, archiving, and analysis of biological samples (fur, feathers, organs) from wildlife killed at renewables; (2) using those samples to biochemically assess the 'catchment area' from which those fatalities are drawn; and (3) integrating catchment area data with demographic models to understand cumulative and population-level consequences of fatalities to wildlife. Here we describe the vision and initial implementation of the physical and scientific infrastructure we have developed. Subsequently, we highlight the utility of this new approach with success stories illustrating how the ~100,000 samples currently archived have supported collaborative and novel population-level vulnerability assessments, leading to tangible products that inform management decisions. We also describe plans to expand the initiative, making biological samples broadly available to the scientific and renewables-wildlife

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communities, and growing our ability to provide science to streamline renewable energy development.

***Utilizing high-resolution genetic markers to track population-level exposure of migratory birds to renewable energy development**

R Harrigan, J Rajbhandary, C Bossu, P Sanzenbacher, T Dietsch, C Gruppi, T Katzner, T Smith, K Ruegg

Presenting author: **Christen Bossu**, Colorado State University, christen.bossu@gmail.com

With new motivation to increase the proportion of energy demands met by zero-carbon sources, there is a need to focus on efforts to assess and mitigate the impacts of renewable energy development on sensitive ecosystems and wildlife, of which birds are of particular interest. One challenge for researchers has been estimating the effects from such development on individual breeding populations of migratory birds. Here, we utilize a high-resolution genetic tagging method to rapidly identify the breeding population of origin of carcasses recovered from renewable energy facilities and combine them with maps of genetic variation across geographic space (called 'genoscapes') for five species of migratory birds known to be exposed to energy development to assess population-level effects on migratory birds. We demonstrate that most avian remains collected were from the largest populations of a given species. In contrast, those remains from smaller, declining populations made up a smaller percentage of the total number of birds assayed. Results suggest that application of this high-resolution genetic tagging method can successfully improve identification of population-level exposure of migratory birds to renewable energy development and may be a powerful tool to inform future siting and mitigation activities associated with renewable energy programs.

***Offsetting fatalities of golden eagles at wind energy facilities in Wyoming with non-lead ammunition distribution programs**

V Slabe, R Crandall, T Katzner, A Duerr, T Miller

Presenting author: **Vincent Slabe**, Conservation Science Global, slabe.vincent@peregrinefund.org

Golden eagles face many anthropogenic risks including electrocution, collision with wind turbines and vehicles, and lead poisoning. Minimizing or offsetting eagle deaths caused by human-caused sources is often viewed as an important management objective. Despite this, there are few available and legally acceptable options to offset deaths of eagles in the US. We implemented a non-lead ammunition distribution program in southeast Wyoming and evaluated its effectiveness as a compensatory mitigation action to offset incidental take (i.e., fatalities) of golden eagles at wind energy facilities. In 2020 and 2022, we distributed non-lead ammunition at no cost to 699 hunters with big-game tags specific to our > 400,000 ha study area. These hunters harvested 296 pronghorn, 14 deer, and 33 elk. We used road surveys in 2020 to estimate a density of 0.036 (95% CI = 0.018 – 0.058) golden eagles per km² during the big game hunting season in our study area. Established mitigation calculations suggest that our non-lead ammunition distribution program offset the fatality of 3.84 (± 6.10 ; SE) eagles over the course of these two hunting seasons. Our work illustrates the usefulness of non-lead ammunition distribution programs as an action to mitigate eagle fatalities caused by wind facilities or other anthropogenic causes of death.

***Large-scale evaluation of associations between bird abundance, wind energy, and the Conservation Reserve Program using eBird data**

E Lassiter, C Duchardt, J Diffendorfer, R Iovanna, A Lopez, K Maguire, S Loss

Presenting author: **Samantha McGarrigle**, Oklahoma State University, samantha.a.mcgarigle@gmail.com

As the U.S. pushes to decarbonize the electricity grid, there continues to be significant expansion of renewable energy in rural and agricultural areas. As a result, the proximity of wind energy infrastructure to lands enrolled in the Conservation Reserve Program (CRP) has steadily increased. Wildlife habitat provided by CRP increases biodiversity, while wind energy development can negatively affect wildlife,

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including birds through direct collision mortality and indirect effects on habitat. We conducted a large-scale evaluation of associations between abundance of grassland-dependent birds and wind turbine locations, CRP lands, and interactions between wind and CRP. To do this, we compiled eBird data for 38 grassland bird species from 2012-2021 and characterized avian abundance, wind turbine characteristics, and CRP characteristics at 1.5 and 4.5 km spatial grains. Using generalized additive models, we found that important CRP and wind-related predictors of abundance differed among bird species. Further, we found evidence that wind-CRP interaction terms were important (i.e., effects of CRP on bird abundance dependent on characteristics of wind development in the landscape), but also that the direction and magnitude of these interaction effects varied among species. Results from our study can provide information to decision-makers that can help adapt CRP program incentives to maximize both wildlife benefits of CRP and local and national benefits of wind development in rural and agricultural communities.

Linkages between landscape characteristics and eagle fatalities at wind turbines in Wyoming

T Miller, T Conkling, T Katzner

Presenting author: **Trish Miller**, tricia.a.miller@gmail.com

Renewable energy production has expanded across the world with negative impacts to some species. In Wyoming, considerable numbers of fatalities of eagles have occurred at some wind turbines. With the expansion of wind energy across areas of Wyoming where large numbers of eagles concentrate, understanding the landscape factors that influence these fatalities can inform future siting of turbines in high-risk areas and mitigation of fatalities at existing sites. We evaluated potential predictors of fatalities at two wind energy facilities in east central Wyoming. For each wind turbine, we calculated vegetative and topographic characteristics within the rotor swept zone, using a circular buffer with a radius equal to the blade length of each turbine. We then assigned each turbine as a fatality or non-fatality based on the reported location of Bald and Golden Eagle fatalities and we used these data in binomial generalized linear mixed models with facility as a random effect. We then extrapolated the results to other areas in Wyoming with existing or planned wind energy facilities and created spatial maps. Finally, we validated our model using fatality data from other existing facilities. The resulting model and spatial maps can help inform safer siting of future wind turbines and guide mitigation for existing facilities.

Being more strategic in your public engagement efforts

C Davis, J DeSimone, E Cohen

Presenting author: **Cathlyn Davis**, University of Maryland Center for Environmental Science, cat.davis@umces.edu

Birds are declining, and conservation efforts require shifting beliefs and behaviors. Bird banding stations and similar place-based research facilities are well positioned to connect with communities on conservation. However, little has been documented about their education engagement efforts including effective practices and impacts on visitors. To gain insight on the state of the field, we surveyed station leaders across North America (n=54), and found that most stations (87%) pursue public engagement and target a wide range of outcomes related to avian research and conservation. The visitors we surveyed at two of these stations were predominantly white, could easily access the station, sought immersive nature experiences, and may only have moderate interest in learning about conservation. Visitors did not only gain knowledge about birds and their habitat but also had positive changes in their attitudes about science and scientists more broadly. Public engagement strategies that build from theory can help increase the efficacy of engagement experiences by (1) aligning long-term conservation goals with short-term, measurable outcomes and the specific tactics that achieve these outcomes and (2) enhancing knowledge gain outcomes with others, such as demonstrating scientists' transparency, shared values, and willingness to listen. Strategic engagement might also help expand the diversity of visitors in terms of their demographics and prior interest in birds and conservation.

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Operating a publicly accessible banding station: balancing integrity of research, training of students, and substantive public engagement**J Owen, K Taylor, R Stewart***Presenting author: Jennifer Owen*, Michigan State University, owenj@msu.edu

The Michigan State Bird Observatory operates a long-term bird banding station, the Burke Lake Banding Station, with the central goal of conducting research on the stopover biology and health of migrating landbirds each fall and training university students in field-based research. In 2013, after a couple years of conducting research, we began to invite members of the public to visit the station and observe the entire process – from capturing birds in mist-nets to the processing, banding, and releasing. Our goals were simple; we wanted to be transparent about how we conducted scientific research and we wanted to foster a deeper connection to nature through birds. Additionally, we wanted to provide students opportunities to engage with the public and gain skills in science communication. Overall, being a fully accessible banding station has been a success and impactful to our local community in ways we did not fully appreciate in 2013. People are eager for these hands-on opportunities that instill passion and inspire people of all ages, and more specifically, foster curiosity about the foods and habitats that support birds throughout their annual cycle. It is our hope that visiting the station and learning about the relationship between the habitat, availability and quality of food, and health of migratory birds will lead to an appreciation for the role of science in advancing knowledge and to promoting better land stewardship practices. We will share preliminary data on assessing visitor experiences and how that information will guide a more strategic approach to public engagement efforts in the future.

Manomet Observatory: Engaging the public in long-term bird research through participatory science and experiential learning**E Dalton***Presenting author: Evan Dalton*, evanndalton@gmail.com

Since the first bird was banded on site in 1966, Manomet Observatory has placed a heavy emphasis on education and public engagement. Given our suburban location, visiting groups from schools and various interest groups have been mainstays at the migratory banding station for decades. Over time, our approach to education has changed; gone are the days where merely showing a bird in the hand moves the societal needle. Although this can be an effective tactic to spark interest, the need for outcome-driven goal-setting is increasingly apparent as we are often faced with a lack of public buy-in for the work we conduct. Through recent changes to our educational approach, Manomet educators strive to achieve our goal of increasing awareness of and appreciation for bird science and the connections between ecological health and human well-being. Our newly developed educational modules feature real-world data from our research operation and involve participants in the process of collecting additional data. Aside from raising awareness for the conservation goals of our work, this method builds public trust in the scientific process as well as the practitioners. Although this case study pertains to a migratory banding station, our framework is applicable to any informal scientific setting where elevating public awareness and trust are desired outcomes.

Engaging the public in watershed restoration with bird banding**M Fyelling, T Rodriguez, E Greene, R Domenech, R Brandl***Presenting author: Megan Fyelling*, University of Montana Bird Ecology Lab, megan.fyelling@mso.umt.edu

The Bird's-eye View Education Program integrates public education and scientific monitoring in the Upper Clark Fork River Basin (UCFRB) of western Montana. The UCFRB has been degraded by over 100 years of mining and smelting activities and is the largest contiguous federal Superfund site in the nation. We began conducting long-term education and outreach programs in 2010, inviting the public to observe research at songbird banding stations and Osprey (*Pandion haliaetus*) nests. We engage with members of the public about the local history of mining, Montana's bird community, and ecological restoration of the watershed. We host high school and undergraduate interns, volunteers, summer camp groups, and members of the community who often arrange repeat visits. We believe the legacy of mining and

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restoration activities should include public outreach so that land-use decisions in the future do not compromise the integrity of the ecosystems that support the region. Birds can not only be used as bio-indicators to measure restoration success, but they are also impactful tools for engaging the public. We aim to interact with the community in a way that promotes scientific literacy and stewardship of this important watershed. Results from an assessment show that participants leave with a positive attitude toward the outdoor science experience and a general knowledge of the riparian ecosystem. In our presentation, we will build on these prior efforts to explore how a strategic approach to engagement can help articulate and broaden outcomes to ensure we meet our scientific literacy and watershed stewardship goals.

***A race to the start: Understanding the biotic and abiotic drivers of timing of breeding and the consequences of breeding early in a changing world**

A Sutton, N Freeman*Presenting author: Alex Sutton, alexosutto@gmail.com*

The decision of when to breed is an important determinant of individual fitness. However, despite a multitude of studies investigating the intraspecific relationship between timing of breeding and reproductive performance, less is known about why the strength of this relationship varies between species. Furthermore, environmental change has the potential to alter the relationship between lay date and fitness, but there is still a limited understanding of what mechanisms drive these differential responses to change environmental conditions. We propose that the potential effects of environmental change on the relationship between timing of breeding and fitness are dependent on 2 primary factors: (1) the potential constraints imposed by breeding early and (2) the drivers of higher fitness of early breeders. We first summarize multiple hypotheses proposed to explain why breeding early, either based on absolute date or relative to conspecifics, increases fitness. We then summarize the factors that may constrain when individuals initiate breeding, including limits on the ability to advance their lay date or extend the length of their breeding season under favorable conditions. Understanding constraints on the timing of breeding allows for the identification of obligate (single-brooded species that do not attempt to breed after a specific date) and facultative (predominantly multi-brooding species that have long breeding seasons) early breeding species that are likely differently affected by climate change. Finally, we propose a simple mathematical formula that incorporates the costs and benefits associated with early breeding to quantify how climate change could influence the benefits of early breeding and either mitigate or exacerbate the costs. Our cost-benefit approach provides a clear framework to predict how species may shift the timing of their breeding to maximize fitness in a changing world.

Phenological shift and climate change: why does responsiveness among birds vary?

K Gurney*Presenting author: Kirsty Gurney, Environment and Climate Change Canada, kirsty.gurney@ec.gc.ca*

Across diverse avifauna, global climate change continues to alter the timing of seasonal events (i.e. phenology). Within and among species, however, the degree to which shifts in phenology match variation in climate differs substantially, and the roles of life history traits and environmental factors in determining phenological responsiveness remain poorly understood. Our ability to predict how ongoing environmental change will affect wildlife is thus limited. To address questions concerning the ecological and environmental drivers of phenological responsiveness among birds, we have conducted studies in multiple species, including ducks, geese, and shorebirds. By using different proxies to estimate climate variation and then quantifying relationships between these proxies and nest initiation dates, we have identified interspecific patterns and have also tested hypothesized mechanisms (migration distance, early versus later breeding) that might explain observed variation. Taken together, our results suggest an important role for organismal differences (i.e., related to physiology) in driving inter- and intraspecific differences in responsiveness. Although we have found less evidence that differences in the magnitude of environmental change experienced by different groups drives variability in responsiveness, this apparent spatial uniformity warrants further study. Further, our research highlights that ongoing monitoring of how

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birds shift timing of life history events in response to climate variability – while also testing for the cues that explain observed responses – is critical to improving future predictions of the impacts of ongoing global change.

The relative importance of temperature, precipitation, snowpack, NAO and ENSO on the spring migratory timing of North American landbirds

B Tonelli, C Youngflesh, T Cox, M Neate-Clegg, E Cohen, M Tingley*Presenting author: Ben Tonelli, bttonelli@ucla.edu*

Climate change is shifting the migratory and breeding phenology of birds resulting in a multitude of downstream ecological effects. Despite decades of studies conclusively determining the near-ubiquitous temporal advancement of bird arrival, an understanding of how climate change might lead to variable shifts across populations, species, and communities remains hampered by limited spatial and taxonomic sampling. In this study, we analyzed 88,965 site-specific arrival dates from 222 bird species over 21 years to investigate the role of temperature, snowpack, precipitation, the El-Niño/Southern Oscillation, and the North Atlantic Oscillation on the spring arrival timing of North American birds. Across species, we find that interannual variation in bird arrival on breeding grounds is most strongly explained by temperature and snowpack, and less strongly by precipitation and climate oscillations. Sensitivity of arrival timing to climatic variation on the breeding grounds exhibited spatial nonstationarity, being highly variable within and across species, highlighting the importance of ecological and geographical context in predicting climate change responses. A high degree of heterogeneity in phenological sensitivity to climatic variation across phylogenetic and geographical space suggests diverging responses to ongoing climatic changes at the population, species, and community scale, with potentially negative demographic and ecological consequences.

Inconsistent shifts in warming and temperature variability are linked to reduced avian fitness

C Taff, R Shipley*Presenting author: Conor Taff, cct663@gmail.com*

As the climate has warmed, many birds have advanced their breeding timing. However, as climate change also changes temperature distributions, breeding earlier might increase nestling exposure to either extreme heat or cold. Here, we combine >300,000 breeding records from 24 North American birds with historical temperature data to understand how exposure to extreme temperatures has changed. Average spring temperature increased since 1950 but change in timing of extremes was inconsistent in direction and magnitude; thus, populations could not track both average and extreme temperatures. Relative fitness was reduced following heatwaves and cold snaps in 11 and 16 of 24 species, respectively. Latitudinal variation in sensitivity in three widespread species suggests that vulnerability to extremes at range limits may contribute to range shifts. Our results add to evidence demonstrating that understanding individual sensitivity and its links to population level processes is critical for predicting vulnerability to changing climates.

***Relative breeding timing and reproductive success of a resident montane bird species**

L Whitenack, B Sonnenberg, C Branch, A Pitera, J Welklin, V Heinen, L Benedict, V Pravosudov*Presenting author: Lauren Whitenack, University of Nevada Reno, lauren.whitenack@gmail.com*

The phenological match-mismatch hypothesis predicts that animals that better synchronize critical life history events with the peak availability of their primary food source should have higher fitness. If phenological match-mismatch determines breeding success, most individuals in a population may be expected to breed simultaneously within a given year because selection has favored mechanisms that allow for the tracking of optimal food abundance. Therefore, individuals that breed too early or too late

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relative to the bulk of the population ('peak' of breeding) should experience decreased fitness. Using 11 years of data, we investigated the effect of relative breeding timing on breeding success in resident mountain chickadees (*Poecile gambeli*) across two elevations in the Sierra Nevada mountains, USA. Chickadees that bred during the peak of nesting did not have the highest breeding success; instead, birds that bred early performed best at high elevation, while at low elevation early and peak nests performed similarly. In contrast, late nests consistently performed the worst. Breeding success decreased linearly with relative timing at both high and low elevations, and the relationship between breeding success and timing differed among years. Our results suggest that phenological match-mismatch may not be the main driver of within-year variation in breeding success in animals residing in montane environments.

Early is relative – fitness consequences of the absolute and relative timing of reproduction in three species of hole-nesting birds

J Burant, N Freeman, A Sutton*Presenting author: Joseph Burant*, Netherlands Institute of Ecology, j.burant@nioo.knaw.nl

Life history theory posits animals should optimize their timing of reproduction to maximize their fitness. For birds living in seasonal environments, the optimal timing of reproduction will depend on the timing and width of peak food availability. Individuals may optimize their reproductive success, both in absolute terms and relative to their contemporaries, by timing egg laying such that food availability is increasing and/or near its zenith during the critical stages of offspring development; selection favours early lay dates. However, shifting abiotic and biotic conditions, such as climate and (its effects on) food availability, may affect changes in the fitness consequence of early laying. We test these hypotheses using 68 years of data from long-term studies of hole-nesting birds breeding at four sites in the Netherlands, focusing on three species: Eurasian Blue Tit, Great Tit, and European Pied Flycatcher. We examined the effects of absolute and relative timing of reproduction on multiple components of fitness, including brood size, number of fledglings, adult survival, offspring recruitment, and lifetime reproductive success. Consistent with our theoretical framework and previous work in these study populations, we show that while lay dates have advanced the fitness consequences of early laying are species-specific and vary through time. In general, brood size, number of fledglings, and offspring recruitment were positively influenced by absolutely early lay dates (save for the most extreme), but there were negative effects of laying either earlier or later than the average conspecific breeding in the same year. Female survival was less influenced by lay date. Thus, selection on the absolute and relative timing of egg laying influences lifetime reproductive success, favouring increasingly earlier lay dates, while fitness is maximized by individuals who optimize their timing to annual conditions.

Post-fledging survival as a potential mechanism for variation in the timing of breeding among songbird species

T Jones, M Zammarelli, M Webster, S Kaiser, S Sillett*Presenting author: Todd Jones*, Smithsonian's National Zoo and Conservation Biology Institute, Migratory Bird Center, jonestm@si.edu

The timing of breeding has an important impact on reproductive performance and individual fitness. In migratory birds, early breeding is considered widely advantageous across species, with early breeders often exhibiting higher reproductive performance through larger clutch and brood sizes, higher nest success, and more fledglings produced. Notably, there are also single brooded species that do not begin a nesting attempt beyond a particular date, even when there appears to be enough time and resources to do so. Thus, central to phenological research are questions of why all individuals do not choose to breed early? And why there is strong selective pressure against some species having longer breeding seasons? Most research seeking to answer these questions has focused on pre-fledging parameters of adult fitness, such as the number of young fledged in a season. Consequently, we still have a poor understanding of the role of critical juvenile life stages, such as the post-fledging period, on the timing of breeding in songbirds. To help fill this knowledge gap, our research compares seasonal variation in post-fledging survival between the Black-throated Blue Warbler (*Setophaga caerulescens*) and Ovenbird (*Seiurus aurocapilla*) at the Hubbard Brook Experimental Forest, NH, USA; two species that exhibit

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differences in the timing and duration of their breeding seasons. Preliminary results from our study suggest that post-fledging survival may be a key mechanism underlying variation in the timing of breeding, and likely the benefits of early breeding, among songbirds species.

***Environmental drivers of female reproductive investment in egg quantity versus quality in a grassland sparrow**

N Freeman, E Sroor, H Castro-Miller, K Hobbs, M Reynaldo, K Silber, N Mohankumar, N Wright, A Boyle

Presenting author: Alice Boyle, Kansas State University, aboyle@ksu.edu

Female investment in reproduction is a critical component of life history that influences both the fitness of the female and her offspring. Oviparous females can allocate energy into egg size and/or clutch size and this allocation can vary over lifetimes and among species. However, less is known about whether investment decisions shift within breeding seasons and the factors that influence female's reproductive strategies at the individual and population level. We studied the endogenous and exogenous factors associated with variation in female reproductive investment by measuring 860 eggs from 240 clutches laid by Grasshopper Sparrows (*Ammodramus savannarum*) between 2014 – 2019 at the Konza Prairie Biological Station in Manhattan, Kansas, USA. As the breeding season progressed, females laid heavier eggs and smaller clutches indicating a shift in investment toward fewer but high-quality young. Females that were heavier than expected given their body size laid heavier and larger eggs, but maternal body condition was not related to clutch size. Brood parasitism by Brown-headed Cowbirds (*Molothrus ater*) reduced the number of Grasshopper Sparrow eggs in nests but did not reduce the total number of eggs a female incubated. Pre-laying ambient temperature and precipitation were not associated with egg size. However, females tended to lay more eggs under rainier conditions. Overall, we provide evidence that both endogenous and exogenous factors shape female reproductive investment. Understanding how reproductive strategies respond flexibly to multiple sources of selection and mediate key trade-offs that influence demographic rates and can be used in forecasting population growth in a changing world.

***Avian conservation in a changing world through citizen science and inclusivity**
M Burgess

Presenting author: Murry Burgess, Mississippi State University, mlb1016@msstate.edu

The changing environment impacts humans just as much as birds. Including elements of citizen science and inclusivity into avian conservation improves our ability to manage populations in urban environments while simultaneously involving and improving the lives of people in urban environments. This presentation covers current issues in urban avian ecology, citizen science, inclusivity, and how to combine all of the above into scientific work.

Causes and consequences of male-biased sex ratio in the Gray-crowned Rosy-finches of St. Paul Island, Alaska

E Greene, W Anderson, S Taylor, R Montgomerie, B Lyon

Presenting author: Erick Greene, University of Montana, erick.greene@mso.umt.edu

Most gray-crowned rosy-finch populations have male-biased adult sex ratios but the mechanisms responsible are poorly understood. We are investigating whether this 2:1 bias in adult sex ratios on St Paul Island is the result of a biased primary sex ratio and/or sex differences in survival. Adult annual survival rates are the same for males and females, based on two years of study, so the first year of life is crucial to understanding this bias. Many of these finches nest in human structures, enabling a robust investigation of the primary sex ratio (so far 132 nestlings and 42 fledglings). Our observations suggest that the excess of adult males in this population is responsible for some intriguing reproductive strategies. Rosy-finches form socially monogamous pair-bonds where both members of the pair raise the brood. With the biased sex ratio, half of the males each year fail to obtain a social mate such that their reproductive success is entirely via extra-pair paternity. As a result, extra-pair mating strategies are overt,

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well-developed, and possibly unique in this species.

Candidate genes correlated with island gigantism in North American rosy-finches (*Leucosticte* sp.)

E Funk, W Anderson, G Spellman, K Winker, J Withrow, E Greene, B Lyon, R Montgomerie, S Taylor

Presenting author: **Scott Taylor**, University of Colorado Boulder, scott.a.taylor@colorado.edu

The North American rosy-finches (*Leucosticte* sp.) are a clade of alpine and Arctic tundra specialist songbirds that breed from the Aleutian and Pribilof islands to coastal mainland Alaska, and south in western North America above the tree line throughout mountainous regions to northern New Mexico. Recent work investigating their evolutionary history provided evidence for (i) widespread gene flow between species and subspecies, (ii) modular genetic architecture underlying the plumage traits used to distinguish species and subspecies, and (iii) rapid adaptation to high-elevation environments. Here we investigate the two island-dwelling subspecies of the Gray-crowned Rosy-finch, *L. tephrocotis umbrina* and *L. t. griseonucha*, that are as much as double the body mass of their mainland counterparts. Both subspecies weigh significantly more than expected from the latitudinal relationship between body size and winter temperatures in mainland populations. Further, using whole-genome data, we also examine the genetic basis of rosy-finch island gigantism using complementary FST and GWAS approaches, which implicate several candidate genes known to be related to body mass and body size in bovids, chickens, and nematodes.

Novel genes identified as underlying beak and feather morphology in an alpine finch species

E Robertson, T Brown, S Deitch, E Zavaleta, C Bossu, K Ruegg

Presenting author: **Erica Robertson**, Colorado State University, ericacnrobertson@gmail.com

Identifying the genes underlying local adaptation helps us understand fundamental questions in evolutionary biology and can guide conservation by elucidating the genetic diversity that allows adaptation to environmental change. In this study we investigated the genetic basis of beak and feather morphology in the Sierra Nevada Grey-crowned Rosy Finch (*Leucosticte tephrocotis dawsoni*), performing a genome wide association study (GWAS) on whole genome sequence data. We found 10 single nucleotide polymorphisms (SNPs) associated with beak morphology and 8 SNPs associated with feather morphology. Two of the genes associated with the beak SNPs were then identified to be potentially related to beak development. The first is Rho GTPase activating protein 26 (ARHGAP26), part of the Rho GAP gene family involved in regulating actin cytoskeleton dynamics. This gene is similar in function to ARHGAP28, a gene associated with environmental adaptation in the Brown-capped Rosy Finch. A second gene of interest is APC down-regulated 1 (APCDD1) which acts as an inhibitor to the BMP and the Wnt pathways, both well established as important to beak development. Neither of these genes has been identified previously as contributing directly to beak development. Two genes were identified as associated with feather morphology, of which desmocollin 1 (DSC1) has been associated with hair growth in pangolin and mice but is as yet unstudied in birds. Our results contribute to understanding the genetic basis of traits that undergo local adaptation and suggest novel roles of these genes in beak and feather development.

***A mechanistic statistical model to identify genomic adaptation in spatially structured populations of Rosy-Finches in heterogeneous environmental conditions**

N Goel, M Hooten, K Ruegg, C Bossu, E Zavaleta

Presenting author: **Nikunj Goel**, University of Texas at Austin, nikunj410@gmail.com

As global temperature rises, high-altitude species face extinction risk due to the rapid contraction of thermally suitable habitats. Theoretical and empirical studies suggest that local adaptation and gene flow

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may rescue these species by introducing beneficial alleles. However, identifying these adaptive genetic variants poses several statistical challenges, such as accounting for the uncertainty in allele frequency estimates from raw sequencing data and propagating this uncertainty through a mechanistic evolutionary model of local adaptation. Here, we present a Bayesian model to identify potential adaptive genetic variants in Brown-capped Rosy-Finch metapopulation that are distributed across the Southern Rocky Mountains of Northern America. The Bayesian model consists of three hierarchical layers. In the first layer, we model the uncertainty in local allele frequencies arising from sequencing errors and finite sampling. In the second layer, we explicitly model the stationary distribution of allele frequencies that are subjected to evolutionary forces-such as selection, mutation, migration, and drift. Finally, in the third layer, we model selection coefficients as a function of the environmental covariate. Thus, our work demonstrates how to build scalable processed-based statistical models to identify genomic signatures of local adaptation.

***Using whole genomes to conserve and understand the Wallowa Rosy-Finch (*Leucosticte tephrocotis wallowa*)**

P Bolton, E Funk, H Watts, S Taylor, B Vernasco

Presenting author: **Peri Bolton**, peri.bolton@gmail.com

Alpine habitats are experiencing significant ecological changes associated with rising global temperatures. Understanding how such changes are influencing alpine-dependent species is limited by a lack of information on their ecology and population status. The North American rosy-finches (Genus: *Leucosticte*) breed in the high elevation mountain ranges that maintain permanent snow. The Wallowa Rosy-Finch (*Leucosticte tephrocotis wallowa*) is restricted to the small and relatively low elevation Wallowa Mountains of Northeastern Oregon and is listed as a sensitive species by USFS. Recent phylogenomic work on most of North America's rosy-finches found weak structure and gene flow among species and subspecies but did not include the Wallowa Rosy-Finch. Therefore, to develop robust management strategies we need to understand how genetically distinct the Wallowa population is from the rest of the North American rosy-finches and begin to understand their population health through levels of inbreeding and genetic diversity. After an expedition to conduct the first non-lethal sampling of Wallowa Rosy-Finches, we sequenced whole genomes from eight Wallowa Rosy-Finches. The Wallowa Rosy-Finch shows similar levels of weak differentiation as other mainland species and sub-species do from each other. However, despite the small area and low elevation of the Wallowa Mountains, we do not find substantially reduced heterozygosity or genetic diversity compared to the already low genetic diversity in all rosy-finches. We discuss how our results can be used to inform conservation of the Wallowa and North American rosy-finches.

***Analysis of fecal DNA reveals spatial variation in the diet of breeding rosy-finches**

B Vernasco, T Brown, J Skelton, H Watts, E Zavaleta, M Jusino

Presenting author: **Ben Vernasco**, Whitman College, benvernasco@gmail.com

Diet represents a fundamental axis of ecological variation that can shape how species respond to environmental change and patterns of diversification. Rosy-finches are a recently diverged group that breed on islands of alpine habitat found across the Western United States. Breeding rosy-finches rely on seeds and insects, but spatial and temporal variation in rosy-finch diet has yet to be quantified. Filling this knowledge gap is important to understanding the causes of phenotypic variation between groups of rosy-finches and why populations may differentially respond to climate-mediated environmental change. Here, we use multi-marker fecal metabarcoding techniques to quantify spatial and temporal variation in insect and plant consumption by breeding rosy-finches. Fecal samples were collected from four sites across three mountain ranges, representing two subspecies of the Gray-crowned Rosy-Finch that occur at different elevations and have contrasting bill morphologies. Samples from one mountain range were collected from 2 sites and one of the sites was sampled at the beginning and end of July, which spans the incubation, nestling, and fledgling period for the mountain range. Our design facilitates quantification of dietary variation within and between mountain ranges allowing for examination of spatial and temporal

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variation in breeding rosy-finch diet. We identify strong differences between subspecies and mountain ranges in the richness and composition of insect and plant items consumed. Our results provide novel insight into potential ecological sources of variable responses to environmental change and causes of phenotypic variation between populations of an alpine-dependent songbird.

***Inferring breeding origins of Rosy-Finches overwintering in New Mexico using stable hydrogen isotopes**

W Watson, C Borgman, S Cox, E Duvuvuei, T Wright, A Lawson

Presenting author: Whitney Watson, wwatson@nmsu.edu

Climate change is projected to affect certain parts of the globe disproportionately, with high latitude and high elevation areas undergoing more rapid changes. With these changes comes concern for species which occur exclusively in these areas. The three North American species of Rosy-Finch - Brown-capped (*Leucosticte australis*), Black (*L. atrata*), and Gray-crowned (*L. tephrocotis*) - breed in tundra or alpine tundra biomes and migrate to lower elevations or latitudes during the winter. Although all three species are particularly vulnerable to climate change, we have limited knowledge of their breeding ecology and migratory movements due to the remote nature of their breeding grounds. In this study, we used stable hydrogen isotope analysis to gain insight into the breeding origins of individuals captured during the winter to infer migratory connectivity of breeding and nonbreeding locations. We analyzed the stable hydrogen isotope composition-measured in $\delta^2\text{H}$, or the ‰ ratio of deuterium (^2H) to protium (^1H)-of 200 feather samples from each of the three Rosy-Finch species collected in the Sandia Mountains of central New Mexico between 2005 and 2022. Through this work, we have been able to ascertain breeding distributions of Rosy-Finches that overwinter in the Sandia Mountains and examine the breeding site fidelity of individuals which returned to this region during multiple winters. This research has the potential to provide valuable information on Rosy-Finch migratory connectivity and life history to inform management initiatives aimed at conserving these high-altitude specialists, their associated biomes, and other similar climate-threatened species.

Estimation of survival and migration timing of two Rosy-Finch species using RFID encounter data

C Cox, J Gardner, K Savides, C Latimer, R Norvell, H Gaya, C Rushing

Presenting author: Cody Cox, University of Georgia, codycox75@uga.edu

Rosy-Finches comprise a genus of songbirds that breed in remote, alpine habitats and winter in lower montane elevations across the western U.S. Inaccessible breeding season habitat and semi-nomadic winter movements have limited research on Rosy-Finch demography, preventing reliable estimates of survival rates in the face of growing threats. We used Radio Frequency Identification (RFID)-equipped bird feeders at three sites in northern Utah to passively monitor wintering populations of two Rosy-Finch species: the widespread Gray-crowned Rosy-Finch (*Leucosticte tephrocotis*) and range-restricted Black Rosy-Finch (*Leucosticte atrata*). Due to challenges estimating daily survival rates for nomadic species, we used a robust design to group detections into three-day intervals. We then developed a hierarchical multi-state capture-recapture model to estimate survival and migration phenology of each species. We tagged 320 Gray-crowned Rosy Finches and 62 Black Rosy-Finches from fall 2018 to spring 2022. Tagged individuals were detected a total of 129,408 times by our RFID feeders. Our model produced the first within-season survival estimates for these species, which were comparable to those found in similar species. Our approach also allowed estimation of wintering-site arrival and departure phenology, which indicated that multiple populations of both species visit the feeders: individuals that overwinter at the feeder sites and individuals that pass through during migration. Our estimates of Rosy-Finch survival and migration timing can inform management and provide baselines in the face of climate change. Our approach can be applied to estimate demographic rates in other species of conservation interest that readily visit feeders.

Where we started and how it went; the story of Idaho's breeding surveys for

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Black Rosy-finches**T Regan, S Knetter, S Thompson***Presenting author: Tempe Regan, Idaho Fish and Game, tempe.regan@idfg.idaho.gov*

Idaho is home to a considerable portion of the breeding range of Black Rosy-finches (*Leucosticte atrata*); an S2 (impaired) Species of Greatest Conservation Need in Idaho. Because of difficulty accessing and safely surveying the rugged alpine terrain these birds use for nesting and breeding, relatively little is known about their range, distribution, and life-history traits. In the summer of 2019, we initiated a pilot study targeting Black Rosy-finches; in 2020, we expanded these surveys across all alpine habitat in Idaho. We drew a spatially-balanced random sample of 4x4 km grid cells that contained $\geq 25\%$ alpine habitat in areas of the state with higher-quality alpine and $\geq 5\%$ alpine habitat in areas with lower-quality alpine habitat. We conducted surveys between July 1 and September 1 each summer from 2019 - 2023 using point count methods and distance sampling to assess occupancy, abundance, and detection probability. Across all years, we conducted 257 surveys within 27 different mountain ranges, detecting 1241 individual birds on 667 occasions. Prior to our work, there were only 18 observations of Black Rosy-finches during the breeding season in Idaho. Other studies have noted that Brown-capped (*Leucosticte australis*) and Black Rosy-finches are most strongly affected by presence of cliffs, snowpack and elevation; we will assess how these, and other habitat and topographical variables affect Black Rosy-finch occupancy in Idaho. We will also examine how detection probability varied by a suite of variables, to increase our survey effectiveness and refine model estimates.

Banding results of wintering Brown-capped, Gray-crowned and Black Rosy-finches at the same location in Estes Park, Colorado over a 22-year period
S Rashid
Presenting author: Scott Rashid, Colorado Avian Research and Rehabilitation Institute, pygmyowl15@gmail.com

Examining our late fall/winter and early spring banding data over a 22-year period shows a steady decline of rosy-finches in Estes Park, Colorado. Having reviewed our data of more than 5500 rosy-finches (of all three species) banded, we have documented a steady decline within the species. Using walk-in traps baited with sunflower seed, we capture large numbers of rosy-finches, frequently more than 100 birds in a day. Each bird is identified by species, brown-capped, gray-crowned (including the Hepburn's race), and Black Rosy-finches. Each bird is then weighed, their wing and tail is measured, their sex is determined then released. Looking at the recoveries of our banded birds both recovered by us and others, were hoping to find that rosy-finches are not in decline but rather have moved to other areas of the west to spend the winter, as rosy-finches are being observed in multiple locations in Colorado each winter. However, we are not obtaining recoveries of many banded birds compared to the numbers of birds we have banded.

***Opportunistic citizen science data reveal shifts in the breeding distribution of a common alpine bird across the Fennoscandian peninsula**
K Brunk, J Hagelin, T Ergon
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The threat of climate change is particularly acute for species in arctic and alpine habitats, where changes are happening the most rapidly. While species are generally expected to shift their ranges northward and upslope in response to changing climates, actual measured shifts in species distributions have been mixed and sometimes unexpected. We tested whether the occupancy dynamics of a common and iconic montane bird, the bluethroat (*Luscinia svecica*), conform to expectations under climate change. Specifically, we leveraged opportunistic citizen science data from across the Fennoscandian peninsula over the last 39 years to test the hypothesis that the breeding distribution of bluethroats has shifted towards higher latitudes and higher elevations. We analyzed over 900,000 observations of bluethroat and 12 background species (to establish non-detection), using spatio-temporal occupancy modeling in a Bayesian framework. We found that the occupancy probability of bluethroats has declined significantly

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over the past four decades and that this decline is particularly striking at lower elevations and latitudes. Our work demonstrates that even common and globally stable species are at risk of breeding habitat loss under the looming threat of climate change.

***Introduced trout shift bird community composition at alpine lakes in the Sierra Nevada, California**

M Clapp, G Patricelli

Presenting author: **Mary Clapp**, The Institute for Bird Populations, mclapp@birdpop.org

Introduction of non-native fishes into over 50% of the Sierra Nevada's historically fishless watershed profoundly has profoundly restructured the aquatic food web, resulting in lower native invertebrate diversity and the endangerment of endemic taxa such as the mountain yellow-legged frog (*Rana sierrae/muscosa*). However, the extent to which the effects of trout introductions cascade into the terrestrial environment is less well understood despite the two habitats being linked by a substantial transfer of nutrients from lake to land via aquatic insect emergences. We hypothesized that the community composition, diversity, and overall abundance of birds differs between fish-containing and fishless lakes due to the reduction of a potentially important prey source. We conducted lakeside bird surveys in Sequoia and Kings Canyon National Parks at 39 fish-containing and fishless lakes between the years 2014-2020 and quantified insect emergence between lake types using sticky traps. Avian community composition differed between fish-containing and fishless lakes, driven largely by turnover. In addition, fish eradication at one lake between 2016-2019 allowed us to conduct a BACI (Before, After, Control, Impact) case study to assess changes in the avian community following fish removal. Overall avian abundance increased more than two-fold at the fish-removal lake relative to the control lake, and two insectivorous bird species appeared that were not detected in any previous surveys at that lake. This study reinforces the importance of studying aquatic and terrestrial habitats as interdependent systems and further motivate the conservation of fishless lake habitat in the Sierra Nevada's alpine waters.

***Fine-resolution historical breeding distribution and niche of Sierra Nevada Gray-crowned Rosy-Finch (*Leucosticte tephrocotis dawsoni*) indicates the importance of snowpack**

R Goljani Amirkhiz, K Leitner, G Hong, T Brown, E Zavaleta

Presenting author: **Reza Goljani Amirkhiz**, rgoljani@ucsc.edu

Mountaintop species are considered vulnerable to climate change, as declines in the availability of alpine habitats potentially escalate their risk of extinction. Quantifying their historical distributions, and understanding what environmental factors shape their niche, can help us understand how changes in these factors have affected their distributions to date and shed light on likely future responses. We compiled historical records of the Sierra Nevada Gray-crowned Rosy-Finch (*Leucosticte tephrocotis dawsoni*, GCRF), an endemic, alpine-breeding taxon, from museums and literature. We utilized a presence-available approach and developed a Bayesian Zero Inflated Negative Binomial model to analyze the GCRF's historical relative abundance and distribution. Based on a suite of hypotheses, we developed seasonal and annual bioclimatic raster layers for the period of 1950-1980, which covers the time period of our historical records. We also developed topographic and land cover raster layers to represent the breeding habitat of this species. Through a variable selection process, we identified the most important factors that shaped the historical distribution and relative abundance of GCRF. We projected the best model to the Sierra Nevada mountains in California at 1km spatial resolution. Annual precipitation as snow was the most important factor, with GCRF favoring areas of intermediate snow totals. We found positive relationships between summer snow water equivalent, vector ruggedness measure (a topographic variable representing cliff nesting habitat) and species relative abundance. We observed negative quadratic relationships between GCRF's relative abundance and both distance to lakes and the frequency of spur and hollow landforms. The prediction map showed that in the mid-20th century, areas with the highest habitat suitability for this species potentially were mainly within and around Sequoia and Yosemite National Parks, King Canyon and Sierra National Forests in

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Mapping the abundance and habitat of the Sierra Nevada Gray-crowned Rosy-Finch (*Leucosticte tephrocotis dawsoni*)**T Brown, R Goljani Amirkhiz, E Zavaleta***Presenting author: Timothy Brown*, University of California Santa Cruz, timbrown@ucsc.edu

The decline in summer snowpack is a critical concern for alpine specialists, such as the Sierra Nevada Gray-crowned Rosy-Finch (*Leucosticte tephrocotis dawsoni*), whose breeding seasons in high-altitude ecosystems are synchronized with spatiotemporal resource availability. Our study examined the influence of key habitat features on breeding habitat for this species. Using hierarchical distance sampling models, we estimated Rosy-Finch density and distribution across 27 high-elevation sites in California from 2018 to 2022. Our integrated approach, which combined point counts with observer distance-based detection probabilities and habitat factors, allowed us to estimate detection probability and relative abundance simultaneously while accounting for imperfect detection in unmarked populations. Our results indicate that the relative abundance of Rosy-Finches was positively associated with proximity to cliffs and snow patches, and negatively associated with the presence of woody vegetation. These findings provide an understanding of habitat preferences and lay the groundwork for developing a predictive map that employs raster layers to depict potential breeding sites, pinpointing areas of highest suitability defined by key predictors including annual snow levels, weather, and topographic variables. These insights underscore the critical role of specific habitat features, particularly persistent summer snowpack, in supporting Rosy-Finch habitat, highlighting the species' vulnerability to climate change. This habitat suitability map, informed by our empirical findings, will support monitoring of Rosy-Finch distribution changes over time and space to guide conservation planning.

****Environmental heterogeneity and abiotic drivers influence population density and constrain habitat for the range-restricted Brown-capped Rosy-Finch (*Leucosticte australis*)****K Bernier, A Seglund, E Zavaleta***Presenting author: Kathryn Bernier*, University of CA, Santa Cruz, bernier.kathryn@gmail.com

Species select habitat at nested spatial scales, from the population level down to individual needs. The Brown-capped Rosy-Finch's (BCRF) alpine cliff-nesting habitat is limited to the Southern Rocky Mountains, and could be affected by disproportionate climate warming at high altitudes. Not all potential breeding habitats are suitable for BCRF due to microhabitat and spatial variation. Our study goals in BCRF breeding areas were to (1) measure population density, and (2) identify variables and mechanisms that further restrict BCRF and influence spatial variation in breeding density. We surveyed breeding BCRF (2018-2020) using modified line transect distance sampling and by comparing used to available habitat. We intersected spatial data layers such as terrain ruggedness, temperature, and snowpack with BCRF presence to identify scales of effect on bird density. Estimated overall density ranged from 16.1-20.9 BCRF/km² by year. BCRF densities were not uniform within alpine breeding basins, but were higher near potential cliff nesting sites, snow, and rocky substrates. Probability of BCRF increased with elevation (range 3422-4106m). BCRF presence was unrelated to water resources like alpine lakes. BCRF foraged preferentially on snow and sparsely vegetated areas. These findings suggest that potential climate change effects, including decreased snowpack, earlier snowmelt, and increased vegetation density, could negatively affect BCRF in the future. Studying species-habitat associations at multiple scales improves understanding of current habitat use, distribution and abundance and can help guide species management in an uncertain future.

Alpine Songbird Habitat Associations and Preferences Amidst a Changing Climate: Black Rosy-Finches (*Leucosticte atrata*)**C Brown, N Rosenberger, G Barrile, K Gerow, A Chalfoun***Presenting author: Carl Brown*, Biodiversity Research Institute, carl.brown@briloon.org

Alpine systems are among those predicted to be the most affected by a rapidly changing climate. Upslope

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movements and shifts in avian composition in response to changing climate are well documented, yet the specific habitat associations and needs of many alpine birds remain uncharacterized. We evaluated the breeding abundance of a suite of songbirds inhabiting alpine habitats in the Rocky Mountains, USA. Focal species included the cliff-nesting Black Rosy-Finch (*Leucosticte atrata*), ground-nesting American Pipit (*Anthus rubescens*), and woody vegetation obligate, White-crowned Sparrow (*Zonotrichia leucophrys*). We conducted line-transect surveys for birds across seven mountain ranges and 46 sites in Northwestern Wyoming during 2016–2017 with transects repeated three times per breeding season (N = 170 total visits). Habitat metrics included alpine and woody vegetation cover, temperature (Heat Load Index; HLI), and distance to cliff. Black Rosy-Finches increased with proximity to cliffs and were inversely associated with woody and alpine vegetation. The abundance of American Pipits decreased with the amount of woody cover and proximity to cliffs. The abundance of White-crowned Sparrows increased with increasing woody vegetation and HLI. Our results demonstrate the unique niches occupied by different alpine songbirds with implications for the effects of changes to alpine habitats with on-going climatic change.

Finding cause for optimism in avian conservation

A Cox, R Boughton*Presenting author:* **Andrew Cox**, U.S. Fish and Wildlife Service, William_Cox@fws.gov

The magnitude of conservation challenges that exist at local and global scales can leave people feeling overwhelmed and pessimistic about the future. This ecological grief may be especially profound for conservation professionals, who often directly witness environmental loss. Nevertheless, many of us need a semblance of positivity in our professional lives to operate effectively, and support from the general public is reliant in part upon positive messaging that conveys our conservation successes. I present a path toward pragmatic professional optimism derived from work in Florida, USA, where numerous conservation successes have occurred in the face of climate change, invasive species, anthropogenic disasters, land use change, and other environmental stressors.

We can do this! Engaging new and broad audiences across the full annual cycle for research and conservation funding

S Kendrick*Presenting author:* **Sarah Kendrick**, U.S. Fish and Wildlife Service, sarah_kendrick@fws.gov

In our world of overwhelming conservation challenges and limited funding resources for migratory bird conservation, we must be creative. Many migratory landbird species are in steep decline and efforts to identify limiting factors and address these threats across the full annual cycle remain important. Meanwhile, many existing conservation audiences and heretofore unengaged new audiences may be interested in supporting research or conservation action through funding support or field assistance. Three recent tracking projects across the Western Hemisphere with international bird-conservation partners have been crowd-funded by Missouri birding groups. That support was matched by state and federal agencies to fill knowledge gaps for declining songbird species of conservation concern, including Cerulean Warbler (*Setophaga cerulea*), Golden-winged Warbler (*Vermivora chrysoptera*), and Wood Thrush (*Hylocichla mustelina*). This funding has allowed for new tracking data for science and has built lasting working relationships across the range of our shared migratory birds. Another research initiative for tracking Wood Thrush has engaged over 40 partners across 25 states and 7 countries via state agencies and international partners, resulting in the largest Motus-tagging project to date with across the species full annual range. As with any successful initiative, personal communication and connection continue to be the cornerstone of these co-produced successes, and education on these issues and a focused ask may allow us to engage these overlooked audiences of supporters. By leveraging funding and collaboration through partner projects including non-traditional, or often overlooked, audiences, we can build a stronger study design, ownership of the work, greater probability of conservation actions using the findings, and sense of community across the hemisphere for migratory birds.

Researching to understand and acting to change: Neotropical milestones in the

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conservation of migratory birds**C Gomez, N Bayly***Presenting author: Camila Gomez, SELVA, camila.gomez@selva.org.co*

The last decade has seen a significant improvement in our understanding of migratory bird ecology throughout the annual cycle. It has also opened our eyes to ongoing negative population trends for many species, several of which are deeply concerning. Our improved scientific understanding and realization of the urgent need to act for change, have also led to the formation of broad collaborations and numerous working groups that are pushing for migratory bird conservation to be at the frontline of conservation action at multiple scales. SELVA's Migratory Ecology program has been one of the cogs at the center of this process since 2009. Here, we describe how our work began by tackling some of the most basic knowledge gaps for migratory landbirds in the Neotropics and has now organically evolved into the coordination and implementation of science-based conservation actions and education programs producing positive outcomes for migratory birds on their Neotropical non-breeding grounds. In the last five years, we have reached thousands of individuals across the Neotropical region with education programs highlighting the wonders and perils of migration, initiated habitat restoration projects in five regions in Colombia and Costa Rica, planted over 40,000 trees providing resources for migratory birds and we are currently supporting the formal protection of over 100,000 ha of mid-elevation forest in priority non-breeding areas in Colombia for species like Cerulean and Canada Warblers. We have learned that having sound knowledge about the ecology of species adds immense value to any planned conservation actions and believe that the process of generating scientific knowledge should always accompany conservation strategies to make them efficient, adaptable, and verifiable.

Savanna and woodland restoration is benefiting disturbance dependent birds**F Thompson***Presenting author: Frank Thompson, University of Missouri, thompsonf@missouri.edu*

Many bird species of conservation concern in the Eastern U.S. are associated with early stages of forest stand development or open ecosystems (i.e., savanna and woodlands) sustained by fire. Many studies have investigated effects of traditional forest management on forest birds in the eastern U.S. and in general early successional birds respond positively to forest regeneration practices for 5-15 years post-harvest if sufficient canopy is removed. Open forest management consisting of tree thinning and periodic prescribed fire to restore and maintain open woodland and savanna is an alternative to closed forest management. A possible concern for the application of fire and thinning in open-forest management for early successional species is that too much tree retention could reduce the benefit for early successional species. This concern seems unfounded, however, as restoration and management of oak and pine-oak woodland management benefits many early successional or disturbance-dependent birds. Abundance of bird species of concern such as Field Sparrow, Blue-Winged Warbler, Eastern Towhee, Prairie Warbler, White-Eyed Vireo, Yellow Breasted Chat, Eastern Whip-Poor-Will and Chucks-Will-Widow is positively related to prescribed fire and thinning or the resulting vegetation structure (reduced canopy cover, tree density). We recently translocated Brown-Headed Nuthatches to restored pine woodland in Missouri where they were extirpated, and they have been breeding there for four years now. Large-scale restoration efforts such as the U.S. Forest Service Collaborative Landscape Restoration Program are restoring open forest ecosystems at a landscape scale and benefitting disturbance dependent birds.

Collective action reverses the population decline of a coastal-dependent shorebird – An American Oystercatcher success story**S Schulte, J Brush***Presenting author: Janell Brush, Janell.Brush@myfwc.com*

The population of the eastern subspecies of the American oystercatcher (*Haematopus palliatus palliatus*) was in decline as recently as 15 years ago. Recent surveys conducted by Manomet documented a 45% population increase in the US wintering population. This incredible conservation success is a result of cumulative local conservation actions guided by range-wide partner coordination, management, research,

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and shared objectives. The Oystercatcher Working Group was formalized as coastal biologists recognized the unique opportunity for collaborative year-round conservation and management to benefit the American Oystercatcher. Population recovery initiatives dedicated resources to oystercatcher conservation which increased capacity, funding, and the size, scope, and scale of the American Oystercatcher Working Group. The working group members applied collective knowledge and developed strategies to improve reproductive outcomes. The working group has achieved countless research, management, and conservation milestones to benefit the oystercatcher. These accomplishments have stemmed from site-specific, regional, and range-wide projects and have contributed significantly to the overall understanding of oystercatcher ecology and informed the development of effective management and conservation actions to conserve the species.

From discovery to recovery: 50 plus years of science, conservation, and outreach lead to delisting in the Kirtland's Warbler

N Cooper, P Marra*Presenting author: Nathan Cooper*, Smithsonian Migratory Bird Center, nathanwands@gmail.com

After decades of fire suppression and high rates of nest parasitism by Brown-headed Cowbirds, Kirtland's Warbler populations plummeted to just 167 males left in the wild and were declared endangered in 1966. After more than 50 years of concerted effort by the recovery team, agency partners, and scientists the species was delisted in 2019. In this talk, we will tell the story of the Kirtland's Warbler from its discovery in 1851 to its successful delisting in 2019. We will highlight the critical science, conservation, and outreach efforts that led to delisting, and discuss what the future holds for this conservation-reliant species.

The recovery of the red-cockaded woodpecker: a conservation success story on a large scale.

J Walters*Presenting author: Jeffrey Walters*, Virginia Tech, jrwalt@vt.edu

The red-cockaded woodpecker (*Dryobates borealis*) (RCW) was listed as endangered in 1970. The first region-wide assessment of the species' status in the mid-1980s revealed that more than half of RCW populations were declining or extirpated, and another quarter were likely declining. None were increasing. In contrast, a species status assessment (SSA) in 2018 classified 72% of the 46 largest RCW populations (>30 family groups) and 82% of 33 smaller populations (10-30 groups) as increasing during the previous 25 years. Five populations were declared recovered during that period, and the species is now in the process of being down-listed to threatened. What transpired between the mid-1980s and today was driven by a paradigm shift in management. Two management tools, construction of artificial cavities to promote new group formation and prescribed burning to improve habitat condition have been especially critical to the success of the 'new' management. Use of artificial cavities was a byproduct of research on the species' breeding system, illustrating the value of basic research generally, and in behavioral ecology specifically, to conservation and species management. The recovery of the RCW has transformed conservation of southern pine ecosystems from the 'woodpecker wars' and clear-cutting of pine habitats in the 1980s to the longleaf pine ecosystems restoration, Safe Harbor programs on private lands and effective conservation partnerships of today, benefitting a multitude of other species. The recovery of the RCW and the pine ecosystems it inhabits is a conservation success story on a large scale.

Rethinking our relationship with nature: the binational restoration process for the Colorado River delta

O Hinojosa-Huerta*Presenting author: Osvel Hinojosa-Huerta*, Cornell Lab of Ornithology, osvelhh@gmail.com

After decades of desiccation caused by water policies focused on consumptive uses, the Colorado River delta in Mexico has been under a binational recovery process, shifting the relationships between water

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users and nature. As a result of a binational agreement between Mexico and the United States signed in 2012, 40,000 hectares of priority wetlands have been restored and protected. These restoration outcomes are based on the collaboration between agencies, ngo's, academic institutions, and water users from both countries, with continuous work on governance, science-based planning, public policy, mechanisms to secure land and water for nature, and the operation of a monitoring program to evaluate the ecosystem responses. Restoration has been based on hydrological modelling, restoration ecology, landscape design and hydraulic engineering, to optimize the available resources to enhance habitat conditions. As a result, bird populations and diversity has increased, as well as the ecosystem services provided to local communities. A new binational agreement was signed in 2017, extending the commitments of funding and water for restoration for another 10 years. This multidisciplinary and collaborative approach is being replicated to build capacity along the Pacific Coast of Latin America through the Coastal Solutions Fellows Program. The goal is to cultivate, train, and catalyze a collaborative network of scientists, conservationists, policy experts, architects, sociologists, and engineers to improve coastal resiliency and shorebird conservation in Latin America. Five cohorts of CSF fellows are already implementing science-based cross-sectoral conservation projects in 37 priority sites from Mexico to Chile, with an estimated conservation impact on 180,000 hectares and benefits to at least 28 shorebird species.

Waterfowl in North America as a model for positive conservation outcomes

K Kemink, S Stephens, M Brasher

Presenting author: **Kaylan Kemink**, Ducks Unlimited Inc., kkemink@ducks.org

In the early 20th century, waterfowl numbers were severely depleted due to the combined impacts of a prolonged drought and over-harvesting, and a complete ban on duck hunting was being considered. Concerned about these challenges, a group of sports-hunters advocated for policies that would eventually help guide hunting seasons and licensing, putting an end to market-hunting and the un-checked depletion of the duck populations. Over the next 50 years American waterfowlers went on to champion other landmark conservation legislation including the Duck Stamp Act, Swampbuster, the Conservation Reserve Program, and the North American Wetlands Conservation Act (NAWCA). These policies, among others, financed programs and partnerships that protected vital habitat for North American waterfowl populations. For example, NAWCA would ultimately serve as a foundational funding mechanism for the North American Waterfowl Management Plan, which represented a partnership among the federal governments of the U.S., Canada, and Mexico; non-profits; and state/provincial governments geared towards conserving wetlands for migratory birds and other wildlife across North America. Without these policies, many waterfowl populations would not have recovered from their slump in the early 20th century nor have been sustained into the present day. Despite the positive impacts leveraged from policies in the waterfowl world, habitat loss continues to be one of the greatest threats facing North American populations. Across their range, waterfowl are challenged with the continued conversion and degradation of their habitat and extreme drought and climate change have created additional stress. To maintain a positive trajectory, vigilance and renewed supporter numbers are needed along with a continued commitment to habitat conservation from agencies at all levels as well as non-profit groups.

Using the Power of the Endangered Species Act to Delist the Interior Population of Least Tern

R Fischer, C Lott, P Hartfield

Presenting author: **Richard Fischer**, US Army Engineer Research and Development Center, Richard.A.Fischer@erdrc.dren.mil

The interior population of Least Tern (*Sternula antillarum*) was removed from Endangered Species Act (ESA) protection in 2021. The path to recovery was paved with significant modeling; and range-wide monitoring, management, and conservation planning. In addition, a key to success was interagency cooperation among the U.S. Army Corps of Engineers, U.S. Fish and Wildlife Service, and multiple state, federal and non-federal stakeholders. Although the ESA is one of the most comprehensive and successful pieces of legislation in our nation's history, there often is confusion and conflict, impeding its intended purpose. Much of this conflict has centered on ESA Section 7, and a failure to fully integrate

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interagency cooperation into conservation culture. Reliance almost exclusively on Section 7(a)(2), or formal consultation, has for the most part, resulted in maintaining the status quo, at best, and at worst, in piecemeal losses and declines of the population and habitat baselines of listed species, with the result of potentially increasing restrictions to Federal programs. This presentation will address a paradigm shift with the use of ESA Section 7(a)(1), which strives for proactive conservation, and improving listed species baselines, to recover the interior population of least tern. When appropriately implemented, Section 7(a)(1) has the potential to facilitate federal agency missions through minimizing and distributing costs and increasing conservation effectiveness; without section 7(a)(1), cost of compliance with section 7(a)(2) likely will continue to rise into the foreseeable future.

***Saving the snail kite: invasive prey and novel ecosystems promote population recovery**

R Fletcher, M Beatty*Presenting author: Meghan Beatty, meghan.beatty@ufl.edu*

Invasive exotic species are spreading rapidly throughout the planet. These species can have widespread impacts on biodiversity by creating novel species interactions and ecosystems that native species experience. We provide evidence of rapid, widespread changes in the endangered snail kite (*Rostrhamus sociabilis*) across its North American range with the invasion of a novel prey, the island apple snail (*Pomacea maculata*), a much larger congener of the kite's native prey. In just over one decade since invasion, the U.S. snail kite population went from near extinction to increasing over four fold in population size. Snail kite distribution has closely tracked the spread of this invasive species and has led to snail kites using novel ecosystems that they formerly did not occupy. While experiments show that snail kites do not prefer exotic snails, the substantial increase in resource availability led to increases in kite survival and reproduction, which ultimately increased both viability and sexual selection on morphology. Our findings suggest evolutionary change may be imminent and underscore that even long-lived vertebrates can respond quickly to invasive species. Further, these results highlight that novel ecosystems can provide unexpected surprises for native species, which in this case has led to renewed hope for the persistence of this endangered species and has provided decision-makers much needed time to develop comprehensive strategies to promote population recovery.

Stable isotopes and diet: using a captive bird model to test for factors affecting trophic discrimination and model performance.

K Gurney, H Classen, R Clark*Presenting author: Kirsty Gurney, Environment and Climate Change Canada, kirsty.gurney@ec.gc.ca*

Discerning assimilated diets of wild birds using stable isotopes is well established where potential dietary items are isotopically distinct. With the advent of mixing models, and Bayesian extensions of such models (Bayesian Stable Isotope Mixing Models, BSIMMs), the statistical techniques used for these efforts have increased rapidly. The accuracy with which BSIMMs quantify avian diet, however, depends on several factors including uncertainty in tissue discrimination factors (TDFs; $\hat{\tau}$) and identification of appropriate error structures. Whereas performance of BSIMMs has mostly been evaluated with simulations, here we test the efficacy of BSIMMs by raising domestic broiler chicks (*Gallus gallus domesticus*) on four isotopically distinct diets under controlled environmental conditions. $\delta^{13}\text{C}$ of liver, but not feather, was negatively related to the rate at which individuals gained body mass. For $\delta^{15}\text{N}$, we identified effects of dietary group, sex, and tissue type, as well as an interaction between sex and tissue type, with females having higher liver $\delta^{15}\text{N}$ relative to males. For both tissues, BSIMMs allocated most chicks to correct dietary groups, especially for models using combined TDFs rather than diet specific TDFs, and those applying a multiplicative error structure. These findings provide new information on how biological processes affect TDFs and confirm that adequately accounting for variability in consumer isotopes is necessary to optimize performance of BSIMMs.

***DNA metabarcoding primer choice influences the dietary characterization of an**

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aerial insectivore, the Purple Martin (*Progne subis*)**A Forsman, J Fischer, J Siegrist, S Gaspar, K Fraser, B Hoenig**Presenting author: **Anna Forsman**, Colby College, aforsman@colby.edu

DNA metabarcoding has become a popular approach for characterizing taxonomic composition of mixed DNA samples such as those extracted from feces and stomach contents. This approach leverages DNA sequence variability among taxa within conserved regions of the genome (e.g., COI), which allows for classification of community constituents by comparing resultant reads against a reference database. Despite the potential power of this technique, it is becoming increasingly clear that the lab methods used, in particular the PCR primer set(s) selected, significantly influence (a) the ability to differentiate between taxonomic units and (b) the classification efficiency of taxonomic units to known taxa, preferably to genus or species. Here, we describe our work to optimize methods for differentiating and classifying insect taxa from fecal samples collected from purple martins (*Progne subis*) to comprehensively characterize the diet of this and other insectivorous bird species. We found a clear difference in both detection and classification efficiency between primer sets used for library prep, which in turn influenced conclusions drawn about dietary ecology across sampling sites. These results will be discussed in the context of a similar study conducted by the authors to use DNA metabarcoding for characterizing more complicated diet compositions in omnivorous species.

****Evaluating the role of aquatically derived fatty acids in aerial insectivorous birds****C Génier, M Pilecky, C Guglielmo, K Hobson**Presenting author: **Corrine Génier**, Western University, cgenier@uwo.ca

In North America, declines in aerial insectivorous birds have been attributed to habitat loss and changes in climate, but the quality of insect prey may also be a contributing factor. Fatty acids, a major part of the building blocks of lipids, are important for the development, growth, and health of young birds. Insects emerging from waterbodies supply more of the beneficial fatty acids (i.e. long-chain omega-3 polyunsaturated fatty acids, LC-PUFA) than terrestrial insects. Some birds may also be able to synthesize LC-PUFA from readily available short-chain fatty acids that can be abundantly found in terrestrial insects. More terrestrial-associated birds such as barn swallows (*Hirundo rustica*) may then rely on a higher fatty acid conversion compared to more riparian purple martins (*Progne subis*). Using bulk $\delta^2\text{H}$ measurements of tail feathers, fatty acid profiles of blood plasma, and $\delta^{13}\text{C}$ compound-specific stable isotope analysis, we evaluated how aerial insectivores acquire key fatty acids through their diet or internal synthesis. We found that both wild barn swallows and purple martins can synthesize their own omega-3 and -6 LC-PUFAs and that omega-3 conversion efficiency was higher than previously reported in riparian tree swallows. Fatty acid conversion, to an extent, can be a way to compensate for deficient diets and our study is the first to demonstrate key differences in conversion efficiencies among aerial insectivorous birds.

Consequences of living near water: An assessment of wetland influence on riparian and upland boreal passerine diets using multiple endogenous markers**K Kardynal, K Hobson**Presenting author: **Kevin Kardynal**, University of Saskatchewan, kevin.kardynal@ec.gc.ca

Wetlands are an important component of the boreal forest landscape that may contribute valuable resources to the diets of terrestrial birds through subsidies of aquatic-emergent insects. Consumption of aquatic emergent insects provides higher levels of beneficial long-chain polyunsaturated fatty acids (LCPUFAs) but may also expose birds to deleterious contaminants such as mercury. Understanding the contribution of aquatic-to-terrestrial flows of nutrients to passerine diets will help determine the potential importance of wetlands to boreal songbirds and aid in their conservation. We sampled multiple boreal passerine species and insects at varying distances (0 to >1 km) from wetlands during the breeding season in the boreal forest of central Saskatchewan 2021-2023. We used feather stable isotopes ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$, $\delta^2\text{H}$), fecal eDNA, plasma fatty acids and feather and blood total mercury (THg) to determine if

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proximity to wetlands influences diets of several species. Isotopic niche space, diet composition and THg differed significantly between riparian (e.g. Swamp Sparrow *Melospiza georgiana*) and upland breeding species (e.g. Ovenbird *Seiurus aurocapilla*). Differences in these assays were also evident but weaker between upland breeding birds occupying habitats near (<100 m) and away (≥100 m) from wetlands. Multivariate statistics indicated that riparian species contained higher proportions of LCPUFAs with distance from wetlands driving this relationship. Together, these results indicate that wetlands are key drivers of exposure of boreal passerines to beneficial fatty acids and deleterious mercury. We discuss the potential trade-offs of living near water for boreal forest birds and how our results can contribute to the conservation of boreal wetlands.

***Insight into Wood Thrush diet in ecological forestry gaps during the post-breeding season using metabarcoding**

C Ziegler, A Bailey, E Bierer, S Latta, B Porter

Presenting author: **Cassandra Ziegler**, Duquesne University, cassandra.ziegler88@gmail.com

Ecological forestry gaps (EFGs), a method used by the Foundation for Sustainable Forests (FSF) charitable land trust in western Pennsylvania forests, removes unhealthy, unfavorable trees in forests to create small openings for early successional plant species to grow, encouraging native plant species growth and potentially supporting migratory bird diets while also improving forest health. Wood Thrush (*Hylocichla mustelina*), a declining species that breeds in mature forest habitat, is present in the EFGs during the post-fledging / pre-migration period. The habitat utilized during this time is critical to support complex bird diets preparing for autumnal migration. We hypothesize that Wood Thrush presence in the EFGs suggests utilization of the food sources made available by the early successional plant growth, with a presumed shift from consuming more arthropods to fruits during this period. DNA extracted from Wood Thrush fecal samples was amplified using arthropod primers (ZBJ) targeting the cytochrome c oxidase I (COI) mitochondrial gene and a novel combination of plant primers targeting the chloroplast trnL (UAA) intron. Results show that Wood Thrush primarily consume arthropods from families in orders Lepidoptera and Coleoptera, but show a more diverse consumption of plant taxa, including a mixture of mature forest and early successional plant genera. Additionally, more individuals consumed plant taxa throughout the season compared to arthropod taxa (June-August). These results indicate the importance of a variety of plant species from mature forests and early successional growth to support bird species. This study will aid in bird conservation, forest management, and habitat recovery efforts.

Yellowstone Birds: Ecology, Conservation and Management

D Smith, W Wehtje, D Tomback

Presenting author: **Douglas Smith**, dwsmith0526@gmail.com

Yellowstone National Park (YNP) is the world's first national park and as such is well protected and studied, except for birds. Formal bird monitoring did not begin until the mid-1980s and park-led research not until the late-2000s. This lack of attention is significant because there are over 150 breeding species and several species of conservation concern. One example is Trumpeter Swans. YNP was one of the last areas in the contiguous US where swans survived and park monitoring dates back to 1931. Other species of more recent monitoring are Bald Eagles, osprey, and Peregrine Falcons with datasets beginning in the mid-1980s; YNP was a peregrine release site for restoration. Beginning in 2008 a more rigorous monitoring and research program was implemented including an expansion of songbird and raptor surveys (including owls), research on golden eagles, common loons, trumpeter swans, harlequin ducks, ravens, and Clark's nutcrackers. Many of these projects were collaborative and were made possible by public-private partnerships. These projects revealed key management issues. Trumpeter swans were suffering from climate induced and human-caused nest failure leading to closures and installation of artificial nesting platforms. Fish nets set for lake trout and human disturbance led to loon mortality and nest failures. Songbird surveys were expanded past BBS surveys into many unique habitats such as old growth forests, burns, grasslands and riparian areas. The results of these studies led to management action and culminated in the book *Yellowstone Birds* which this symposium is loosely structured around. The book, program re-design, and research were all intended to increase visibility and focus on

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Yellowstone birds.

Trumpeter swans (*Cygnus buccinator*) in Yellowstone: the decline and ongoing recovery of an iconic species

D Smith, E Sheilds, W Long, R Shea, L Walker, J Rotella, W WehtjePresenting author: **Walter Wehtje**, Ricketts Conservation Foundation, wwehtje@rickettsconservation.org

The Trumpeter Swan (*Cygnus buccinator*) was once one of North America's most endangered bird species. Yellowstone National Park provided a refuge for the species during the late 19th and early 20th century when habitat destruction and hunting nearly drove this species to extinction. While swan numbers have recovered nationwide since the 1930s, the park's swan population declined from an average of 50-60 birds in the 1950s, to a low of two in 2010. The reasons for this decrease are obscure, but human disturbance during the nesting season and increased predator pressure on cygnets are two possibilities we will discuss. Despite no firm agreement on the reasons for this trend, the park decided to counteract this decline through a concerted reintroduction effort. Since 2012, captive-raised swan cygnets have been released inside the park every year, resulting in the establishing of three successful nesting pairs inside the park by 2023. While this outcome is encouraging, nesting habitat for this iconic species may shrink within the park during the next few decades. Climate models suggest that many wetlands within Yellowstone National Park will become more seasonal as the climate grows warmer and drier. Due to the swans' long nesting season (140 -160 days from egg laying to fledging), if wetland habitats dry up during the summer months, there may not be enough time for nesting swans to fledge young successfully under predicted climate conditions.

Harlequin Ducks of Yellowstone National Park: What we know, what we don't, and the state of current research

D Meattley, L Savoy, S PatlaPresenting author: **Dustin Meattley**, Biodiversity Research Institute, dustin.meattley@briwildlife.org

One of the most beautiful birds in Yellowstone National Park is also one of the region's least well-known or studied wildlife species. The Harlequin Duck, by waterfowl standards, is a relatively small, stout, charismatic bird, most recognizable by the male's striking colorful and seemingly odd-patterned appearance. Fittingly, the origin of the term 'harlequin' is in reference to the clown-like performers in Italian theater. Harlequin Ducks are among the family of waterfowl classified as sea ducks. As with most sea duck species, the Harlequin Duck occupies interior freshwater habitats during the spring and summer breeding season, and then migrates back to the ocean, utilizing the near-shore marine ecosystem during the longer, non-breeding portion of the year. Its current breeding range in Wyoming has been reduced and restricted to the northwestern regions including Grand Teton and Yellowstone National Parks, and the Bridger-Teton and Caribou-Targhee National Forests. Wyoming represents the most southeastern breeding population of harlequins in western North America, and they are currently designated as a Species of Greatest Conservation Need. Field observations over the decades, plus aerial surveys, indicate that Yellowstone National Park supports a significant portion of Wyoming's breeding harlequin population, hosting upward of 16-24 pairs (of an estimated 70 pairs statewide). As harlequins are specialists at remaining unnoticed and nest on remote breeding streams, inventorying this species is incredibly difficult and time intensive. In recent years, field studies of Yellowstone National Park and Wyoming's Harlequin Ducks have started to unlock some of the mysteries of the distribution of harlequins within the park and surrounding Greater Yellowstone Ecosystem, as well as movements of these birds from their breeding areas to the Pacific coast. Using traditional survey methods such as ground surveys and helicopter flights, as well as newer more advanced methods s

Loons in Yellowstone: Persistence of an Isolated Population

V Spagnuolo, J Fair, A Leavitt, D Smith, D Evers, W Wehtje, L WalkerPresenting author: **Vincent Spagnuolo**, Ricketts Conservation Foundation, vincent.spagnuolo@gmail.com

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In the 1900s, Common Loons (*Gavia immer*) experienced a population decline and northward range retraction throughout North America. The retraction created a small, isolated population in the Greater Yellowstone Ecosystem (GYE). This island population was understudied relative to many loon populations at the species' southern edge. In 2011, GYE loons experienced poor reproductive success, and some long-standing territories went vacant. Yellowstone National Park (YNP) and the Wyoming Game & Fish Department identified loons as a species of conservation concern, which sparked an extensive private-public partnership study to understand the issue and enact management actions to mitigate identified threats. Since 2013, the authors have conducted a comprehensive survey of loon presence and reproductive success in the GYE, and investigated threats to survival, reproduction, and habitat quality. Identified threats include human disturbance of nest sites and mortality as bycatch in gillnets set for lake trout control in Yellowstone Lake. We adapted well-established loon conservation strategies developed in other population areas to this unique population including nesting and brooding area closures, nest rafts, outreach, and education. The population fell to as few as 14 territorial pairs during our work but now numbers over 25 territorial pairs. Emerging threats include elevated levels of biotoxins produced by cyanobacteria, which impacts various lake-system trophic levels. Continued conservation of the GYE loon population by state and federal agencies in concert with non-profit and academic researchers will enable the persistence of this island population as well as offer unique research opportunities.

Environmental Drivers of Reproduction by Golden Eagles in the Northern Range of Yellowstone National Park

D Haines, V Dreitz, T Katzner, D Smith

Presenting author: David Haines, National Park Service, dbhaines@gmail.com

Golden Eagles (*Aquila chrysaetos*) are a North American species of conservation concern throughout their range. Within the northern range of Yellowstone National Park (YNP), territories of golden eagles occur at relatively high densities. However, average reproductive rates over the past ten years (2011-2023) have been low (productivity = 0.32, nest success = 27%), stimulating questions as to what environmental factors limit reproductive success. Hypotheses include extreme weather, variation in prey availability, and the recovery of large carnivores within YNP. We evaluated spatial and temporal components of golden eagle habitat that could explain reproductive output of eagles in YNP's northern range. Preliminary results indicate that increasing periods of prolonged precipitation during winter was negatively associated with apparent nest initiation. Nest success was negatively associated both with increased snow levels and with increasing periods of severe weather during early spring when eagles initiate nesting. Additionally, we found evidence to suggest that territories with more rugged terrain and in closer proximity to neighboring territories tended to have greater nest success than flatter, less densely packed territories. Our findings highlight potential drivers for the contrasting trends in territory density and nest success of YNP eagles and could be used to inform management of this population.

Peregrine Falcon presence within the Yellowstone National Park landscape

J Pagel, D Haines, D Smith, K Duffy

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We provide a synopsis of known Peregrine Falcon (*Falco peregrinus*) data from Yellowstone National Park (YNP), including cooperative work that helped its resurgence in the Rocky Mountains and Greater Yellowstone Ecosystem. YNP offers a unique higher elevation ecosystem to discern peregrine population resurgence, with most nest territories being in long-untrammeled areas having potential for unique prey and iconic nest sites. The first recorded sightings occurred in 1914, and later field efforts peaked in the mid 2010's, with continued monitoring of known territories to the present day. Nest site monitoring and limited nest data indicate that Peregrine Falcon eggshell thicknesses appear to be approaching pre-DDT thickness. YNP peregrines produce young at occupied known territories with a nesting success average of 72% per annum. We noted productivity varied per year; monitoring revealed an average output of 1.6 young per occupied territory, and 2.2 young per successful brood. Passerines and gulls have been found to be the most frequent prey, but we have recorded unusual prey items not seen elsewhere. We believe the peregrine population has resurged in YNP to levels where the park-centric population may have

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achieved a post de-listing stability of 32 known territories.

Territorial Common Ravens (*Corvus corax*) commute to distant anthropogenic foods in the Greater Yellowstone Ecosystem

J Marzluff, M Loretto, C Ho*Presenting author: John Marzluff, University of Washington, corvid@uw.edu*

Territorial birds typically restrict ordinary movements to remain near their defended foraging, nesting, and roosting sites. Territorial Common Ravens (*Corvus corax*) restricted movements to within ~8 km of the nest and roost during the breeding season. Throughout the year, they rarely traveled more than 10 km to natural foods (insects, small mammals, wolf kills). However, territorial ravens regularly commuted 30-50 km from their traditional roost sites on territory to anthropogenic foods. Such long-distance flights were non-stop and directly to areas where hunters regularly killed elk, bison, and deer or to sites where garbage and grease floating on wastewater were processed. During flights, ravens typically traveled 45 km/hr. In contrast, non-territorial ravens regularly traveled 20-30 km daily regardless of the season and type of food exploited. We suggest that the certainty of obtaining food of high caloric content repaid the energetic costs of commuting. A raven expends up to 1200 Kcal / day, which would be repaid with approximately 300 g of protein or 130g of fat. Obtaining this quantity of food by a dominant raven is possible throughout the year, but especially during the hunting seasons outside Yellowstone National Park. However, exploitation of anthropogenic foods in the Greater Yellowstone Ecosystem exposes ravens to risks (lead and other chemical contaminants). The apparent ease with which ravens travel to distant foods emphasizes the need to manage anthropogenic sources near rare species that are incidental prey of ravens.

Clark's Nutcracker spatial movements in Yellowstone National Park: Maintaining an iconic mutualism

D Tomback, K Li, W Wehtje*Presenting author: Diana Tomback, University of Colorado Denver, diana.tomback@ucdenver.edu*

Fundamental to species conservation planning is understanding important interspecific interactions. Whitebark pine (*Pinus albicaulis*), an ecologically important high elevation conifer, is declining rangewide from several threats including exotic disease. Clark's nutcrackers (*Nucifraga columbiana*) are primary seed dispersers for whitebark pine and key to maintaining the tree. In Yellowstone National Park (YNP), long-term monitoring confirms whitebark pine decline, but little is known about nutcracker population dynamics, seed resource use, and spatial movements. Questions concerning spatial use include whether birds have home ranges within YNP or whether ranges extend beyond park boundaries, how home ranges vary seasonally and annually, and if birds leave the park, whether they return (residency vs. emigration). In March 2021, we placed GPS tags with limited fixes and variable intervals on six breeding nutcrackers. Three were captured in Douglas-fir forest and three in spruce-fir forest. All birds remained in the vicinity of capture until late May/late June. One nutcracker repeatedly returned to the same area between trips to higher elevation forests in late summer, suggesting seed caching at lower elevations. In June, two birds left the park and overwintered outside park boundaries. In March 2023, five nutcrackers were captured in Douglas-fir forest and fitted with solar-powered doppler tags. Preliminary analysis of 95% confidence intervals for AKDEs for three birds ranged from 139 to 384 km² but for one bird was only 15 to 29 km². All home ranges included the point of capture. Two birds briefly visited locations outside YNP. In sum, all tagged birds remained within YNP or the Greater Yellowstone.

***Clark's nutcracker forest community visitation: Whitebark pine maintains a keystone seed disperser**

T McLaren, D Tomback, N Grevstad, M Wunder, W Wehtje, L Walker, D Smith*Presenting author: Tom McLaren, Klamath Bird Observatory, thm@klamathbird.org*

Clark's nutcrackers (*Nucifraga columbiana*) are obligate seed dispersers for the threatened whitebark

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pine (*Pinus albicaulis*), but they often use other conifer seed resources because of annual variability in cone production or geographic variation in whitebark pine availability. Whitebark pine is declining from several threats, including invasive disease, leading to potential population declines in both species. Where there are few additional seed resources, we propose that whitebark becomes the limiting resource supporting nutcracker populations. We established sites in five forest community types, including whitebark pine, lodgepole pine (*P. contorta*), Engelmann spruce (*Picea engelmannii*), limber pine (*P. flexilis*), and Douglas-fir (*Pseudotsuga menziesii*) to study how nutcrackers use conifer forests within Yellowstone National Park, and determine potential seed resources including whitebark pine's importance. We collected point count, conifer cone production, and forest community data, as well as seed resource use observations. We compared models estimating nutcracker density and its relationship to forest community type, seed harvesting time-period, year, site, and cone seed energy. Cone production varied across years indicating annual variability in available energy. Nutcracker density was best predicted by forest community type and harvesting time-period and was highest in whitebark pine stands during the mid-harvesting season. Nutcracker density was comparatively low for all other forest community types. This underscores whitebark's importance as a key seed resource for Clark's nutcracker in Yellowstone National Park. The potential for a downward spiral in the two species necessitates further monitoring and restoration action.

Passerines: Documenting the Little Ones

K DuffyPresenting author: **Katy Duffy**, katyduffy@mt@gmail.com

Passerines account for seventy-five bird species known to nest in Yellowstone National Park, with an additional twenty-three species that occur during summer, migration or winter. Because of concerns about severe declines in songbirds across North America, we conduct several studies that focus on these species. Point counts and line transects serve to monitor bird populations in several habitat types: riparian willows, grassland/sagebrush steppe, recently burned forests, and mature forests. In addition to point counts in riparian willows, a banding program occurs in this habitat type and follows Monitoring Avian Productivity and Survivorship (MAPS) protocol. Although only 1% of Yellowstone National Park consists of willows, this habitat type attracts the most nesting songbirds. We banded >1,300 individuals during the first six seasons. Surveys in grassland/sagebrush steppe document the diversity and abundance of species occurring in this habitat. We also initiated counts of birds in recently burned forests. Because wild land fires, augmented by warming and drying due to climate change, pose threats to mature mixed conifer habitats in the park, we count bird species and abundance in these forests. Counts in lodgepole pine forests found fewer than half the number of bird species when compared with more diverse forests.

Long-term population monitoring of bald eagle and osprey in Yellowstone National Park: patterns of decline and recovery in a high-elevation lake ecosystem

L Walker, D SmithPresenting author: **Lauren Walker**, Yellowstone National Park, lauren.seckel@gmail.com

Bald eagles (*Haliaeetus leucocephalus*) and osprey (*Pandion haliaetus*) are highly visible raptors that breed along waterways and lakes throughout North America and Yellowstone National Park. The invasion of the non-native lake trout (*Salvelinus namaycush*) to Yellowstone Lake in the early 1990s, and the subsequent decline in native cutthroat trout (*Oncorhynchus clarkia bouvieri*), has had diverse implications for the trophic web. Systematic and park-wide monitoring efforts of Yellowstone's bald eagle and osprey were initiated in 1984 and 1987, respectively. We analyzed patterns in eagle and osprey breeding populations, nesting success, and the number of young fledged to assess differences between species and locations within the park. Since 1984, the number of breeding pairs of eagles in the park has remained largely stable over time ($F_{1,37} = 0.65$, $p = 0.42$), increasing slightly in areas away from Yellowstone Lake ($F_{1,37} = 5.49$, $p = 0.02$). In contrast, osprey populations have declined since 1987 across the park ($F_{1,34} = 54.35$, $p < 0.001$) and both on and off the Lake (Lake: $F_{1,32} = 54.64$, $p < 0.001$; Non-Lake: $F_{1,34} = 9.97$, $p = 0.003$). The osprey decline on Yellowstone Lake has been particularly

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precipitous, with a peak presence of 62 nesting pairs in 1994 but none in 2021 or 2022. Differences between species reflect different dietary strategies. Bald eagles are a dietary generalist that feed on fish, waterbirds, and other resources, providing eagles some flexibility in responding to the dramatic decline in the native fish stock. In contrast, osprey are obligate piscivores well-suited for foraging on shallow-swimming and medium-sized cutthroat but not adapted for the deeper and larger lake trout.

Moving ahead: Improving the interface between research and management in Yellowstone National Park

D Tomback, D Smith, W Wehtje

Presenting author: **Diana Tomback**, University of Colorado Denver, diana.tomback@ucdenver.edu

Protected areas and the biodiversity they conserve are facing unprecedented challenges from local to global scales. Yellowstone National Park's bird program was not established until the mid-1980's and remained limited in scope and poorly supported until recently. Resources are stretched in managing or monitoring the 150 or more breeding birds and species of special concern which include migrants, year-round, or part-time park residents. In addition, many bird populations range across multiple jurisdictions in the Greater Yellowstone Region (GYR), complicating management. During the last 30 to 50 years, the GYR has experienced profound changes within and in proximity to the park, including the impact of climate change, increasing risk of wildland fire, carnivore restoration and riparian vegetation regrowth, the spread of invasive disease and species, increasing park visitation, and expansion of the built environment both regionally and locally. Focus on the bird program was timely, because research and monitoring indicate that many of the aforementioned factors are impacting avian biodiversity, habitats, and population persistence. In the symposium presentations, we have heard key case histories that illustrate issues and, in some cases, management solutions. In general, we suggest that research and monitoring information may provide insight into population declines, and some of these may be reversed or mitigated with management actions. In this overview and wrap-up session, the organizers and speakers answer questions and welcome input from the audience.

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Contributed Oral Presentations

****Discerning vocal activity patterns of Eastern Black Rails with Passive Acoustic Monitoring (PAM)**

B Kephart, S McRae*Presenting author: Bailey A Kephart, East Carolina University, kephartb22@students.ecu.edu*

The Eastern subspecies of the Black Rail (*Laterallus jamaicensis jamaicensis*) is one of the rarest marsh birds in North America, and was recently uplisted federally to 'Threatened'. Cryptic and secretive, Black Rails are notoriously difficult to observe, and their ecology and behavior are poorly understood. Passive acoustic monitoring using Autonomous Recording Units (ARUs) offers a minimally invasive strategy for detecting Black Rails. It can also be used to determine appropriate time windows for scheduling traditional callback surveys in specific geographic regions. In this study, we used ARUs to document the circadian and seasonal patterns of Black Rail calls over the course of two breeding seasons. We programmed ARUs to record continuously for 24 hours and between 17:00-10:00 hours at four study sites. Audio recordings were run through an automated software recognizer (BirdNET Analyzer GUI 1.0.2, Cornell Lab of Ornithology) trained with Black Rail calls from the local population as well as the Macaulay Library of Natural Sounds. We then manually verified flagged portions of recorded audio files. We used verified detections to determine how Black Rail calls were distributed over the 24-hour cycle as well as the breeding season (May-August). Preliminary results suggest peak calling activity occurred during late evening and early morning hours with calls occurring through the end of July. However, we detected more variability in circadian patterns among sites than expected. We relate these activity patterns to environmental variables. Our results will help inform future monitoring efforts for this imperiled species.

****Passive Acoustic Techniques to Monitor a Cryptic Galliform**

D Tonnessen, R Luna*Presenting author: David Tonnessen, davidtonnessenx@gmail.com*

Passive Acoustic Monitoring has been touted as an efficient and cost-effective method of monitoring wildlife but thus far has largely been deployed as a method of monitoring whales, songbirds, and amphibians. Effectively surveying for members of Galliformes requires different methods than for songbirds, and due to its secretive nature and little existing literature, no standardized survey protocol has been applied for the Montezuma Quail *Cyrtonyx montezumae*. In this study, we test the efficacy of using passive acoustics to estimate densities, comparing results with in-person flush surveys. With 40 Autonomous Recording units in the Davis Mountains of West Texas, we 1) use the BirdNET detection software to calculate Montezuma Quail densities, comparing results with physical observer flush-counts over corresponding detection radii, and 2) inspect phenology of vocal activity over wet and dry periods of a seasonal landscape. We expect to find 1) similar estimates in density between acoustic methods and flush-counts, and 2) higher vocal activity during wet periods. This is the first attempt at deploying passive acoustic techniques to estimate populations of a gamebird species, and could determine the best acoustic methods to monitor Galliformes in the future.

Performance and accuracy of unmarked abundance models with data derived from machine-learning classification of passive acoustic recordings

C Fiss, S Lapp, J Larkin, J Cohen, H Parker, J Larkin, J Kitzes*Presenting author: Cameron Fiss, University of Pittsburgh, fisscameron@gmail.com*

The ability to conduct cost-effective wildlife monitoring at scale is rapidly growing due to availability of low-cost autonomous recording units (ARUs) and automated species recognition. However, estimating abundance with such methods remains challenging because most abundance models require data difficult for low-cost monaural ARUs to gather (e.g., counts of individuals), especially using the output of automated species recognition. Models not requiring counts/distances to individuals in combination with low-cost ARUs could provide a means of obtaining abundance estimates for large-scale wildlife

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monitoring but remain untested. We collected avian data in forests of Pennsylvania in Spring 2020 and 2021 using both traditional point counts (PCs) and ARUs. We tested the ability of Royle-Nichols (RN) and time-to-detection (TTD) models to estimate abundance of two species from detection histories generated by applying a machine-learning classifier to ARU data. We compared abundance estimates from these models to estimates from the same models fit using PC data and to two additional models appropriate for PCs, the N-mixture and distance models. We found that RN and TTD models fit with ARU-based data produced abundance estimates congruent with PC-based models across all six sites. ARU-based estimates had confidence intervals that were on average 17.3% smaller than PC counterparts. This result was consistent across two species with differing abundance and habitat use patterns. Higher precision of models fit using ARU data is likely due to higher detection probability, which itself may be due to greater survey effort using ARUs and machine-learning classifiers to sample more time at any given point. Our results support the use of ARUs in abundance-based study applications, and thus may afford researchers a better understanding of habitat quality and population trends, while allowing them to make more informed conservation actions and recommendations.

Evaluating the performance of passive acoustic monitoring and BirdNET to monitor avian communities

P Panwar*Presenting author: Pooja Panwar, Dartmouth College, Pooja.Panwar.GR@dartmouth.edu*

Passive Acoustic Monitoring has emerged as a technological advancement to assess the impacts of environmental changes on avian diversity in space and time. Autonomous recording units (ARUs) can reduce the need for expertise in the field but their utility is limited by hardware costs and challenges in efficiently extracting species richness data from large audio datasets. Machine learning tools automatically identify bird vocalizations, which may reduce the expert time needed if classification is sufficiently accurate. In this study, we assessed the performance of BirdNET (a machine-learning approach to analyze large audio datasets) against the output of human-annotated recordings and point count surveys in the field to estimate the species richness of avian assemblages. We analyzed bird census and acoustic data collected at 100 locations in the forests of the northeastern US across the 2022 and 2023 breeding seasons. We extracted four 10-minute recordings from each location, manually annotated the species detected on recordings, and analyzed the recordings using BirdNET. We compared the species richness estimated from point count surveys, manually annotated recordings, and BirdNET output. The species richness of avian communities estimated from manually annotated recordings was similar to point count surveys. Our results show that BirdNET's precision for detecting common and abundant species in our study area was relatively high, but precision for some rare species was low. Advances in automated classifiers such as BirdNET provide the opportunity to expand bird research and monitoring efforts greatly and improve our understanding of avian communities.

*Evaluating the effectiveness of BirdNET Analyzer for detecting migratory landbirds in Minnesota

J Fuller, N Michel, D Gentry, M Worland*Presenting author: Jennifer Fuller, National Audubon Society, jennifer.fuller@audubon.org*

The use of autonomous recording units (ARUs) is rapidly growing in the field of avian monitoring. While in-person surveys are often limited by the availability of trained observers and survey duration, ARUs enable researchers to control survey timing and drastically increase sampling frequency and duration. This improves the probability of detecting species and accurately assessing characteristics such as species richness or individual species occupancy. However, until recently, ARU recordings were manually processed by human listeners, which is inefficient and highly time-consuming. Today, numerous publicly available classifiers exist to expedite this process, but these classifiers still require human-assisted validation to confirm whether they can accurately detect species of interest. We performed a pilot study examining the effectiveness of a popular classifier, BirdNET Analyzer, for detecting 24 different breeding landbird species within the Riverbend Nature Center, in Fairbault, MN. Three ARUs were deployed by the Minnesota Department of Natural Resources (DNR) May 11th through May 31st, 2023, for four hours after

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sunrise. ARU recordings were analyzed using BirdNET Analyzer, with up to 100 random samples per species extracted and validated manually in Raven Lite software as either true or false detections. We then identified species-specific confidence thresholds where we were 90-95% confident detections were true positives using a logistic regression. Our results identify species-specific thresholds for migratory landbirds in Minnesota, as well as examine the overall effectiveness of BirdNET Analyzer for remotely monitoring avian species in this region. These findings provide valuable insight for designing effective ARU analyses of migratory landbirds.

***Can individual movement behavior explain connectivity between isolated wetlands for an endangered raptor?**

C Poli, R Fletcher*Presenting author:* **Caroline Poli**, Caroline.Poli@myfwc.com

Functional connectivity, defined as the influence of the landscape on movement or flow of organisms, depends on habitat composition and animal responses to features of the landscape. However, as animals move among habitats, movement behavior and therefore selection of resources can differ in purpose and with age. Additionally, information on behavior is often not included in connectivity assessments, leading to a potential disconnect between connectivity estimates and actual movement. For the critically endangered Snail Kite, a wetland specialist, habitat selection during travel may differ compared to other behavioral states because traveling snail kites must move through non-wetland areas, often soaring at altitude. We therefore investigated the extent to which resource selection in Snail Kites differs during travel compared to other behaviors, and determined whether it is necessary to account for distinct behavioral states to fully understand connectivity. We collected GPS tracking information from 116 juvenile Snail Kites between 2018-2023 and validated connectivity from GPS-tagged birds against independently observed movements of color-banded Snail Kites. We found that birds are less selective during travel compared to other behaviors, and that between-patch habitat matters: considering resource selection (via least cost paths) was more important for understanding connections between wetlands than geographic isolation (straight-line distance). However, knowledge of behavioral state only improved connectivity estimates slightly. For snail kites, these results underscore the importance of wetland management for movement of birds, and show that the landscape can have strong impacts on populations and connectivity.

Investigating the Activity Pattern of Hudsonian Godwit Chicks Using an Automated Radio Telemetry Network

F Huang, N Senner*Presenting author:* **Feipeng Huang**, feipenghuang@umass.edu

Shorebird chicks at northern latitudes are under strict time constraints to achieve high growth rates. While the long daylight hours provide ample time to acquire food, movements associated with foraging lead to high rates of energy expenditure. To understand how flexible foraging behaviors are for shorebird chicks, we studied the fine-scale movement of Hudsonian Godwit (*Limosa haemastica*) chicks in Beluga, Alaska, using an automated radio telemetry network, a recent technological advancement that allows small animals to be tracked continuously. In the summers of 2022 and 2023, we fit 44 chicks with radio transmitters that relayed radio signal strength (RSS) values every 2-9 seconds to an array of nodes. We then derived the locations of the chicks and assessed how their movement rates changed over the course of the day, across the season, and in relation to weather conditions and resource availability. Our study will shed light on the degree to which shorebird chicks can behaviorally adjust their activity in response to the increasingly unpredictable environment under climate change.

****Diel activity of a winter adapted species at its southern range edge: behavioral responses to a temporally dynamic environment**

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Adaptive behavioral responses to fluctuating spatial and temporal patterns of available energy and predation risk are a critical determinant of a species' fitness. Ruffed grouse (*Bonasa umbellus*) are a forest-dependent, winter-adapted bird whose overwinter survival is strongly linked to dynamic winter conditions. During winter, grouse must balance their activity to reduce exposure to inclement weather conditions as well as reduce predation risk. We hypothesized that grouse are more active during the warmest times of day (i.e. diurnal) when the risk of cold exposure exceeds that of predation. However, when risk of cold exposure is low, we hypothesized that grouse will minimize temporal overlap with their primary predators (i.e., crepuscular). We used triaxial accelerometers to measure grouse activity across 2 winters (2022/23 and 2023/24) in Wisconsin. We evaluated the influence of winter temperature and snow depth on grouse activity patterns using a generalized additive mixed model. Results suggest that temperature is a significant determinant of grouse diel activity during winter. This study provides important inference into the adaptive capacity of this winter adapted species to rapidly changing winter weather at the southern edge of its range. Implications of these results on grouse survival and regional population persistence will be discussed.

Fruit-frugivore interactions from the Choco rainforests of northwest Ecuador**J Karubian, C Chenevert, L Anderson, T Lamperty, K Narasimhan, J Olivo, J Cabo, D Cabrera, L Carrasco Camacho***Presenting author: Jordan Karubian, jk@tulane.edu*

There is an abundance of fruit in most tropical rainforests, each representing an investment by the adult plant to successfully reproduce by having its seeds dispersed to a favorable site for germination. In the hyper-diverse Chocó rainforests of the community-led FCAT Reserve in northwest Ecuador, much of this dispersal is provided by iconic Neotropical frugivores such as toucans, umbrellabirds, and manakins. What factors determine which individual plant these birds will select to forage upon, and which they will snub? How many fruits will a bird consume, and thereby disperse the seeds of? These questions have enormous implications for plant fitness and, by extension, patterns of species-level and genetic-level floristic diversity. For frugivorous birds, these questions are likely to shape physiological condition and downstream behavioral interactions, potentially including mate choice dynamics. In this talk, we summarize recent advances in avian frugivory studies from the FCAT Reserve. From the plant perspective, we show how fruit removal at both canopy and understory palm species by large-bodied avian frugivores is shaped by a complex interplay of surrounding environment (surrounding fruiting trees), tree-level traits (height) and fruit-level traits (sucrose content). From the bird perspective, we use lek-breeding manakins to demonstrate how surrounding fruit abundances influence movement, behavior and indices of mating success. These findings highlight the need for more research at the intersection of animal behavior and plant ecology in tropical rainforests, and beyond.

****Diverse nonbreeding movement behaviors in a common, but understudied bird****E Williams, A Jahn, J Johnson, H Mann, C Gesmundo, P Taylor, P Marra***Presenting author: Emily Williams, Georgetown University, ffyngau@gmail.com*

Understanding how and why animals use space is core to virtually all aspects of ecology, from influencing individual fitness, to predicting impacts of global change. Yet, most of what we know comes from studies focused on the breeding season, which represents just a small percentage of the full annual cycle. To better understand the patterns and drivers of space use during the nonbreeding period, we tracked multiple populations of American Robins (*Turdus migratorius*) across their distribution, using small, high-resolution satellite transmitters during 2019–2024. We hypothesized that interannual variation in temperature and precipitation would influence differences in individual movement strategy and space used during winter. We quantified the nonbreeding space use behaviors of 108 individuals, and found that robins ranged from more territorial to nomadic in their movements during winter. We found that robins coming from breeding areas with greater interannual variation in snow conditions and temperature showed much greater displacement during winter than robins originating from breeding areas with less interannual variation in those conditions. Our results showcase the large variation in nonbreeding movement behaviors within a single species. Such variation likely typifies the flexibility inherent within

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species with large ranges, but which is also an important characteristic needed for keeping pace with ongoing environmental change. By examining intraspecific variation in space-use behaviors, we will not only gain a better understanding of the scale of space species need across the entire annual cycle, but also how species may track future environmental change.

***Songbird nest box occupancy and selection in vineyards of Napa Valley, California**

B Martinico, C Pham, F Jomaa, E MacDonald, E Wilson-Rankin, H Wilson, D Karp, M Johnson

Presenting author: Breanna Martinico, bmartinico@ucdavis.edu

Integrated pest management (IPM) often focuses on enhancing the control of pests by arthropod natural enemies (i.e., predators/parasitoids), but less work has focused on vertebrate predators of insect pests. In California, winegrapes are a key crop that may benefit from bird-mediated pest control of insect pests. Insecticide use by California winegrape growers has increased over time, with approximately 45M lbs applied in 2018. Promoting birds that are natural enemies of key winegrape pests could provide vineyard managers with alternatives to pesticides, especially on organic fields where fewer insecticides can be applied. Despite the potential for birds to contribute to IPM, more research is needed to understand and harness their benefits for winegrape growers. Our goal is to determine how to optimize nest box use by songbirds in vineyards and understand the associated pest management outcomes. In this study, we documented the use of songbird nest boxes to attract Western Bluebirds (*Sialia mexicana*) and Tree Swallows (*Tachycineta bicolor*) and investigated patterns of nest box selection in vineyards of Napa Valley, California. We surveyed existing songbird nest boxes ($n = 1,007$) at 17 vineyards and documented species occupancy, nest box attributes, and local habitat characteristics. We used generalized linear mixed-effects models to understand how occupancy is influenced by nest box attributes and local habitat. We found that both species preferred nest boxes in more open areas farther from wooded habitats and fitted with predator guards. Future work will examine the diet of both species, assess their capacity to affect pest numbers, and examine their response to local and landscape habitat features.

Nesting on new ground: Do human-made habitats provide refuge for breeding Nelsons Sparrows?

K Owen, M Mallory, N McLellan, J Nocera

Presenting author: Kiirsti Owen, kiirsti@gmail.com

The Acadian subspecies of Nelson's Sparrow (*Ammodramus nelsoni subvirgatus*) breeds in saltmarshes from northern Massachusetts to New Brunswick and eastern Quebec. In the Canadian Maritimes, these birds also successfully breed in diked agricultural lands (i.e., 'dikelands') that were originally created by Acadian settlers in the 1600s. Little is known about the reasons for or consequences of using dikelands for breeding. To fill this knowledge gap, we monitored nest fates in natural saltmarsh and human-made dike habitats. We collected fecal samples on adults and nestlings to examine which habitat type they were foraging in, and we also quantified competition and vegetative cover. We hypothesized that flood risk in saltmarshes played an important role in Nelson's Sparrows' decision to nest in dikelands given that the Bay of Fundy has the highest tides globally. Based on nest monitoring, we estimated higher overall nest success in dikelands than saltmarshes. Fecal sample analysis showed distinct differences in diet between birds using dikelands compared to saltmarshes. We also observed differences in vegetation and competition. These results suggest that the Acadian Nelson's Sparrow are able to take advantage of a readily available human-made habitat for breeding. With rising sea levels threatening coastal habitats, it's important to understand if coastal breeding birds can adapt to changes and what trade-offs exist for birds who shift to alternative habitats.

A mechanistic basis for the effects of extreme heat and agriculture on bird reproduction

K Lauck, P Gonzalez-Gomez, K Goldberg, D Karp

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Presenting author: **Katherine Lauck**, UC Davis WFCB, kslauck@ucdavis.edu

As climate change progresses, human-dominated landscapes expose birds to new temperature extremes by removing trees and other natural vegetation that insulate the understory. Our previous work has found that extreme heat disproportionately reduces bird nesting success in agriculture relative to forest. We tested for two mechanisms that could drive this interaction: increased thermoregulatory energy demands and reduced food provisioning to nestlings. We monitored Tree Swallow and Western Bluebird nestlings across 235 nest attempts during April-August 2021-2023 in California's Central Valley. We recorded nest box temperature and weekly nestling growth, corticosterone responses, and parental food delivery rates. We are using structural causal modeling to trace the direct and indirect effects of land cover types and nest box temperatures on nestling growth and survival through corticosterone responses and nest box visitation. Our initial results demonstrate that hot temperatures inside nest boxes significantly reduce Western Bluebird nestling growth in row crop agriculture and grassland (but not orchard and forest). For Tree Swallows, extreme heat reduced growth in row crop only. The additional stressors present in row crop agriculture (e.g. agrochemicals, human presence) may reduce nestling birds' resilience to hot temperatures. Our findings will suggest concrete ways to modify working landscapes to better accommodate birds as climate change progresses. Designing cooler nest boxes may increase nestling resilience to the direct effects of heat, whereas adding non-crop habitat to working landscapes to support food resources or provide thermal refuges for parents may offset reduced food provisioning.

****Avian Functional Trait Diversity in a Heterogeneous Agroecosystem****C Cormier, E Scordato***Presenting author:* **Christian Cormier**, Cal Poly Pomona, christian.j.cormier@gmail.com

Agricultural intensification can cause the functional homogenization of bird communities relative to natural environments. It has been proposed that bird communities in agricultural systems close to contiguous native habitats may experience reduced losses of taxonomic and functional trait diversity, but variation in functional diversity between native and agricultural habitats is highly context dependent. Here, we evaluated the functional diversity of bird communities in the Santa Clara River Valley (SCRV), a heterogeneous agroecosystem in Southern California. We have conducted seasonal point counts in avocado, citrus, and riparian habitats throughout the valley in order to calculate avian functional richness, functional evenness, and functional dispersion, which together provide a complementary assessment of a community's functional trait diversity. Preliminary analysis indicates that orchard bird communities have lower taxonomic diversity and functional richness compared to natural habitats, but avian communities in orchards closer to native habitats are more functionally rich relative to more isolated orchards. Orchards in general were more functionally even than natural riparian habitats, though there were not strong differences in functional dispersion. Across all trait metrics, avocado orchards had greater variation than citrus orchards or riparian habitats, indicating that orchard structure influences avian functional trait diversity. Our results support the distance from native habitat hypothesis and display the complex interplay between avian community assembly, functional traits, and habitat structure.

Avian biodiversity in central California vineyards**L Peria, C Francis***Presenting author:* **Lindsay Peria**, California Polytechnic State University, San Luis Obispo, lperia@calpoly.edu

Avian biodiversity is declining across the country, and conservation lands alone will be insufficient to support vibrant avian communities long-term. However, the integration of bird friendly practices into agricultural lands could support species that have lost habitat to development. Here, we evaluate how avian distributions and diversity vary with land cover characteristics among vineyards, such as percent remnant habitat, other agriculture, presence of surface water, and vegetation structural complexity. Point counts will be completed in Spring 2024 throughout vineyards in Edna Valley, San Luis Obispo. Satellite imagery and LiDAR data will be used to measure land cover and structural complexity. We will use occupancy models to estimate how occupancy of species varies with vineyard characteristics while controlling for detection probability, and we will use a variety of community metrics to quantify how

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environmental gradients influence diversity patterns, including overall richness and evenness. We predict that more heterogeneous vineyards, especially those with remnant habitat interspersed, will have the highest occupancy rates and hence species richness. Because most of the research at the nexus of conservation and vineyard management has been conducted outside of North America, this project brings contextual relevance for conservation among the expanding viticulture industry in the Western USA. Specifically, the findings will help identify environmental features that vineyard managers can use to promote diverse avian communities on these working lands.

Pesticide exposure and plant damage in natural areas in agricultural landscapes: implications for birds

T Benson, T Beveroth, C Johnson, E Price, T Rye, E Lain, B Charles, D Zaya

Presenting author: Thomas Benson, University of Illinois at Urbana-Champaign, tjbenson@illinois.edu

Starting in the second half of the 20th century, agricultural intensification increasingly involved the use of chemicals for pest control. The development of numerous synthetic pesticides, including herbicides, insecticides, and fungicides, led to widespread use and, in some cases, widespread non-target effects on organisms. Our understanding of the potential effects of these pesticides on non-target organisms generally lags behind their widespread adoption, as does our understanding of the extent to which these chemicals travel beyond the fields in which they're applied into natural areas. In 2023, we examined the extent of plant damage consistent with non-target herbicide exposure and quantified concentrations of pesticides from natural areas throughout Illinois. We sampled >180 sites in Illinois and found at least moderate damage to plants at almost all sites, with >50% of sites having severe damage and oak species most frequently affected. We found pesticides in nearly all natural areas, with 40 different chemicals detected. Herbicides were found in the greatest concentrations, with Atrazine and 2,4-D most common. Later in the season, fungicides and insecticides were more commonly detected. The amount of row-crop agriculture in the surrounding kilometer predicted concentrations of pesticides and severity of plant injury. The longer-term effects of this exposure and plant injury are unknown, as are the effects on insects and insectivorous birds. Given that oaks were the most frequently observed with plant damage, and the disproportionate importance of this group for caterpillars and the migrating and breeding birds that consume them, more work is needed to explore these implications.

Effectiveness of public-private efforts to conserve Tricolored Blackbird (*Agelaius tricolor*) colonies on agricultural lands in the San Joaquin Valley, California

X Castañeda, I Souza-Cole, D Airola, N Clipperton

Presenting author: Ian Souza-Cole, Audubon California, iansouzacole@gmail.com

Since the early 1990s when much of the population of the Tricolored Blackbird (*Agelaius tricolor*) began nesting in fields of triticale grown for dairy silage in the San Joaquin Valley, many colonies have been destroyed inadvertently during harvest. After previous inconsistent efforts, in 2015 a Regional Conservation Partnership Program brought the dairy industry, Natural Resource Conservation Service, Audubon California, California Department of Fish and Wildlife, and other partners together in an effort to stem the losses. The program located colonies and compensated farmers for crop value lost when the harvest was delayed until after the blackbirds fledged and encouraged creation of alternative nesting habitat to attract nesting birds away from agricultural fields. Before 2015, data on the numbers of colonies in silage fields, and on the blackbirds' productivity conserved and lost, are complete only for 2005-2009, when only 43% of colonies encompassing 60% of the monitored nestings avoided destruction. From 2015 to 2022, 93% of colonies representing 96% of nesting attempts were conserved, and the number of birds nesting in silage increased by as much as 100,000. The program's success resulted from the adequacy of federal funding, protection provided by the species' listing as endangered by the state of California, and effective communications and cooperation among the partners and within the dairy industry. Protection of colonies in silage fields since 2015 likely contributed to the substantial increase in the numbers of birds nesting in this habitat and perhaps to an increase in California's Tricolored Blackbird population as a whole. Continued effort is needed to achieve the species' recovery.

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Maximizing bird foraging habitat in coffee farms through shade tree selection*R Bennett***Presenting author: Ruth Bennett, Smithsonian Institution, bennettr@si.edu*

Coffee farms with shade trees provide habitat for a diverse communities of birds. Although on-farm tree diversity typically correlates with bird diversity, little information exists about which tree species provide the most important food resources to the bird community. This is a critical gap, as carbon offsetting and sustainability programs increasingly incentivize coffee farmers to add trees to their farmland, often prioritizing non-native and fast-growing trees that may provide low biodiversity value. To determine if food resources for birds vary among coffee shade tree species, we conducted bird foraging observations on 27 tree species (mean 11 individuals per species) over 8 seasons from 2020-2022 in Villa Rica, Peru, where coffee farming is the dominant economic activity. For foraging birds, we analyzed their richness, abundance, and time foraging per tree species, correcting for crown area. Bird use varied among trees species, with 14 species supporting 90% of all foraging individuals and minutes. Trees in genus *Inga* were the most common shade trees in the region and showed intermediate use by insectivores and high use by hummingbirds. Frugivores strongly selected trees in genera *Ficus* and *Trema*, particularly when ripe fruits were available. Unexpectedly, *Eucalyptus grandis*, a non-native timber tree, showed intermediate use by the entire bird community, although *Pinus tecunumanii*, a non-native pine, had extremely low use across guilds. These results demonstrate that coffee shade tree species provide differential resources to associated bird communities and provide a basis for selecting shade tree species that maximize bird foraging habitat.

****Bobolink (*Dolichonyx oryzivorus*) breeding and site selection are not macro-scale processes in highly fragmented habitats****M Oliver, J Nocera***Presenting author: Meghan Oliver, meghan.oliver@unb.ca*

Bobolinks (*Dolichonyx oryzivorus*) rely on nesting habitat created from hayfields and pastures. The species is area-sensitive and their fitness and habitat connectivity are positively correlated. The environmental correlates of breeding site selection have been well-studied, particularly in areas of contiguous habitat (e.g., prairies, extensive agricultural regions). However, much less is known about their breeding site selection in areas of low connectivity and limited habitat choices. We examined Bobolink abundance and nest success near the northeastern range edge (the Wolastoq/Saint John River Valley, New Brunswick, Canada) where agricultural areas are highly fragmented and surrounded by a wooded matrix, unlike most areas in the Bobolink's breeding range. We collected abundance and breeding data using point count surveys and developed a reproductive index. We used geospatial modelling to quantify four predictive variables: field area, edge length, maximum distance to edge, and proportion of agriculture in the landscape (at three spatial scales). Despite their known importance in more contiguous habitats, our models indicate these variables do not predict breeding success at our study sites. Further modelling will assess whether this is also true for abundance, which varies throughout the breeding season and peaks in mid- to late-July. Our results suggest that when choice is limited and habitat is fragmented, Bobolinks are not guided by large-scale spatial characteristics but may be limited to focusing on territory-level attributes. Ultimately, the findings from this study can be used to better describe critical nesting habitat for this threatened grassland bird in jurisdictions not dominated by agriculture.

Forest cover and coffee cultivation system influence bird community functional diversity in the Sierra Nevada de Santa Marta, Colombia*L Morse, R Bennett, J Valente***Presenting author: Liza Morse, University of Vermont, liza.morse@uvm.edu*

Although coffee agroforestry systems are renowned for maintaining high avian richness and abundance, community composition often differs from native forests and species diversity declines with production intensity. Increasingly, functional diversity is recognized as a critical aspect of biodiversity though it has been less well explored in agroforestry systems. In this study, we explored the impacts of coffee

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cultivation and forest cover on bird functional diversity using community occupancy models. Community occupancy models were built using data from 250 locations in forests and heterogeneous coffee systems in the Sierra Nevada de Santa Marta, Colombia. We then used model predictions to simulate 100 ha farms with (i) shade (>40% canopy cover) or sun (<20% canopy cover) coffee, (ii) 0-85% forest cover within the farm, and (iii) 0-100% forest cover within the surrounding landscape (6 km²). Occupancy rates from these farms were used to calculate functional diversity – including measures of richness, evenness, and redundancy – and trends in functional diversity were evaluated using nonlinear regression. Functional richness demonstrated a quadratic relationship with forest cover, peaking at intermediate levels of cover in both coffee types. Functional redundancy decreased with forest cover at both scales and was consistently higher in sun-grown coffee. Trends in functional evenness varied between breeding and non-breeding seasons and between scales of forest cover. These results suggest that the size of functional space occupied by the bird community is maximized at intermediate levels of forest cover, though the extent to which that functional space is filled and resilient to trait loss varies by season, coffee type, and the amount and scale of forest cover.

****American Kestrels in Northeast Arkansas: Nest Box Use, Nesting Success, and Impacts on Potential Agricultural Pests**

T Sharrow, T Boves, V Rolland*Presenting author: Ty Sharrow, Arkansas State University, tysharro@ptd.net*

The American Kestrel (*Falco sparverius*) is a declining generalist predator that can be found in agricultural landscapes where they can potentially provide pest control services, especially during their breeding season. However, removal of most woody vegetation in agricultural regions such as in the Lower Mississippi Alluvial Valley (LMAV) has eliminated most suitable nesting sites for kestrels (which are cavity nesters), and has likely contributed to low breeding densities of kestrels in this, and other, agricultural regions. Fortunately, kestrels can be attracted to otherwise suitable habitats by adding artificial nest boxes. In this study, we installed 40 nest boxes adjacent to row crops (rice, cotton, corn, and soy) in two counties in the LMAV of northeast Arkansas, USA, to assess kestrel nest box occupancy, nesting success, and impacts on potential pest populations. We monitored nest boxes biweekly and conducted annual small mammal, avian, and insect surveys at both occupied and unoccupied nest boxes, and at random points, in May-July 2022–2024. In the first breeding season following deployment in 2021, four boxes (18%) were occupied each successfully producing young, seven boxes (29%) were occupied in 2022 with four successfully producing young but in 2023, nine boxes (23%) were occupied but only one attempt successfully produced a fledgling. Despite relatively low occupancy and nest success, abundances of small mammals and avian pests were lower than at unoccupied sites; insect abundances did not differ. Our findings support that kestrels can be attracted to agricultural areas within the LMAV using nest boxes and provide pest control services in this region.

A golden opportunity: investigating relocation effectiveness and day-time habitat selection of Golden Eagles (*Aquila chrysaetos*) in Wyoming

K Amicarelle, C Ramos, N Bickford*Presenting author: Kristen Amicarelle, Colorado State University Pueblo, k.amicarelle@pack.csupueblo.edu*

Eagle depredation of sheep is a concern raised by Wyoming landowners. This human-wildlife conflict is potentially due to the modern anthropomorphic and environmental challenges eagles face. Relocation is a proposed tool to mitigate this wildlife conflict and decrease eagle persecution. Our objective was to investigate if relocation of Golden Eagles (*Aquila chrysaetos*) could be implemented for management of sheep depredation and understand which habitat variables relocated eagles are selecting. We predicted that age and relocation distance would influence the return rate of individuals, and that habitat selection would reflect similar preferences between relocated and non-relocated eagles. Surveys were conducted to find relocation sites that were safe from human development and had suitable habitat. We trapped 12 eagles and fitted them with cellular GPS transmitters to provide insight into their movement patterns and habitat preferences post release. Eagles were relocated at distance intervals, ranging from 100-400

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miles. We modeled resource selection using general linear mixed effect models and correlated random paths to determine habitat selection between the relocation and stopover locations using multiple covariates. Eighty percent of relocation events resulted in the absence of the eagles for at least three weeks and were deemed successful by landowner's standards. Adult eagles returned to the capture site more quickly than younger individuals ($P < 0.05$), whereas relocation distance and season did not influence the return time ($P > 0.05$). Our return analysis showed little evidence that eagle translocation would be an effective management strategy long-term, and would have various logistical and biological challenges if implemented statewide.

Barn owls exert direct and indirect effects on rodent pests

K Larson, R Baldwin, M Johnson*Presenting author: Katherine Larson, katherinelarson01@gmail.com*

Ecological theory predicts that raptors exert top-down effects on their prey by direct consumption, indirectly by imposing risk of predation, or a combination of both. However, empirical evidence for these effects is mixed and inconsistent. Understanding relationships between raptors and their prey is especially important where raptors may contribute to the control of agricultural pests. Earlier work shows promise that barn owls may control rodent pests, but empirical evidence is limited and the distinction between direct and indirect effects remains unresolved. Here, we investigate the top-down effects of barn owls on rodent pests in winegrape vineyards in Napa Valley, California. We monitored barn owl occupancy, reproductive status, and fledgling success in over 300 nest boxes in 2023. We used this to create a spatially and temporally explicit barn owl hunting pressure model from hunting locations and from prey delivery rates that vary as nestlings develop. The hunting pressure layers were used to examine the direct effect of barn owls on rodent abundance (measured with chew blocks), and the indirect effect of barn owls on rodent perceived predation risk and activity (measured with giving-up density trays and game cameras respectively). We found that barn owls exert both direct and indirect effects on rodent pests and that dense vegetation favors the acoustically attuned barn owls over the visually-oriented rodent pests. We contribute to growing evidence that barn owls can be used as biological control in agricultural systems, and we show that growers can manipulate vegetation to enhance the effect of barn owls and to induce more fear in rodents.

***Bird-friendly beef: Investigating the impact of regenerative forage systems on grassland bird reproductive success**

B Rigley, J Gilley, D Luther, A Johnson*Presenting author: Bernadette Rigley, Smithsonian Institute, rigley.bw@gmail.com*

In the Southeastern United States, managed hayfields and pasturelands represent a significant portion of remaining available grassland bird habitat, hosting several declining species including the eastern meadowlark (*Sturnella magna*). This provides an opportunity for landowners to implement land management practices that help foster the recovery of grassland bird populations. However, for conservation to be effective, land management must aim to benefit both producers and birds. Regenerative agriculture is a holistic approach that integrates management practices that benefit agricultural ecosystems and production. While regenerative forage production has demonstrated correlations with increased bird abundance, there remains a notable research gap in assessing whether these practices contribute to population declines. We evaluated how regenerative forage systems impact both the reproductive success of grassland birds and the quality of forage for cattle. Four experimental grazing and haying treatments were implemented on privately owned working lands in the Shenandoah and Piedmont Valley regions of Virginia. For each treatment, we collected forage samples for nutrient analysis and quantified reproductive success using a combination of territory mapping and systematic nest searching. Preliminary data suggests that early pasture grazing and stockpiling for fall and winter grazing not only yield standing forages suitable for multiple livestock production classes, reducing reliance on harvested hay, but also enhance survival among grassland birds by minimizing disturbances during peak nesting periods.

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Can deploying boxes for Barn Owls trigger managed trophic cascades?**M Johnson, J Carlino, C Cortez, K Larson, J Rodriguez, S Kross***Presenting author: Matthew Johnson, Cal Poly Humboldt, mdj6@humboldt.edu*

Many farmers worldwide deploy nest boxes to attract Barn Owls (*Tyto spp.*) in hopes they will contribute to the management of rodent pests, which cause enormous crop losses. Recent empirical evidence suggests this practice has promise, but the underlying theories have not yet been examined. In this presentation, we first briefly review the attributes of Barn Owls that make them good candidates for delivering pest control ecosystem services. Second, we describe the deployment of nest boxes for pest-eating birds as a 'managed trophic cascade,' and we review theoretical conditions under which this practice is likely to operate in agroecosystems. Third, we highlight evidence from American Barn Owls (*Tyto furcata*) nesting in winegrape vineyards in Napa Valley, California, where the presence of hunting barn owls significantly reduced rodent activity (18-63%) and increased perceived predation risk by rodents (up to 71%). We also provide evidence that the owls' reproductive output likely outpaces mortality, suggesting this practice is not posing an ecological trap for this species. Together, these results indicate that Barn Owls can exert meaningful top-down effects on rodent pests in vineyards, but the hypothesized indirect benefits to crop plants remain unresolved and difficult to quantify. We identify attributes of other systems that could lend themselves to more fully testing all constituent hypotheses of a suspected trophic cascade caused by Barn Owls.

Direct and Indirect effects of migratory shorebirds on nitrogen cycling in agricultural fields managed for fall-winter wetland habitat**V Blocker, J Taylor, J Hoeksema***Presenting author: Victoria Blocker, USDA-ARS, victoriamsimek@gmail.com*

The global human population continues to grow exponentially, and agriculture will need to become more productive to meet growing food demands. Humans also need clean water and other services that ecosystems provide. This requires future agriculture production to reduce environmental and wildlife impacts through improved efficiencies and best management practices. Migratory shorebirds rely on wetlands throughout North and South America as stopover habitat for rest and refueling during migration. Temporarily flooded farmlands in the Mississippi Delta have proven to be beneficial locations for shorebirds during migrations along the central flyway. This conservation practice also enhances wetland properties that promote excess nitrogen (N) retention or removal. However, little research has been conducted to evaluate how shorebird activity influences N cycling in these temporary wetland habitats on agricultural lands. Soil cores collected from shorebird enclosure plots and shorebird accessible plots were used to measure N cycling processes including denitrification, N uptake, and oxygen consumption. The paired enclosure plots were also used to measure invertebrate densities to identify the relationship between shorebird presence, invertebrate densities, and their relationship to nitrogen cycling. Enclosure plots had a significant impact on total invertebrate densities and oxygen consumption while showing no effect on nitrogen cycling. Using these results, we can better understand how interactions between wildlife and habitat created through best management practices may enhance ecosystem services in managed agroecosystems.

Physiological conditions of barn owl nestlings as indicators of habitat quality in the Napa Valley wine-growing region**C Cortez, M Johnson, J Cornelius***Presenting author: Christian Cortez, Cal Poly Humboldt, cc554@humboldt.edu*

The adaptive breeding-habitat hypothesis posits that birds will select nest sites with attributes that favor reproduction. For species with generally high nest success, physiological measures of offspring condition, such as fault bars, growth bars, feather corticosterone, and heterophil-lymphocyte ratios, may provide meaningful measures of habitat quality near nest sites. As a sustainable, cost-effective approach to protecting crops while minimizing the reliance on chemical pesticides, many farmers in Napa Valley, California attract rodent-eating barn owls (*T. furcata*) to their vineyards with nest boxes, where the owls

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typically have high nest success. Previous research in this agroecosystem shows that owls select boxes with uncultivated land cover nearby, such as oak savanna, grassland, and riparian habitats. We assessed the relationship between these physiological conditions of barn owl nestlings and the composition and configuration of land cover surrounding their nest boxes with generalized linear mixed models. In initial findings, barn owl nestlings had lower values of chronic stress, as identified by low heterophil to lymphocyte ratios, with more grassland and oak savanna habitats in close proximity to their nest boxes, and higher ratios with more developed and fragmented land cover. Ongoing analyses will determine whether these same patterns hold for a shorter term measure of stress as revealed by corticosterone concentration in the nestlings' feathers. Our results contribute to a growing body of literature suggesting physiological measures can be useful indicators of habitat quality, and they help emphasize the importance of conserving native habitats for the provisioning of pest control services in agricultural landscapes.

****Examining environmental and life history correlates of winter movement in a nomadic Arctic-breeding passerine**

S Simard-Provençal, E McKinnon, O Love

Presenting author: **Samuelle Simard-Provençal**, samsimpro@gmail.com

The Snow Bunting (*Plectrophenax nivalis*) is an Arctic-breeding passerine facing population declines. The cause for these declines, however, is not well understood. Therefore, there is still much to learn about this species at the life history level. The goal of this research is to understand patterns of nomadic winter movements of Snow Buntings overwintering in Ontario, Canada. Specifically, we will investigate which environmental factors are influencing space use in the wintering period and determine spring migration initiation. This will be accomplished using automated radiotelemetry (Motus Wildlife Tracking System) tags deployed on 72 wintering Snow Buntings in southwestern Ontario. Additionally, while some birds were banded, tagged, and released where they were caught, some birds were strategically displaced by several hundred kilometers to causally test their response to different weather conditions (i.e. moved from a preferred northern site to a less preferred southern site). The high density of radio-receiver towers in southwestern Ontario makes it an ideal location to conduct this research. Preliminary data analysis resulted in 22 individuals where winter movement was detected. We assessed differences in bird movements between sexes, ages, and experimental treatments across the landscape and looked for correlations between bird movements and fine-scale weather correlates. With climate change increasing ambient temperatures and affecting weather systems at a global scale, quantifying the movement ecology and connectivity patterns of this species will help to determine whether buntings have the capacity to adapt to an increasingly changing landscape across multiple life stages.

****Assessing the Effects of Environmentally-Mediated Phenological Matching of the Snow Bunting (*Plectrophenax nivalis*), an Arctic-Breeding Songbird to its Arthropod Prey**

A Riquier, G Gilchrist, O Love

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Snow Buntings are an Arctic-breeding passerine species that relies on arthropods to provision their offspring. Previous studies have shown the importance of matching laying phenology and arthropod abundance relating to the peak of offspring food demand. However, it is still unclear if buntings can flexibly adjust their laying date in response to environmental cues to match the chick-rearing period with the peak of arthropods as well as how climate change is affecting the emergence of arthropods in the Arctic. Our aim is to determine whether buntings can track changes in environmental conditions to phenologically match the chick-rearing period with the timing of arthropods. Our objective is to examine the links between climate, food availability and bunting laying phenology, and use these relationships to forecast whether the synchronicity of timing between arthropods and buntings will diverge as climate change accelerates. To examine these questions, we are using a long-term dataset (2007-2019) supplemented by two years of my own research (2022-23) to relate variation in climate to arthropod abundance and diversity data (collected from pitfall traps) and bunting lay date, clutch size, and success

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outcomes from Qikiqtakuluk, Nunavut. The results of this study will provide insight into whether Snow Buntings have the adaptive capacity to respond to increasing variability in spring weather conditions. This work will provide broader insight into whether climate change induced mis-matching timing is a mechanism behind population declines. Results will help us to understand whether other Arctic species relying on arthropods are also facing similar stressors.

Monitoring, citizen science, and field data reveal a novel alpine breeding distribution and vegetation associations of a migratory, habitat-specialist songbird

B Walker, A Yappert, C Brennan, C Bossu, A Jones*Presenting author: Brett Walker, Colorado Parks and Wildlife, brett.walker@state.co.us*

Understanding the breeding habitat and distribution of migratory songbirds is essential for accurately assessing their conservation status. The 'sagebrush' Brewer's Sparrow (*Spizella breweri breweri*) breeds in greatest abundance in sagebrush (*Artemisia* spp.) shrublands of western North America, and the 'timberline' subspecies (*S. b. taverneri*) breeds in shrubs or krummholz at or above treeline in mountain ranges from Alaska to Montana. Brewer's Sparrows have also been reported at alpine sites in summer in mountain ranges across the western United States, but their taxonomic affiliation and breeding status are unknown. We reviewed monitoring, citizen science, and specimen data for Colorado and identified 186 historical summer observations of Brewer's Sparrows at 59 alpine sites (3334–4288 m elevation). We surveyed 39 alpine sites in June–July 2021–2023, detected a total of 100 adults at 26 alpine sites, and confirmed breeding at three sites. Males occupied mixed-species willow patches 0.9–1.8 m tall, often intermixed with sparse conifer krummholz. Vegetation associations and timing of breeding at alpine sites closely matched those of *taverneri*, but songs, morphology, coloration, and genetics of alpine birds overlapped with sagebrush birds and most closely matched those of range-wide *breweri*. Our results indicate that western Colorado supports a widely-distributed breeding population of alpine *breweri* in willow-krummholz at or above treeline. Whether alpine birds are itinerant breeders that first nested in sagebrush remains unknown. Our results complicate interpretation of differences in breeding habitat and breeding phenology as supporting criteria for subspecific identification and taxonomic delineation in this species.

What drives seasonal habitat selection patterns of the alpine-endemic white-tailed ptarmigan?

N Parker, G Wann, M Mahoney, S Oyler-McCance, C Aldridge*Presenting author: Nicholas Parker, nick.parker@colostate.edu*

While it is predicted that many wildlife species will shift their ranges upward in response to climate change, species in alpine ecosystems already exist at the highest elevations with no opportunity to move. The white-tailed ptarmigan (*Lagopus leucura*) is an alpine endemic grouse species found across Colorado facing an uncertain future in the state due to climate change, land use change, and increasing human recreation. To help guide management and predict future changes in white-tailed ptarmigan habitat, we first need an understanding of current habitat requirements across seasons. We combined 10 years (2013–2023) of location data from a long-term mark-recapture study on white-tailed ptarmigan at two sites in Colorado with recently collected data from radio- and GPS-collared birds. We used a resource selection framework with remotely sensed environmental covariates to model seasonal habitat relationships. We found white-tailed ptarmigan shift habitat use seasonally, moving to higher elevations with greater permanent snow cover during the warmest summer months. Anthropogenic effects were overall weak, but white-tailed ptarmigan avoided areas with higher road density. Land cover and vegetation characteristics also had relatively little influence on habitat selection, yet white-tailed ptarmigan selected increased shrub cover. Overall results from these analyses indicate white-tailed ptarmigan habitat use in Colorado is largely driven by abiotic factors that are predicted to change under future climate scenarios, which will ultimately reduce usable habitat. Ongoing research aims to model white-tailed ptarmigan habitat across Colorado to help prioritize areas that can be protected to allow for their continued persistence.

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Infidelity in the Alpine: The Mating System of White-tailed Ptarmigan Evaluated with Behavioral and Genetic Information**M Mahoney, C Aldridge, G Wann, N Parker, S Zimmerman, S Oyler-McCance***Presenting author: Meghan Mahoney, Colorado State University, Meg.mahoney@colostate.edu*

Mating systems have traditionally been characterized through direct behavioral observation. From these studies it is estimated that over 90% of bird species exhibit social monogamy. However, advances in molecular techniques have allowed researchers to determine whether the observed parents of a clutch are also the biological parents, a concept known as the genetic mating system. Genetic studies have revealed that true monogamy is rare across the class Aves, with most monogamous pairs partaking in extra-pair mating (EPM). The prevalence of infidelity in birds suggests this behavior may be evolutionarily adaptive, whereby individuals may seek an extra-pair mate with higher fitness or more compatible genes than their within-pair mate, all while retaining the benefits of a pair bond. The white-tailed ptarmigan is an alpine-endemic grouse observed to be monogamous, with previously undetermined rates of EPM. Leveraging recent advances in high-throughput sequencing, we have sequenced and annotated the entire genome of the white-tailed ptarmigan. From this assembly, we have developed a panel of single-nucleotide polymorphisms (SNPs) that we are using to genotype white-tailed ptarmigan samples collected in Rocky Mountain National Park and Mt. Bluesky Wilderness between 2011 and 2024. We have constructed a pedigree for each white-tailed ptarmigan population and, by comparing these pedigrees to field observations of social pairs, we will calculate rates of EPM. These findings have important implications for understanding the adaptive behaviors of white-tailed ptarmigan and other bird species, especially as related to selective pressures from alpine ecosystems.

Are white-tailed ptarmigan negatively impacted by warming in the alpine? Using 55 years of data to estimate correlations between growth and climate**G Wann, C Aldridge, C Braun, P Coates, S Oyler-McCance***Presenting author: Gregory Wann, U.S. Geological Survey, wannng@usgs.gov*

Alpine birds are interesting to study in the context of warming temperature and changing precipitation because the alpine ecosystem is largely defined by cold temperatures and snow, and empirical examples demonstrating how populations have responded to long-term changes remain uncommon. White-tailed ptarmigan studied at two sites in Colorado's Front Range offer some useful insights. We collected monitoring data in the form of mark-recapture and brood surveys from 1966 to 2020 (55 years) at Mount Blue Sky in Clear Creek County and Trail Ridge in Larimer County. We use population models fit to three datasets (annual study-site abundance, chicks per female produced, and annual rates of survival) to investigate if temperature and precipitation effects influenced annual variation in growth rates, and if interactions between climate and density were able to explain such effects (we predicted effects would be strongest at highest densities). Preliminary results from our modeling indicate the presence of density dependent feedback in the populations we studied, but no obvious interactions with the climate variables we examined. Overall, annual rates of change declined at the Trail Ridge population ($\hat{\lambda} = 0.98$), but slightly increased at Mount Blue Sky ($\hat{\lambda} = 1.02$). We discuss the different growth trajectories at the two populations and attribute these differences to local factors, and highlight uncertainties of climate effects, and whether the sites are representative of other areas along the Front Range.

Molting strategy relates to life history evolution in migratory birds*P Dougherty, M Carling***Presenting author: Paul Dougherty, University of Massachusetts Amherst, pdoughe1@uwoyo.edu*

An organism's ability to invest time and resources into the maintenance of biological functions defines its survivorship potential. In birds, molt, the systematic replacement of feathers, represents an individual's most significant and consequential investment in annual survivorship. We combined stable isotope analyses and captive studies to compare molting speed and individual flexibility between Indigo Buntings (*P. cyanea*) and Lazuli Buntings (*P. amoena*). Feather stable isotope ratios indicate that *P. amoena*, which

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molt during an extended migratory stopover in monsoonal areas, molt more slowly than *P. cyanea*, which molt prior to post-breeding migration. Additionally, comparison between feather stable isotopes and observations of captive birds suggest that individual *P. amoena* are more flexible in their prebasic molt phenology. Prolonged yet flexible investment in feather growth supports higher adult survivorship in *P. amoena*, which is consistent with exploration of age ratios of museum specimens and banded birds as well as the fact that *P. amoena* typically raises fewer broods per year than *P. cyanea*. Overall, our results demonstrate that molting strategy can modulate life history evolution in migratory birds. Furthermore, the slower life history of *P. amoena* (and presumably other species that breed in western North America and have similar natural history) should be a consideration in conservation. If the persistence of *P. amoena* populations indeed depends on relatively high adult survivorship, ongoing shifts in precipitation phenology that reduce the time available for individuals to molt may contribute to population declines.

Bendires Thrasher (*Toxostoma bendirei*) winter and migratory movements: New discoveries and opportunities for full life-cycle conservation

C Borgman, C Kondrat*Presenting author:* **Corrie Borgman**, U.S. Fish and Wildlife Service, corrie_borgman@fws.gov

Bendire's Thrashers (*Toxostoma bendirei*) are among the fastest declining avian species in North America (Rosenberg et al. 2016, Sauer et al. 2020). Significant data gaps exist for basic information on their breeding season and winter distributions, migratory patterns, habitat associations, and population limiting factors. This thrasher species occupies flat, sparse deserts, grasslands, and shrublands of the southwest United States and adjacent northwest Mexico. In the northern part of their range, they are considered migratory, while southerly birds are expected to be resident year-round. However, where exactly this distinction lies, as well as any details about migratory timing, wintering locations, wintering habitat associations, and migratory connectivity are unknown. We tagged 54 birds with Lotek PinPoint 10 GPS tags at five breeding sites in Arizona and New Mexico between 2019 and 2022. We recovered 23 tags (43%) and determined migratory departure timing and wintering locations. Seventy-six percent of the birds we tagged made migratory movements. The majority migrated to Sonoran desertscrub habitats in a broad area surrounding Hermosillo, Sonora, Mexico. There was no distinction in wintering locations for birds from different breeding populations; in fact, some individuals wintered within 5 – 10 km of others from separate breeding populations. These results show the importance of habitats in Sonora to this species. Future direction includes surveys to evaluate habitat characteristics, winter, and breeding season abundance at these sites and similar locations in Sonora. This effort is accomplished through partnerships in Mexico and facilitated through the Desert Thrasher Working Group.

Annual and overwinter survival of Blackpoll Warblers derived from non-breeding sites in Colombia

A Morales Rozo, C Gomez, P Taylor, N Bayly, K Hobson, G Colorazo Zuluaga*Presenting author:* **Andrea Morales Rozo**, Universidad Nacional de Colombia, Universidad de los Llanos, anmoralesr@unal.edu.co

Conservation of declining migratory species requires estimates of vital-rates from their entire annual cycle. However, in the Neotropics, there are few species for which we have annual, or within non-breeding period survival data, and this considerably hinders our ability to identify population limiting processes. Blackpoll Warbler populations have declined drastically, and until recently, data on their non-breeding ecology and survival were scarce. Using Cormack–Jolly–Seber models to analyze mark-resighting data collected over six years (2017 to 2022) at two non-breeding sites in Colombia, we estimated inter and intra annual apparent survival and examined variation in survival by site, age, and sex. Our results indicate large annual variation in survival during the 6 years of study (0.4-0.7), where 2018 had the lowest annual survival coinciding with a weak to moderate El Niño event (El Niño = drier conditions). We found differences in annual survival among landscapes and between sexes, but not between age groups. Within-winter monthly apparent survival probability varied from 0.92 to 0.96. These high monthly survival rates within the non-breeding period are similar to rates found in other species, suggesting that survival in non-breeding sites may not be a limiting factor contributing to declines in

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Blackpoll Warbler populations.

Carry-over effects of climate on Prothonotary Warbler (*Protonotaria citrea*) feather quality*A Spasic, L Bulluck, A Bressette**Presenting author: **Alyssa Spasic**, spasican@vcu.edu

Avian species have inspired numerous studies on ornamentation, exploring its role in intra- and intersexual selection as a marker for individual quality. Male birds have been the focus of most of these studies while females, which can also display ornamentation, have been studied less. Coloration achieved through molt, particularly carotenoid-based pigments, requires energy derived from food resources. As climate affects insect abundance, there may be a link between climate conditions during molt and feather quality the following season. We assessed the relationship between temperature and precipitation during molt and female Prothonotary Warbler (*Protonotaria citrea*) breast and crown feather reflectance metrics the following year. We collected breast feathers from 448 females and crown feathers from 417 females across 13 years (2010-2023) in eastern Virginia, USA. Breast and crown carotenoid content and breast yellow intensity tended to be higher following cooler and wetter conditions during molt. The negative impact of temperature on breast yellow intensity was greater in younger females. These results indicate that temperature and precipitation during molt carry over to influence female feather quality, which likely serves as an indicator of individual quality to potential mates. These results provide insight into how climate conditions affect individual plumage quality and may aid in understanding the impacts of climate change on mating systems. Future study is needed to explore how conditions during molt may interact with species' thermoneutral zones to influence energy tradeoffs toward important events in a species' annual cycle.

****Understanding the annual life cycle of Horned Grebe (*Podiceps auritus*) breeding in Canada****C Howell, K Kardynal, E Reed, A McKellar, K Gurney**Presenting author: **Christina Howell**, University of Saskatchewan, christina.howell@usask.ca

Migratory birds use a variety of habitats and are exposed to a wide range of environmental conditions throughout the annual cycle, which can influence population demographics and species abundance in subsequent seasons. Within Canada, some indicators suggest that breeding populations of Horned Grebe (*Podiceps auritus*) have significantly declined since 1970, yet factors influencing populations and reasons for the apparent declines remain unknown. The objectives of my research were to (i) identify wintering areas used by Canadian breeding horned grebes, and (ii) understand the extent to which breeding populations mix, segregate, and/or spread out during the non-breeding season (i.e. migratory connectivity). Using light-level geolocators, 18 birds from two study sites were tracked across one full annual cycle. Stable isotope values carbon (^{13}C) and nitrogen (^{15}N) from feathers were used in conjunction with geolocator data to assign individuals to distinct wintering populations. Tracked birds followed a southeast migratory pathway to a wide geographic range of marine and freshwater non-breeding locations; most occupied Atlantic Coast ($n = 7$) and freshwater continental ($n = 7$) sites, followed by Gulf Coast ($n = 2$) and the Great Lakes ($n = 2$). Isotope cluster analysis suggest that populations likely mix on wintering areas. Strength of migratory connectivity of horned grebe breeding in Canada was estimated as weak ($\text{MC} = 0.07 \pm 0.08$). Overall, my results fill important knowledge gaps surrounding the migration ecology of horned grebe. My results also have conservation implications, as a more complete understanding of the annual life cycle will improve the development and implementation of management strategies for this species.

****Bald Eagle Habitat Selection in an Urbanizing Landscape****M Middleton, R Conrey, L Pejchar**Presenting author: **Miranda Middleton**, Colorado Parks and Wildlife, miranda.middleton@state.co.usBald eagles (*Haliaeetus leucocephalus*) have made a dramatic recovery since being placed on the

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endangered species list in 1978. Historically bald eagles were largely found in areas close to water (e.g., lakes and rivers) and with relatively little human development. To inform appropriate policy and management, it is important to understand how growing bald eagle populations utilize increasingly developed landscapes. The bald eagle population in Colorado's northern Front Range, a semi-arid environment, has grown from just a few known nests 40 years ago to over 120 known nests today with numbers still increasing. At the same time, this region is currently experiencing a high rate of urbanization. Our objective was to evaluate which landscape characteristics are selected or avoided by bald eagles during five periods of the annual cycle: pre-nesting, incubation, nestling, post-fledge, and non-nesting. From July 2020 through the present, Colorado Parks and Wildlife outfitted 24 breeding bald eagles with GPS/GSM transmitters from a rural to urban gradient along the northern Front Range. Using a third order resource selection function we found that bald eagles in this area selected areas closer to water and herbaceous wetlands and avoided areas with more agriculture. Our findings suggest that water continues to be an important resource for bald eagles, and that this species appears to co-exist with low-moderate density human development. This study advances understanding of habitat use of bald eagles and could help inform local wildlife agencies on how to better manage for an urbanizing landscape that can support bald eagles.

***The role of tropical rainfall in driving range dynamics of a long-distance migratory bird**

B Dossman, C Studds, S LaDeau, S Sillett, P Marra

Presenting author: **Bryant Dossman**, Georgetown University, bd618@georgetown.edu

Predicting how range dynamics of migratory species will respond to climate change requires a mechanistic understanding of the factors that control distribution and abundance throughout the year. Yet, most studies typically focus on breeding season even though a migrant's fitness is influenced by myriad of conditions experienced across their annual cycle. Using multiple lines of evidence, we revealed that environmental conditions during the nonbreeding season influences the range dynamics of the American redstart (*Setophaga ruticilla*). We estimated the breeding origins of our winter population using stable hydrogen isotopes in tail feathers; directly linking our winter population to its breeding origin and providing individual estimates of migration distance. Using long-term data from this nonbreeding population, we found that the relationship between annual survival and migration distance is mediated by tropical precipitation but only during dry years. Prolonged drought in the Caribbean and subsequent higher mortality for individuals from the northern portion of the species' breeding range (i.e., longer migration distances) has resulted in an approximate 500 km southward shift in the breeding distribution of this wintering population. Using breeding abundance data, we demonstrate that this shift in connectivity mirrors changes in the redstart's breeding distribution and abundance. While northern breeding populations are negatively influenced by drought in the Caribbean, more southern populations are unaffected. These results demonstrate the nonbreeding season actively shapes range dynamics in a migratory bird and emphasize the need for full annual cycle approaches to understand how animals will respond to climate change.

****Widespread evidence of carry-over effects of nonbreeding habitat in the Prothonotary Warbler**

R Ralston, C Tonra

Presenting author: **Rebecca Ralston**, Ohio State University, ralston.119@osu.edu

While many North American bird species are advancing their spring migration timing due to climate change, other species demonstrate little sensitivity to rising spring temperatures or earlier vegetation green-up. However, few studies have explored alternative drivers of variation in species-level arrival timing or intraspecific variation in drivers. We used eBird data from 2012-2022 to determine the effects of nonbreeding and stopover habitat quality on Prothonotary Warbler (*Protonotaria citrea*) arrival phenology. We predicted that stopover habitat quality would drive arrival timing at northern latitudes while nonbreeding habitat quality would drive arrival timing at southern latitudes. To measure habitat quality, we calculated monthly enhanced vegetation index (EVI) values and average precipitation for the nonbreeding

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range and high-use stopover sites in Central America and the southern United States. Using generalized linear mixed models, we determined that Prothonotary Warblers arrive later during years with lower seasonal nonbreeding EVI. This effect most strongly impacts warblers in the Atlantic Flyway. Understanding how carry-over effects of nonbreeding habitat impact a species' phenology may assist in explaining patterns of differential population decline, as late arrival has high productivity costs. Additionally, climatic trends predict a growing risk of drought in tropical regions, which may decrease nonbreeding habitat quality for many neotropical migrants and increase delays caused by carry-over effects of nonbreeding habitat.

Evo-eco mechanisms underlying nesting phenology shifts of American Kestrels

J Heath, B Pauli, S Galla, J Winiarski, B Powers, C McClure, A Hunt*Presenting author: Julie Heath, Boise State University, julieheath@boisestate.edu*

Changes in nesting phenology are one of the most predominant responses to climate change. Critical knowledge gaps remain, however, about the underlying genetic and ecological factors that affect the potential for populations to undergo phenological shifts. Individual-based models (IBMs) provide a method to forecast phenological shifts using empirical data that is representative of risk exposure (e.g., climate projections), species sensitivity (e.g., fitness), and adaptive capacity (e.g., evolutionary mechanisms). We developed an integrative IBM that combines evolutionary mechanisms affecting circannual rhythms (i.e., putatively functional genetic markers and heritability), and ecological mechanisms (demographic and life-history traits), to test hypotheses about shifts in egg-laying dates of American Kestrels (*Falco sparverius*). Experiments showed that seasonal declines in adult survival associated with mismatch were the strongest driver of earlier nesting. This was an unexpected result given the attention to the effects of mismatch on productivity. Additionally, changes in migration tendency and distance have small carry-over effects on the rate of egg-laying advancement, suggesting that migration may not limit phenological advancement. Finally, heritability and genetic mechanisms increased the speed of egg-laying-date advancement, reflecting the importance of representing evolutionary processes in IBMs. This work provides methodological approaches for integrating genetic and ecological information into models that simulate both evolutionary and ecological processes, which is an important advancement for understanding and predicting population responses to environmental change.

****Navigating the Anthropocene: Investigating the Habitat Use and Movement of Overwintering Sparrows to Guide Conservation Efforts**

J Morgan, K Williams*Presenting author: Jacob Morgan, Ohio University, jm311216@ohio.edu*

Anthropogenic development into natural ecosystems has resulted in habitat loss, fragmentation, and degradation, contributing to the decline of 55.2% of North American birds since 1970. In recognizing the impacts human development has had on avian populations, there is an urgent need to comprehensively study how birds use current landscapes throughout the full annual cycle. However, until 2015, many ecological studies disproportionately prioritized breeding seasons and overlooked critical aspects of overwintering periods. We delineated the landscape at three field sites in southeastern Ohio into nine habitat classes: Edge, Forest, Wooded Pasture, Shrub, Tall Grass Field, Short Grass Field, Burnt Field, Road, and Residential. We used automated and manual radiotelemetry to quantify overwinter habitat use and monitor movement and migration of 61 Slate-colored Juncos (*Junco hyemalis hyemalis*) and 22 American Tree Sparrows (*Spizelloides arborea*) during 2023 and 2024. Our findings enable us to provide concise, evidence-based recommendations to public and private landowners on how to enhance existing habitats and support avian conservation efforts.

Drivers and consequences of breeding-molt overlap across North American bird species

C Check, C Rushing*Presenting author: Courtney Check, cc34105@uga.edu*

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Avian annual cycles are characterized by distinct but interrelated life-history events, including breeding, molt, and migration, which generally must be completed multiple times through an individual's lifetime. Because birds have finite resources with which to carry out these life history events, investment in one stage often results in corresponding costs in another. Molt is one of the most physiologically straining periods in the avian annual cycle, but little is known about how birds balance the energetic costs of molt with other phases of their life history. Quantifying inter- and intra-specific variation in the extent of breeding-molt overlap is needed to understand how bird species adjust and prioritize life history trade-offs, a process that will be increasingly important for navigating environmental change. We used long-term banding records from the Monitoring Avian Productivity and Survival (MAPS) database to quantify the occurrence of breeding-molt overlap across several hundred North American bird species. Using generalized linear mixed models, we then examined what physiological, environmental, and taxonomic factors influence the occurrence of breeding and molt overlap. We found that the occurrence of breeding-molt overlap depends on a wide variety of factors, indicating that completing molt is a stressor to which birds can respond flexibly in order to maximize their fitness in any given year. As anthropogenically-induced climate and habitat shifts further modify the time frame and resources available for birds to complete their annual cycle, understanding how birds navigate life-history trade-offs will be vitally important for understanding where and how demographic costs will manifest.

Environmental variation shapes life history of the world's birds*C Youngflesh, K Kapsar, A Uscanga, P Williams, J Doser, L Kounta, P Zarnetske***Presenting author: Casey Youngflesh, Clemson University, cyoungf@clemson.edu*

Fluctuating environments pose a challenge for species, which must cope with variability both within and across years. Theory suggests life history plays a key role in persisting under fluctuating conditions. A slower pace of life, characterized by longer generation lengths, allows individuals to distribute reproductive effort across longer periods of time – a bet-hedging strategy against inter-annual variation. However, this notion has gone largely untested using empirical data. In contrast, evidence from a variety of birds supports the opposite pattern when considering large seasonal variation. High intra-annual variability is thought to be associated with a faster pace of life. Synthesizing a collection of global data resources on climate, traits, and ranges, we characterized the role that environmental variability has played in shaping pace of life across nearly the entirety of the world's resident bird species ($N = 7476$). In support of existing theory, we find that high inter-annual variability is associated with a slower pace of life. Intra-annual variation had the opposite relationship, likely due to high winter mortality in highly seasonal environments. These observed patterns were apparent despite strong evidence of phylogenetic constraint. Finally, borrowing an approach from evolutionary biology, we derived rates of environmental change over the last 70 years relative to intrinsic variability and species pace of life. Rates of experienced temperature change were alarming, considering proposed maximum rates of phenotypic adaptation. Quantifying these interactions is key for not only understanding observed macroecological patterns but also for determining which species might be most susceptible to climate change.

Using Long-term banding data to investigate phenological shifts in life-history events in Pacific Northwest Landbirds*R Terrill, J Wolfe, J Alexander, J Stephens, P Martins, C Ralph***Presenting author: Ryan Terrill, Klamath Bird Observatory, ornithoterrill@gmail.com*

The effects of anthropogenic global climate change on bird populations is of acute interest to the conservation and ecology of birds. Because the timing of life-history events in birds results from endogenous cascades triggered by photoperiod changes that have evolved to coincide with environmental conditions, these rapid changes may induce phenological mismatches between the proximate timing of a life history event and ultimate drivers in the form of a selective landscape, potentially reducing a population's overall fitness. The abundance of distributional data on birds have facilitated studies into shifts in distributions and phenology of presence (i.e. migration); but more detailed data are required to understand life-history events, particularly breeding and molt, which are the primary investments birds make into fitness. Here, we use bird banding data from over 30 years of constant-effort

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monitoring to model timing shifts in the phenology of breeding and molt in landbirds of the Pacific Northwest.

The ecology of Eastern Whip-poor-wills on their wintering grounds and why are they so difficult to locate on their Latin American wintering grounds.

M Ward, I Souza-Cole, A Skinner, C Tonra, G Witynski, R Sosa, H Coates, D Edlund, M Avara, T Benson

Presenting author: **Mike Ward**, University of Illinois, mpward@illinois.edu

The eastern whip-poor-will (*Antrostomus vociferus*) is a declining, though still widely distributed nightjar of eastern North America. The whip-poor-will's distinctive vocalization given at dusk, dawn, and night make them a species that can be readily monitored on their breeding grounds. Recent research using archival GPS tags have found that populations from Canada, the northeast United States and the Midwest generally winter in southern Mexico and northern Central America. We also know from historic and more recent eBird records that eastern whip-poor-wills also winter in Florida. We have searched for eastern whip-poor-wills in Oaxaca and Chiapas, Mexico on three occasions in winter in locations where eastern whip-poor-wills are known to winter (via archival GPS locations). While eastern whip-poor-wills are easily monitored on the breeding grounds and we detected many other species of nightjars, we had only one confirmed sighting, and 2 other potential detections. In January of 2024 we visited Florida in search of wintering eastern whip-poor-wills and over the course of six nights detected more than a dozen birds and archival tagged 10 individuals. We will discuss why eastern whip-poor-wills are so difficult to locate on their wintering grounds (outside of Florida), what habitats the species uses on the wintering grounds, and what research is needed to understand if the species is being impacted by loss of habitat on the wintering grounds.

Full annual cycle comparisons of the Western Cordilleran Flycatcher (*Empidonax difficilis occidentalis*) from southwestern Colorado and southern Arizona USA

C van Riper

Presenting author: **Charles van Riper**, US Geological Survey and Univ. of Arizona, charlesvanriper3@gmail.com

From 2007-2023 full annual cycles of Western Cordilleran Flycatchers (*Empidonax difficilis occidentalis*) breeding in southwestern Colorado were compared to flycatchers in southern Arizona. All breeding individuals were color-banded and 10 geolocators attached each summer during 2012-15 in Colorado and 2019-2021 in Arizona. We found no statistical differences in any physical measurement of breeding flycatchers from either location. Return rates of 17-19% were similar at each study area and only one of 700 banded flycatcher nestlings returned to their natal area for breeding and one Colorado bird was found breeding in Arizona. Breeding flycatchers arrived in Arizona one month before Colorado birds, with arrival tied closely to increasing flying insect biomass. There were no significant differences in clutch size, incubation periods, or nestling periods between the two areas, but predation rates were higher in Arizona. Fall migration was 1-month earlier in Arizona with initiation of migration at both sites related to decreasing flying insect biomass. Migration routes closely followed riparian corridors and the Sierra Madre mountain ranges in Mexico with migration taking an average of 23 days in the spring and 28 days in the fall. The Colorado flycatchers followed the eastern Sierra Madre Oriental migration corridor, whereas Arizona birds utilized the western Sierra Madre Occidental corridor. Winter flycatcher locations were south of Mexico City, through the Guadalajara, and west to Acapulco. Some of the flycatchers changed home ranges to more southern locations during the winter. Habitat types utilized during the winter were different than those selected for breeding. Although the Western Flycatcher is not presently a species of concern, this information provides a baseline for understanding parameters of full annual cycles, especially when working to conserve Neotropical migratory birds of the Americas.

Developing a bird-friendly campus: An architect's perspective

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K Sullivan, J Guth*Presenting author: Kimberly Sullivan, Utah State University, yejunco@biology.usu.edu*

Bird-window collisions are a major anthropogenic cause of avian mortality with estimates of 1 billion birds/year dying in collisions each year in the United States. A significant fraction of this mortality occurs during the day at low-rise office buildings which are commonly found on university campuses. Over the past seven years Utah State has engaged in efforts to decrease bird-window collisions by mitigating problematic windows at six buildings and using bird friendly design for seven new buildings. We report here on the success of using solar shades, feather friendly dots, bus wrapper type vinyl overlays, ceramic fritting on windows, UV signature windows, UV light projections and landscaping design in preventing bird-window collisions. We review the role of the architect and interested members of campus in the process from building design to completion and identify some of the challenges encountered.

Field testing window markers designed to reduce bird-window collisions**R Lawson, T O'Connell, S Loss, C Riding, J Elmore, G Riggs***Presenting author: Riley Lawson, Oklahoma State University, riley.lawson@okstate.edu*

Globally, numbers of annual bird fatalities from collisions with windows are likely in the billions. Research into bird-window collisions has yielded valuable information on the attributes of windows, buildings, and their surrounding environments where collisions occur. Numerous commercially available products have been designed to mitigate collisions by altering the appearance of glass on windows to make it more visible to birds. To test the efficacy of one of the most frequently used commercial products, we conducted a before-after control-impact field study of Feather Friendly® markers that were installed on 6 façades at two Oklahoma State University buildings that were monitored for collisions in a previous study conducted between 2015 and 2017. We monitored the two treated buildings, plus eight untreated buildings, for collisions ~6 days a week during spring and fall migration of 2023 and 2024. Preliminary results for fall 2023 indicate an apparent reduction of collisions at treated façades compared to untreated façades in the same time period and compared to the pre-treatment period at the same façades. Additional analyses based on spring migration data are still ongoing. This study provides insight into the potential benefits of more widespread installations of bird-friendly window products to reduce the significant global threat of bird-window collisions.

Examining nocturnal flight calls in relation to weather, topography, and avian collisions**M Chudzik, J Garcia, B Van Doren, S Lipshutz***Presenting author: Madison Chudzik, madison.chudzik@duke.edu*

Billions of migratory birds travel across North America each fall and spring. Among cities in the U.S., Chicago poses the greatest risk to this phenomenon due to the combination of high migration intensity and dangerous levels of light pollution. Acoustic monitoring of nocturnal flight calls, vocalizations emitted during migration, can provide insight into taxonomic composition and migration intensity at a local scale. We deployed a network of recording units across Chicago during the spring and fall 2023 and spring 2024 migration seasons. In addition, we obtained collision data sets from a well-established monitoring program at Loyola University. We then examined the relationship between migration intensity, topography, and the meteorological variables that best predict nocturnal flight call count, as well as collision frequency. Preliminary data reveals that sites closest to Lake Michigan had the highest number of nocturnal flight call detections, suggesting that the migrants may use the lake as a landmark when flying through the city. Furthermore, we expected a taxonomic bias when examining collision rates to the number of nocturnal flight calls detected. Results from Loyola University indicate that warbler species account for a disproportionate number of collisions relative to nocturnal flight call detections. Understanding the mechanisms of migratory success and failures at a fine geographic, temporal, and taxonomic scale can help inform when, where, and for which species mitigation efforts should focus.

Delayed mortality and migration after colliding with windows

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L DeGroot, M SarverPresenting author: **Lucas DeGroot**, degrootel@carnegiemnh.org

Bird-window collisions are the second greatest source of direct mortality for birds, and it is often asserted that 'half' or 'many' birds that hit windows and live to fly away will later die of internal injuries. But, our knowledge of these injuries is limited to a small number of birds that collided with windows and sacrificed to compare their injuries to birds that did not survive a window collision. In this study, we used the Motus WTS to monitor 133 Lotek nanotags on American Woodcock and five species of migrating landbirds found by citizen science volunteers in Cleveland, OH; Columbus, OH; Pittsburgh, PA; and Baltimore, MD 2019 - 2023. We compared their survival and migratory behavior to 88 of the same species captured via mist nets at Black Swamp Bird Observatory (NW OH), Erie Bird Observatory (NW PA), Powdermill Avian Research Center (SW PA), and Foreman's Branch Bird Observatory (MD). American Woodcocks were significantly less likely to be successfully rehabilitated and released (92.2%) than migrant landbirds (99.3%). Similarly, rehabilitated American Woodcock were less likely to be detected departing the release site than Wood Thrush (38% vs 7%); however, both were equally likely to be detected as non-rehabilitated birds en-route after departure. Rehabilitated birds spent 5 to 16 days in rehabilitation on average, and American Woodcock spent an additional five days at their release site in comparison to birds captured at banding stations. Our results indicated that bird-window collisions may have previously unmeasured direct and indirect effects through delayed mortality and delayed migration, particularly during the pre-breeding season as migrants attempt to reach the breeding grounds to establish territories.

A test of using UV light to prevent bird-window collisions.**M Koven, K Sullivan**Presenting author: **Mark Koven**, Utah State University, mark.lee.koven@usu.edu

Bird-window collisions are a major anthropogenic cause of avian mortality with estimates of 1 billion birds/year dying in collisions each year in the United States. In recent years, a number of mitigation techniques have been developed to prevent these collisions. Some building managers and homeowners are hesitant to apply these techniques as they may alter the view or change the appearance of the building. Passerine birds have UV-sensitive (UVS) visual pigments and their lenses transmit UV light while human lenses block 95% of UV light. This presents an opportunity to provide a visible signal to birds that is not visible to humans. We present here the first test of projecting UV lights on a building to prevent window collisions. We projected UV lights onto the southwest façade of the University Inn at Utah State University from June to November 2023 during the daylight hours using commercially available lights used for concerts and dances. The southwest façade of the University Inn is covered with mirrored tiles that reflect trees planted in front of the Inn, sky and mountains. We documented 174 fatal collisions from 2017-2020 (averaging 4.8/month) at the University Inn with most collisions occurring in October and November. A mass collision of 75 birds was recorded on October 31, 2019. During the six-month test period with the lights we recorded six collisions; two of these were on days when the lights were not on and three were on the edge of the facade where the light did not reach. We observed extensive use of the trees in front of the façade by birds during October and November and video recorded birds flying up to the building, hovering and then flying away. We recorded eleven fatal collisions in the four weeks after the lights were removed. The UV projection was not visible to humans and we received no complaints from guests at the University Inn nor staff working in offices in the building.

****Comparing human and dog carcass surveyors to quantify avian mortality and drivers of detection****K Boland, A Lawson, D Osterhaus, P Cutler, G Davidson, M Desmond**Presenting author: **Kelley Boland**, kcboland42@gmail.com

Birds migrating over New Mexico in the fall of 2020 experienced mass mortality-hundreds of carcasses were collected at White Sands Missile Range (WSMR) alone. Recent studies have highlighted the synergistic potential for anthropogenic disturbance and extreme weather to generate mass mortalities during migration, though other factors such as wildfire and drought may contribute. As there was no standardized data collection during the 2020 mortality event, we were unable to effectively quantify avian

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mortality. Therefore, we designed standardized carcass surveys on WSMR to (1) quantify avian mortality during fall migration; and (2) identify drivers of variation in human and conservation detection dog rates of avian carcass detection. We performed carcass surveys at 23–25 sites on WSMR during fall migration 2021–2023. Over 300 surveys were conducted each year. Fewer than 10 mortalities were detected per year during 2021 and 2022, and 136 carcasses were collected in 2023. In 2023, most birds necropsied died from emaciation, and many live birds exhibited signs of heat stress. To measure surveyor detection rates, we placed carcasses on surveys without surveyor knowledge. We conducted 1096 detection trials using 237 carcasses, representing 50 species. Humans detected 57% of carcasses (85% CI = 54%, 60%) and dogs detected 86% (85% CI = 83%, 87%). We used generalized linear mixed models to examine the effect of visual, olfactory, and effort-related variables on detection and found carcass size and ground substrate to be the primary drivers of both human and dog detection. This research is aimed to provide decision support to managers for designing rapid response surveys to accurately quantify avian mortality.

Avian Response to Heavy Mineral Surface Mine Reclamation in Southeastern Georgia

D Watson, E Hunter

Presenting author: **Dan Watson**, Virginia Tech, danwatson@vt.edu

Loss of pine savanna habitat has contributed to the decline of many disturbance-dependent or grassland birds, such as Bachman's sparrow (*Peucaea aestivalis*), northern bobwhite (*Colinus virginianus*), and common nighthawk (*Chordeiles minor*) in the U.S. southeastern Coastal Plain. Prescribed fire is the best way to maintain habitat for these disturbance-dependent species, but alternative land uses, such as timber production, can also provide habitat. However, reclaimed mining sites following heavy mineral surface mining have garnered little attention as potential habitat for these birds, nor has any study assessed the effects of this type of mine reclamation on birds within the region. Reclamation practices may alter vegetation regrowth and create distinct habitats. We compared bird occupancy and species richness across pine habitats in different site treatments (mine reclamation, timber production, prescribed fire) in southeastern Georgia. We intensively monitored communities across site treatments using autonomous recording units (ARUs) and identified bird calls using BirdNET. Initial results show all aforementioned birds of conservation concern are using mine reclamation sites (in addition to other site treatments). Estimates of species richness are 17, 20, and 28 species for timber production, mine reclamation, and prescribed fire sites respectively. Occupancy increased with increasing shrub cover for some bird species, such as Bachman's sparrow, and mine reclamation sites on average contained less shrub cover than timber production or prescribed fire sites. These initial findings show that habitats across site treatments contain different vegetation structure and may support different avian community assemblages.

**Response of boreal songbird communities to the width and on-footprint recovery of linear features created by the energy sector in Alberta, Canada

T Kalukapuge, L Leston, J Martínez-Lanfranco, E Bayne

Presenting author: **Tharindu Kalukapuge**, University of Alberta, Canada, kalukapu@ualberta.ca

The energy sector linear feature network is responsible for most of the forest dissections that have been done in the boreal forest of Alberta. From a human perspective, habitat subdivision by linear features is obvious. However, considering the vast variations in width and vegetation recovery in linear features, understanding whether songbirds include these linear features within their territories or move away from them, and under what conditions this occurs, is important. The objective of this study was framed as a question: How do songbird communities respond to linear features of varying width and on-footprint vegetation recovery? From 2021 to 2023, we surveyed bird communities associated with three types of soft linear features: seismic lines (width: 4 to 8 m), pipelines, and transmission lines (width: 15 to ~100m) in the boreal forests of northern and northeastern parts of the province using autonomous recording units (ARUs). Our results indicate that at the community level, species richness and diversity increase as the width of linear features increases, showing a clear affinity of early seral and shrub-associated species for wider linear features compared to narrower ones. At the species level, distinct differences in response to

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line width were observed, with numerous decrease and increase, with many species showing different threshold responses. The findings offer important insights into considering linear feature width and on-footprint recovery in bird models for regulatory decisions regarding boreal forest restoration in the areas affected by the energy industry.

Piping Plover (*Charadrius melodus*) demography during trophic downgrading and expansion of feral cats (*Felis catus*) at Fire Island, NY

C Wails, H Ludwig VanDerwater, H Bellman, K Black, S Dorsey, K Oliver, S Robinson, D Catlin, S Karpanty, J Fraser

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Along Atlantic coast barrier islands, red foxes (*Vulpes vulpes*) function as apex consumers that take shorebirds and impact populations of smaller mesopredators. Starting in 2015, we observed a multi-year sarcoptic mange epidemic among red foxes at Fire Island, NY. The mange epidemic severely reduced the red fox population and was followed by the expansion of feral house cats (*Felis catus*). We monitored this transition in the predator community to understand the potential impacts to the federally threatened Piping Plover (*Charadrius melodus*). Using trail cameras, we identified individual feral cats and estimated their abundance, survival, and distribution. We then compared the effects of red foxes and feral cats density on Piping Plover nest and brood survival. Following the sarcoptic mange outbreak among red foxes, the feral cat population grew from 14 to 42 identifiable individuals and feral cats had high annual survival rates ($\hat{\phi} \pm SE = 0.77 \pm 0.06$). Prior to and during early years of the mange outbreak (2013 - 2015), red fox activity was negatively correlated with plover nest and chick survival. During the predator transition (2015 - 2019), Piping Plovers fledged fewer chicks in areas with feral cat activity (mean $\hat{\phi} \pm SE$ fledging rate in low cat activity areas 0.63 ± 0.08 vs fledging rate in high cat activity areas 0.54 ± 0.05), though we did not detect a strong, population-level effect. However, in recent years (2021 - 2023), we detected a strong, negative correlation of feral cat activity and density on plover nest and chick survival. Our results underscore the importance of long-term monitoring of non-native predators during periods of trophic downgrading, which may have delayed impacts to native fauna.

Effects of a chemical repellent on reducing bird abundance and altering behavior at airports

K Urchek

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Bird aircraft collisions pose a serious risk to both avian and human safety. Non-lethal chemical repellents show promise as a tool to help reduce this risk but have not been well-studied in airport settings. We tested a non-lethal chemical repellent, Flight Control® Max (active ingredient 9,10-anthraquinone; Arkion Life Sciences, New Castle, DE), to evaluate its potential as a bird repellent in airport settings, specifically aiming to address the questions: 1) can a non-lethal chemical repellent reduce the relative abundance of common bird species on airports? and 2) does species richness vary among control sites and sites where the repellent was applied? Using a Before After Control Impact Paired study design, we surveyed birds on replicated plots at six Wisconsin airports from May to September of 2022 and 2023. The foliar repellent was applied a total of 5 times each season at three airports, and birds were surveyed at paired control and treatment plots at these airports before and after application. Three airports were left untreated, and birds were also surveyed at paired plots at these sites at the same frequency and over the same time period. Some of the most common bird species observed at airports during the study period were red-wing blackbirds (*Agelaius phoeniceus*), brown-headed cowbirds (*Molothrus ater*), and American crows (*Corvus brachyrhynchos*). Preliminary analyses suggest that the Flight Control® Max repellent may be associated with reduced abundance on treated plots and increased abundance on control plots for bird species. Our findings could be used to inform bird management practices within airport settings and explore non-lethal ways of resolving human-wildlife conflicts.

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Identifying a pathway forward for transmission and clean energy that accounts for birds: Audubons Birds and Transmission Report

B Bateman, J Fuller, L Taylor, N Seavy, J Grand, C Wilsey

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To achieve climate change stabilization, we need a rapid build-out of clean energy and the transmission infrastructure needed to support it. However, because of the complex relationships between birds and transmission it is imperative that the expansion of clean energy and transmission is done thoughtfully. Here we provide an overview of the current scientific understanding of the impacts of transmission infrastructure on birds as well as key bird-friendly solutions that can be implemented to help reduce negative consequences. We also identify and map areas of high priority for birds in the US that coincide with existing, planned, and potential transmission build-out. These high priority areas for birds were developed by integrating multi-scale spatial prioritizations to identify the most important places for birds within the US. This brings together key areas for migratory birds that breed in North America across their full annual cycle alongside 'climate strongholds' that are predicted to have high climate suitability and low human modification for bird species at present, and under contemporary climate change scenarios in both breeding and nonbreeding seasons. We identified areas of potential for collisions with transmission as well as areas of potential habitat degradation and disturbance and found that roughly a third of existing, planned, and potential transmission lines coincide with areas that are important for birds. These areas are identified as high priority for where conservation organizations and practitioners should engage in project planning and development to ensure that the bird-friendly practices are integrated in each project from the beginning.

Impacts of wildfire at whole ecosystem scales: Leveraging remote sensing to model bird-habitat associations across historical and contemporary piñon-juniper landscapes

R Crafford, I Breckheimer, H Jones, J Coop

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Changing fire regimes in the western United States raise questions about how fauna will respond. Piñon-juniper (PJ) ecosystems historically have experienced infrequent, high-severity burns, but on the Mesa Verde cuesta in southwestern Colorado (Ní'u-agma-té'vê%-pê%l± [Ute] Lands), recent repeat burns have led to widespread shifts in vegetation structure and composition. While the relatively recent availability of remote sensing technology has shown promise for monitoring habitat changes at large spatial scales, to our knowledge no prior studies have used these methods to model fire-driven shifts in PJ bird communities. We fit Bayesian N-mixture models to explore bird species density and abundance across PJ woodlands and areas that are experiencing little to no PJ regeneration after fire. We used field-based point count data, discrete-return aerial LiDAR data, and Landsat satellite imagery to quantify habitat associations for 18 different bird species, and found numerous supported responses to canopy cover, vegetation height, and deciduousness, though most species exhibited supported responses to covariates explicitly related to fire. Burned habitat showed the most predictive power for birds associated with PJ woodland habitat, all of which decreased in abundance. Notably, 58% of PJ birds increased with time-since-fire, suggesting that while conditions immediately following fire are unsuitable, these species may not be lost in the face of fire-driven habitat conversion. We offer a framework for using widely available remote sensing technology to predict fire-induced changes in bird communities at the ecosystem level and contribute to our understanding of ecological cascades that may occur in the aftermath of contemporary burns.

Nesting success of Tree Swallows at abandoned mine drainage treatment ponds is relatively high but absolutely low

J Kellam

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The presence of abandoned mine drainage treatment ponds in the vicinity of nesting Tree Swallows

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(*Tachycineta bicolor*) could have contrasting effects on their reproductive success. The ponds may, like any other body of freshwater, provide habitat for the larval stage of aerial insects that the birds feed their young; or the ponds may act as an ecological trap, attracting the birds to habitat that is poor in quality and negatively impacting their productivity. We monitored nests in artificial boxes to determine whether distance between the ponds and the nests affected various reproductive parameters including clutch size, hatch rate, number of nestlings, nestling size and mass, number of fledglings, fledging rate, and fledge date. We found that the group of nests closest to the treatment ponds had significantly more nestlings and fledglings, earlier fledge dates, and a better fledging rate when compared to the group of nests more distant from the ponds. However, all these parameters were well below previously published values, which suggests the mine drainage ponds provide good nesting habitat relative to what is available in the region, but that they do not represent high quality habitat for this species overall.

Using modelled distribution maps to create sensitivity maps for wind turbines and recreation zonation

H Sierdsema

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Modelled distribution maps are a valuable tool for planning and impact assessments. By combining information on the known impact of human pressures like wind turbines and recreation with distribution maps an assessment can be made how existing and planned pressures may influence bird populations. By combining bird data from various sources with environmental data detailed distribution maps at a scale of 250x250 m are available for both breeding and non-breeding birds in The Netherlands. We combined these distribution maps with known information of the impact of wind turbines and recreation on birds to create sensitivity maps. This process starts with converting the distribution maps, ie abundance maps, into so-called hotspot maps by defining the smallest possible areas where x per cent of the population occurs. These are referred to as 'quantile maps' that transform abundance maps into binary maps that are comparable between species. Information on the impact of the pressure and policy status like Red List status is used to give different weights with respect to the pressure to each species. The weighted quantile maps are then combined into sensitivity maps, either for all species combined or for example for different habitat groups. These sensitivity maps are used by both policymakers and civilians to preventing or mitigating the effects of these pressures on bird populations

Differential neonicotinoid exposure between migrant and resident birds: testing hypotheses at a high-volume spring stopover site in coastal Texas

M Anderson, B Blackwell, E Sanchez Rivera, C Farrell, A Janik, E Cohen, E McBride, J Fair, S Hamer

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Neonicotinoids are the most used insecticides in the world and are an important threat to migrating birds. Neonicotinoids' high water solubility and long half-lives promote accumulation in soil and water. Birds can be exposed to them by ingesting contaminated insects, seeds, water, nectar, or soil; migrating birds may be predisposed to neonicotinoid exposure through consuming large quantities of food at unfamiliar stopover sites. Neonicotinoids have been experimentally shown to affect migrating birds through severe mass loss, impaired orientation, and delayed departure timing. These effects could carry-over as lower condition birds arrive later to breeding grounds, resulting in worse reproductive outcomes. Across spring migrations in 2022 and 2023 we collected 496 blood samples and 135 fecal samples from birds at a high-volume stopover site in the Gulf of Mexico, with focal representation of Gray Catbirds (*Dumetella carolinensis*; a migrant) and Northern Cardinals (*Cardinalis cardinalis*; a resident). We will test these samples for seven neonicotinoids and seven metabolites using high performance liquid chromatography and mass spectrometry at the Mass Spectrometry Center at Los Alamos National Laboratory. Detection of parent compounds in plasma indicates acute exposure (<24 hours) whereas detection in feces can indicate weeks-old exposure, allowing us to build novel 'exposure timelines' for each bird. We will determine if migratory strategy, phenology, and foraging guild predict neonicotinoid quantities. We expect

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later-season and insectivorous migrants to have the highest overall exposures. This field study is critical to future mechanistic studies to understand how pesticide exposure impacts migratory bird health.

Insecticide exposure and associated physiological effects to migratory shorebirds in the Prairie Pothole Region

S McCahon, C Conway, K Christie, C Morrissey*Presenting author: Shelby McCahon, University of Idaho, smccahon@uidaho.edu*

Many shorebirds in North America use agricultural areas in the Prairie Pothole Region to refuel during critical migratory stopovers, but rapid increases in neonicotinoid insecticide use may pose risks to their ability to efficiently refuel and migrate. Neonicotinoids can suppress appetite, lower refueling rates, and cause rapid mass and fat loss. Our project objectives are twofold: 1) quantify neonicotinoid concentrations in water, invertebrates, and shorebird plasma at wetlands in North and South Dakota, and 2) document the relationship between shorebird body condition and neonicotinoid concentrations. During spring migration, we detected neonicotinoids in 47% of 48 water samples (66% in 2022 and 41% in 2023). During fall migration, we detected neonicotinoids in 7% of 52 water samples (33% in 2021 and 2% in 2023). Water neonicotinoid insecticide concentrations were below levels known to affect aquatic organisms (Toxic Units < 1; max. = 0.18) in all seasons despite frequent detections. However, higher concentrations during spring migration after snowmelt but before crop seeding suggest a long-term exposure risk. During spring migration, we detected neonicotinoids in 60% of 66 shorebird plasma samples (96% in 2022 and 32% in 2023). During fall migration, we detected neonicotinoids in 20% of 108 shorebird plasma samples (33% in 2021 and 16% in 2023). Our results are the highest neonicotinoid concentration reported in a wild bird that consumes neonicotinoids indirectly (1012 Åµg/L). Given our results, more studies are warranted to better understand the extent of neonicotinoid insecticide exposure and associated physiological effects to the many shorebirds in this region.

Factors modulating habitat selection near roads by golden eagles during winter in Wyoming

J Layfield, B Bedrosian, A Chalfoun, R Domenech, S Lewis, B Smith, J Merkle*Presenting author: Joshua Layfield, University of Wyoming, jflayfield@gmail.com*

When foraging, animals often face trade-offs wherein foraging opportunities may coincide spatiotemporally with higher risk of mortality, especially within landscapes altered by humans. Resolving such tradeoffs can depend on intrinsic and extrinsic factors within the surrounding environment, yet both are rarely assessed simultaneously within the same context. Roadways are a widespread form of habitat change that simultaneously offers potential food rewards (i.e., roadkill) and danger (i.e., risk of vehicle collision). We evaluated the extent to which suites of intrinsic and extrinsic factors modulated the selection for areas near roads by golden eagles overwintering in Wyoming during 2014 to 2023. We used a large, collaborative GPS dataset that included 51 eagles representing 175 ID-Years. Adult males and residents were more likely to select areas closer to roads than any other demographic. Moreover, individuals were more likely to select areas near roads during years with low primary prey availability as assayed by cottontail harvest by hunters. Our results suggest that both intrinsic traits of individuals and extrinsic factors can influence proximate habitat decisions and the use of risky landscape elements. Moreover, our work has important implications for the contexts under which efforts to reduce eagle mortality, such as the removal of carcasses from roadways, would be most effective.

Landscape changes lead to declines in local Golden Eagle (*Aquila chrysaetos*) territory occupancy in the Morley Nelson Snake River Birds of Prey National Conservation Area

A Santiago, J Cruz, D Delparte, M Kochert, K Steenhof, J Weldon, J Heath*Presenting author: Ashley Santiago, Boise State University, ashleysantiago@u.boisestate.edu*

Rapid loss of native shrubs and expansion of invasive annuals like cheatgrass (*Bromus tectorum*) have

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extensively altered shrub-steppe systems. A drastic change in vegetation can have bottom-up effects on the ecosystem dynamics including the availability of prey species that rely on shrub-steppe habitats like black-tailed jackrabbits (*Lepus californicus*), the preferred prey of Golden Eagles (*Aquila chrysaetos*). We used a multi-season occupancy model that accounts for imperfect detection to investigate the relationship between landscape variables associated with habitat quality and eagle territory occupancy of 36 Golden Eagle territories in the Morley Nelson Snake River Birds of Prey National Conservation Area (NCA), Idaho, USA from 1986-2022. Preliminary results revealed that the probability of Golden Eagle occupancy decreased 25% from 0.84 in 1986 to 0.59 in 2022. Territory occupancy was negatively associated with annual herbaceous cover ($\hat{\beta}^2$: -0.86, 95% CI: -1.53 to -0.24) and positively associated with shrub cover ($\hat{\beta}^2$: 0.63, 95% CI: -0.11 to 1.39) and time since last burn ($\hat{\beta}^2$: 0.25, 95% CI: -0.28 to 0.83). Territories that were farther from other occupied territories had a higher probability of occupancy ($\hat{\beta}^2$: -3.56, 95% CI: -4.218 to -2.92), likely because as habitat degraded, eagles compensated by expanding their territories into nearby vacant territories. The probability of detection was high at 0.90 but improved in surveys conducted earlier in the day and later in the breeding season. Together, these results show that habitat degradation has bottom-up effects on Golden Eagles, resulting in an overall decrease in the local carrying capacity for eagles.

***The impacts of avian ecology on the distribution of lead pollution in the environment**

J Brown, M Salazar, A Specht, S DuBay

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Lead (Pb) is a highly toxic heavy metal that is now common in the environment due to human activity. Pb pollution has been well studied in soils, water, and organisms, but we know surprisingly little about how Pb pollution moves through food webs or why Pb accumulates differently among species and populations. Answering these questions would allow us to identify species and habitats that are most susceptible to Pb contamination. This research requires measuring Pb levels in different species over time and space, which has been difficult with conventional methods of Pb testing and field sampling. Here, we measure Pb in bird specimens in natural history collections. These specimens are abundant, representing numerous species, life history strategies, trophic levels, localities, and time periods (late 1800s to present). We use a rapid and non-destructive method of measuring Pb levels in bird specimens using a portable X-ray fluorescence (pXRF) analyzer. We have refined this method to obtain accurate measurements of bone Pb content ($\mu\text{g per mg bone tissue}$) by scanning leg bones of bird specimens. As we obtain Pb data from thousands of bird specimens from the Great Lakes region in the US (which has a long history of industrial pollution), we can determine how Pb levels in birds vary in association with ecological traits (like diet type, trophic level, or habitat preference). Uncovering these relationships would support the general hypothesis that the long-term fate of Pb pollution in the environment is shaped by organismal ecology. This work will also serve conservation efforts of birds affected by Pb pollution.

Responding to pressure: Changes in air pressure as anticipatory cues for bird behavior

W Hochachka, T Auer, C Crowley, D Fink, S Ligocki, L Oldham Jaromczyk, O Robinson, A Rodewald, M Strimas-Mackey, C Wood

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Anticipating changes in weather, rather than reacting to changes as they are occurring, will likely lead to better responses to changing weather. Migrating birds have been shown to be able to anticipate appropriate atmospheric conditions for migration by sensing changes in air pressure. For our presentation, we are asking whether changing air pressure is being used by birds to alter their behavior in other ways, at times of year outside of migratory seasons. We will present evidence suggesting that birds are responding to changes in air pressure by altering their behavior. For our analyses, we combined records of bird observations from eBird with information about meteorological conditions at the times that these observations were being made. For diverse passerine bird species, the rate of change in air pressure at the time of observation is associated with detectability of these species. The patterns of

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change in detectability are more consistent with alterations in the activities of birds in response to changing air pressure, rather than with changes in observers' ability to detect birds (e.g., lower detection rates with higher wind speeds). For applied research, our results suggest that controlling for changes in detectability with changing air pressure will improve estimates of occurrence and abundance from bird survey data. More broadly, our results suggest the potential for future research that examines a range of behavioral responses of birds to cues provided by changing air pressure.

What's the Rumpus? The Intercontinental Perception of Avian Alarm Calls*J Dominguez, M Rakovic, D Li, H Pollock, S Lawson, I Novcic, X Su, Q Zeng, R Al-Dhufari, M Bolger, S Johnson-Cadle, J Boldrick, A Bush, M Chamberlain, M Hauber***Presenting author: Jonah Dominguez, University of Illinois at Urbana-Champaign, jonahsd2@illinois.edu*

Alarm signals have evolved to communicate imminent threats to conspecifics but animals may also perceive other species' alarm displays to obtain adaptive information. In birds, mixed-species foraging flocks are often structured around a focal sentinel species, which produces reliable alarm calls that inform eavesdropping non-sentinel heterospecifics about predation risk. Ongoing work has revealed that several species can recognize the alarm calls of certain sentinel species even without prior encounters, including when these are from a distant biogeographic region. We tested for the responses to the alarm calls of a Neotropical sentinel forest bird species, the dusky-throated antshrike (*Thamnomanes ardesiacus*), by naive resident temperate forest birds across three continents during the winter season. However, this did not examine whether naive subjects' responses to unfamiliar sentinel calls differ from responses to non-sentinel calls. We played the alarm calls of three subtropical Asian bird species that participate in mixed species flocks, for temperate North American birds. Here birds responded most to the alarm call of a core sentinel and a local positive control species, less so to a secondary sentinel, and least so to a non-sentinel and a negative control stimulus. These patterns provide evidence that broad phylogenetic and geographic recognition is a pertinent aspect of sentinel alarm calls in general.

****Influence of floral orientation on feeding behavior in Anna's Hummingbirds****J Choi, S Glassman, R Dudley***Presenting author: Sierra Glassman, sierraruyi@gmail.com*

Hover-feeding by hummingbirds from pendent relative to horizontal flowers increases the metabolic cost of flight, but in nature a large proportion of hummingbird-pollinated flowers are oriented near-vertically downward. Here, we investigated via binary-choice tests the behavioral preference of Anna's Hummingbird for particular artificial floral orientations. Rates of nectar depletion and feeding durations between the two flower orientations differed significantly, with captive birds showing a clear preference for the horizontal over the pendent configuration. Opportunistic measurements of wild hummingbirds also suggested a preference for horizontal flowers through a significant difference in feeding durations. These observations suggest that the increased metabolic cost of hover-feeding from pendent flowers is matched by an associated behavioral aversion, at least under the conditions studied here. Pendent flowers pollinated by hummingbirds are nonetheless common in nature, suggesting that additional behavioral or ecological factors underpin persistence of this floral presentation.

Assortative behavior in North American Barn Swallows (*Hirundo rustica erythrogaster*)**O Morosse, T Tsunekage, R Safran, H Kenny-Duddela, D Schield, I Levin***Presenting author: Iris Levin, Kenyon College, levin1@kenyon.edu*

While female mate choice is well established, mutual choice may play a larger role in mate selection than recognized. One possible outcome of mutual mate choice is assortative mating, which occurs in many species of birds. We asked whether North American Barn Swallows (*Hirundo rustica erythrogaster*) paired, mated, and interacted socially with individuals of similar phenotype. We investigated patterns of assortativity in ventral plumage color, tail streamer length, wing length, mass, age, arrival date, and social interactivity for adult Barn Swallows breeding in Ohio and Colorado. Social interaction data came from

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proximity loggers, which recorded close contact between tagged individuals when birds were mating and laying eggs. Social pair formation was strongly constrained by arrival timing to the breeding colony since pairs formed between birds who arrived at similar times. Because after-second-year birds typically arrive earlier than first-year breeders, social pairs also tended to assort by age. In Ohio, where there is more variation in ventral plumage color, birds paired with individuals of similar plumage color, but only when we considered color relative to the colony- and sex-specific means. Barn swallows regularly engage in extra-pair copulations, and mating pairs were more strongly assortative by ventral plumage color than social pairs. Birds also exhibited strong social network assortativity, interacting more often with individuals of both sexes who had relatively similar phenotypes. Investigation of assortative behavior beyond the level of the social pair provides a more complete understanding of the fine scale details of the mating process.

***Accipiter visual discrimination corresponds to squirrel pelage coloration supporting the background matching hypothesis**

S Mahoney, B Pasch

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Coloration can help animals avoid predation from visual predators like hawks by matching the background environment (i.e., crypsis). Diurnal tree squirrels may be especially vulnerable to hawk predation as they forage for food. For example, fox squirrel (*Sciurus niger*) pelage is associated with variation in ground substrate and tree bark coloration, supporting the background matching hypothesis to avoid hawk detection. However, previous studies on prey pelage color are often biased to human visual systems, despite hawk sensitivity to both ultraviolet and visual light spectra (300-700 nm). We integrated reflectance spectrometry of museum specimens and the environment with avian visual discrimination models to test if *Accipiter* hawks can distinguish the color of Abert's (*S. aberti*) and southwestern red squirrel (*Tamiasciurus fremonti*) pelage against cache locations in the Pinaleno and White Mountains, Arizona, USA. Red squirrels larderhoard evergreen cones in central larders termed middens, while Abert's squirrels scatterhoard food throughout the forest floor. The background matching hypothesis predicts that hawks are unable to distinguish squirrels against their cache locations. Consistent with the background matching hypothesis, hawk visual models indicated that larderhoarding red squirrels are concealed against their middens but conspicuous against the forest floor. Conversely, scatterhoarding Abert's squirrels were conspicuous against middens but concealed against the forest floor. Our results highlight the utility of incorporating predator umwelt and indicate that hawk predation can drive interspecific variation of prey color based on background matching.

****Bivouac-checking behavior: an understudied mode of resource tracking in ant-following birds**

M Castaño, H Pollock, C Tarwater, J Kelley

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Mixed Species Animal Groups (MSAGs) are the result of complex interactions that act as a significant selective force driving behavioral evolution. A commonly observed MSAG in the tropics is that of army-ant-following bird flocks. Army ants are voracious nomadic insects that form large raids in search of food driving away invertebrates and small vertebrates, providing a profitable resource that attracts multiple bird species. The most dependent birds to this interaction exhibit bivouac-checking behavior (BCB). However, this specialized behavior remains unstudied and may be more common between ant-followers of different dependency levels (obligate, facultative, and occasional followers). In central Panama, we deployed camera traps for 812 days at bivouacs (n=30) and at control (non-bivouac) sites (n=18) to examine how BCB is used by the bird community over the stationary and nomadic phases of the life cycle of army ants. We detected 1324 individuals of 25 species exhibiting BCB, of which we described BCB for 17 new species. Obligate species were the most detected, followed by four facultative species, representing 59.3% and 28.2% of detections, respectively. Occasional species comprised the remaining 12.5% of detections. Obligate species displayed different patterns of visitation influenced by the activity stage of army ants, throughout the day and year. Eight species were detected checking old

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bivouac locations of nomadic swarms between 1-4 days after the ants entered their nomadic phase. These results suggest that birds exhibit episodic-like memory for temporal and spatial information related to an unpredictable resource. This study helps us understand how BCB impacts the formation and maintenance of complex communities.

California Condor presence, vigilance, and competition at foraging sites

A Blanche, M Conover, N Frey*Presenting author: Alex Blanche*, Utah State University, a.blanche@usu.edu

California condors (*Gymnogyps californianus*) were reintroduced to Southern Utah relatively recently, and while foraging is a necessary component of their survival, their presence at carcasses may impact the historic scavenger community. Condors are large and feed socially, and therefore may monopolize food resources. If condors can exclude other scavengers, unintended, widespread shifts in trophic interactions could occur. Little is known about condors' foraging patterns, including amount and type of carcasses consumed, diversity of foraging habitat, and interactions with other scavengers. There is a scarcity of information regarding avian scavenger behavior across habitat and group size, which may impact the extent to which communities are affected. I set out camera traps to record scavenger activity at 89 carcasses over summer 2022 and 2023, including natural mortalities and carcasses that I set out. I describe foraging efficiency of condors by the duration of time spent feeding and the proportion of each carcass consumed. Condors were most likely to arrive at carcasses with less understory cover, and condor vigilance was most affected by wind and temperature. Eagles displayed an interactive effect between distance to roads and understory cover, displaying similar foraging site preferences as condors when close to roads. Eagles increased their vigilance with larger group sizes and more displacements. Vultures were more likely to arrive earlier in the season and were more vigilant at larger carcasses. Future research should monitor population densities of avian scavengers in relation to condor reintroductions, especially where the majority of carcasses are accessible to condors.

Solitude, monogamy, competition, and cooperation: do social structures drive alarm calling patterns in neotropical birds?

V Weber*Presenting author: Vincent Weber*, University of California - Santa Cruz, viweber@ucsc.edu

The threat of predation poses significant risks to animal survival, and many species have developed anti-predator defenses in an ecological arms race to offset this risk. Alarm calls are a common strategy to mitigate such danger, however, there is a lack of direct tests that explore variation in alarm call propensity across social group structures. We classified five different social groups expecting predictable differences in alarm frequency among them: 1) solitary individuals, 2) monogamous pairs, 3) competitive groups, 4) single-species flocks, and 5) mixed species flocks. Using an artificial predator stimulus—a model hawk fly-by—we conducted experiments in the Peruvian Amazon to investigate alarm calling behaviors across different social groups. Our results indicate a positive correlation between social complexity and alarm call frequency, with singles showing the least likelihood, pairs exhibiting some alarm calling, and competitive groups not alarming. In larger groups, single-species flocks show heightened alarm calling, and mixed-species groups generate alarm calls with the highest frequency, likely because multiple species generate alarms. These findings support our hypotheses, highlighting the importance of social dynamics, group size, and species richness in shaping alarm calling behaviors among neotropical birds, reinforcing the significance of collective defense strategies in enhancing survival. This research provides insights into the adaptive significance of alarm calling and the complex association between variable social structures and anti-predator defense strategies in avian communities.

***Empirical tests of the hygric niche model: Unveiling tropical avian responses to rainfall through bioacoustic analyses**

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Hygric niche theory predicts that in very wet areas, increased rainfall will constrain certain avian behaviors and result in elevated energetic costs for birds. Such responses are expected to be more pronounced when birds are exposed to cooler temperatures, such as those experienced at higher elevations. In wet tropical forest spanning lowlands and premontane forest in Costa Rica, I tested behavioral predictions of the hygric niche model. Working in leks of white-collared manakins (*Manacus candei*), I evaluated how the rate of display behavior varied in the presence of different rates of rainfall, predicting either a linear or step function reduction in display activity in response to increased rainfall. I expected similar rainfall conditions at higher elevations (cooler temperatures) to elicit a steeper reduction in display behavior. I deployed rain gauges and audio recorders at a total of 16 display courts and analyzed ~900 hours of bioacoustics data informed by over 72 hours of behavioral observations. I quantified display behavior using Open Soundscape, training a convolutional neural network to identify display behaviors at the appropriate volumes. Rain inhibited display behavior, and display rates dropped off more steeply at high elevations than at low elevations when comparing the same rainfall rates. Like other aspects of climate, rainfall is critically important to birds – but in ways that are poorly understood relative to effects of temperature. Understanding the mechanistic relationship between environment and rainfall can elucidate climate's influence on demography, ultimately informing mechanistic species distribution models.

***Color pattern differences reduce aggression between closely related species in sympatry**

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Signals like color patterns mediate interactions among animals that live together, and are thus important for reducing costly encounters, such as fights. Color pattern divergence is common among closely related species of birds that live together, largely due to the role that signals play in species recognition, enabling individuals to distinguish members of their own species (conspecifics) from other species (heterospecifics). We still, however, have much to learn about the selective pressures that drive this pattern and the other forces that influence it. Specifically, the importance of signal divergence for coexistence remains controversial due to the idea that species recognition can be enhanced in the absence of selection for signal divergence, simply through learned responses to heterospecifics or the evolution of refined species discrimination in areas of co-occurrence. To test whether color pattern divergence reduces between-species aggression in sympatry, we conducted field experiments in a contact zone between chickadee (*Poecile*) species, where interactions between species are common. In both breeding (territory defense) and wintering (competition for food) contexts, we tested whether birds are more aggressive towards models of sympatric or allopatric males. We compared these responses to those of naïve birds far from areas of range overlap. We found that contact zone birds were less aggressive towards the more divergently colored sympatric heterospecifics in some contexts, suggesting that experience with heterospecifics may influence color-based species recognition in aggressive contexts.

Sexual dimorphism in flight morphology drives sexual dimorphism in flight performance under some, but not all, conditions in House Sparrows (*Passer domesticus*)

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Sexual dimorphism in bird flight structures, including the flight muscles, is likely widespread, but the functional implications of this morphological dimorphism are unknown. In House Sparrows (*Passer domesticus*), males' flight muscles, relative to overall body size, are about 5% larger than females'. We tested how these differences in flight muscle size affect flight performance under multiple conditions. First, we investigated natural, escape-style takeoffs where birds flew horizontally away from the experimenter, conducting multiple trials per bird: with an added 1.4g weight (ca. 5% of body mass) and unweighted. Sex did not significantly predict takeoff velocity under either condition in these trials. Flight muscle size significantly predicted takeoff velocity for weighted, but not unweighted, trials. Next, we tested flight

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performance in vertical escape-style takeoffs, where birds were constrained to fly straight up to escape the experimenter. All birds were tested twice: unweighted in the first trial, and half with an added 1.4g weight, half unweighted in the second trial. In these vertical experiments, males flew significantly faster than females when weighted, but not when unweighted, and flight muscle mass was correlated with takeoff velocity when birds were weighted, but not unweighted. Our results indicate that differences in flight muscle size cause differences in flight performance when birds are particularly challenged.

***Using power to test if the theory of resource holding potential applies to male-male fighting in hummingbirds**

R Elting, M Anwar, D Powers, B Cheng, H Luo, B Tobalske

Presenting author: Rosalee Elting, University of Montana, rosalee.elting@gmail.com

An organism's ability to maneuver is critical for escaping predators and intraspecific fighting and is likely a focus of intense selective pressure. In hummingbirds, escapes are stereotypical, brief (~200ms) and require extreme power. Here we measure what occurs when an animal engages with an encroacher, a behavior regularly seen in territorial agonism in this group. Combat success of an individual provides access to mates and/or food resources. We predicted there should be tradeoffs between these benefits to fitness versus energetic costs of fighting and of maintaining flight morphologies for enhanced maneuverability. These tradeoffs are evident in some taxa (e.g. ungulates) where fighters are making choices based on their resource holding potential (RHP). Tradeoffs and the influence of RHP are largely unstudied in hummingbirds, so to improve understanding of the evolution of maneuvering flight in this group, we studied male-male fighting in calliope hummingbirds (*Selasphorus calliope*, n=4). The birds fought in paired trials in a flight arena, and we measured metabolic power requirements and tested the utility of power for predicting resource use and dominance hierarchy. In contrast with escape, agonistic interactions between male hummingbirds typically occurred over multiple seconds and featured a rich array of maneuvers. Fighting escalation and de-escalation were consistent with governing principles of contest theory, indicating mutual assessment of RHP. Suggesting evolutionary tradeoffs, metabolic power requirements for fighting exhibited greater variance in competition and were elevated when competitors were close to each other for RHP. ONR N000141912540

Vertical territory mapping of songbirds in the H.J. Andrews Experimental Forest

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In a seminal study of niche partitioning, MacArthur (1959) described how five species of warblers occupy different vertical strata in forests in the northeastern United States. However, studies of interspecific territoriality of songbirds have traditionally been conducted in two-dimensional, horizontal space rather than three-dimensional space. We investigated the vertical distributions of songbirds in the H.J. Andrews Experimental Forest (Oregon) to test whether vertical partitioning can explain coexistence of species with similar dietary habits. On the basis of niche partitioning theory, we hypothesized that different species of birds restrict their territories to distinct vertical strata. We conducted conspecific playbacks across the vertical extent of seven old-growth and seven second-growth Douglas-fir (*Pseudotsuga menziesii*) trees to map vertical territories of nine focal species (Wilson's Warbler, Hermit Thrush, Swainson's Thrush, Pacific-Slope Flycatcher, Hammond's Flycatcher, Chestnut-backed Chickadee, Golden-crowned Kinglet, and Hermit Warbler). We selected focal species on the basis of their expected height associations (understory, midstory, or canopy) from the literature. We collected data on the vertical extent of territorial behavior. Our results show that several species (e.g., Pacific Wren, Swainson's Thrush) showed remarkably strong upper limits to territoriality, whereas others (e.g., Hermit Warbler) responded aggressively to playback across the entire vertical gradient, which in some cases ranged >70 m. However, we found considerable intraspecific variation in vertical territory distributions, which we speculate could be due to variability in the presence of heterospecific competitors.

Female black-capped chickadees (*Poecile atricapillus*) exhibit different pairing

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patterns based on body size than female mountain chickadees (*Poecile gambeli*)**S Padula, K Grabenstein, W Anderson, N Addison, A Patel, H Kenyon, A Theodosopoulos, M Larrieu, S Taylor***Presenting author: Sara Padula, University of Colorado Boulder, sara.padula@colorado.edu*

In biparental species, choice of a social mate can heavily influence an individual's fitness; thus, selection should favor both males and females to pair with a high-quality social mate. When females are the choosier sex, they typically rely on either morphological signals or behavioral signals as indicators of male fitness. A common trait that influences social partner choice is body size because it is often associated with higher fecundity, competitive ability, and overall quality. Black-capped (*Poecile atricapillus*) and mountain chickadees (*Poecile gambeli*) are monogamous songbirds that coexist along an elevational gradient in the Rocky Mountains of Colorado. Given their ecological similarity but disparate evolutionary histories, they are an excellent species pair for exploring differences in female size preferences in biparental bird species. Using five years of morphometric and reproductive data from a transect of 400 nestboxes in the Rocky Mountains of Colorado, we constructed linear models and performed simulations to determine if females tend to pair with males smaller, slightly larger, or much larger than themselves, whether patterns of mate choice differed between the two species, and whether preferential pairing resulted in better reproductive outcomes. We found that females of both species avoid males smaller than themselves, but that black-capped chickadees females prefer males much larger than themselves, and that mountain chickadees prefer males slightly larger than themselves. Despite this significant difference in mate choice behavior, we found no positive correlation between mate size differential and reproductive success.

Provisioning in a cooperative bird with multiple breeding females per group**C Poje, D Thrasher, W Feeney, M Webster***Presenting author: Colleen Poje, Cornell University, clp226@cornell.edu*

When reproduction is costly, maternal investment strategies are central to life-history decisions. Cooperative breeding can lead to a diversification of maternal investment strategies. This diversification hinges on the amount of help provided by the additional group members. Most studies of maternal investment in cooperative breeders have utilized kin-based systems where one breeding female dominates reproduction. Few studies have looked maternal investment in more genetically complex cooperative groups and how it is influenced by the addition of independently nesting co-breeding females. By studying variegated fairywrens, *Malurus lamberti*, we explore the impact of additional breeding females on maternal investment in a genetically complex system. We compared patterns of nestling provisioning by breeding females at their own nests in groups that were singular non-cooperative, singular cooperative (one breeding pair) or plural cooperative (multiple breeding pairs). Our findings suggest that the addition of breeding females to a social group may result in the loss of investment benefits seen when only one breeding female is present in a cooperative group.

Breeding stage-specific habitat use of the Mountain Plover in Colorado*C Weissburg, A Pierce, M Wunder, C Ramos***Presenting author: Casey Weissburg, cmweissburg@gmail.com*

Factors like habitat structure, food availability, and predation risk have spatiotemporal variation on the landscape, creating tradeoffs between risk and rewards for animals as they use habitat, and these tradeoffs can vary by life stage or breeding stage. We investigated habitat use in the Mountain plover as an exemplar of a ground-nesting species with precocial young that breeds in grasslands, providing an opportunity to explore site- and breeding stage-specific responses to three categories of environmental covariate: habitat structure, food availability, and predation risk. We monitored nests and broods at two study sites in distinct breeding regions of Colorado and quantified the three covariate categories across a standardized site-wide grid in 2021 and 2022. We employed a used vs. available framework in a logistic regression for nest and brood locations and developed a series of a priori models hypothesizing which of the three categories best explained plover use relative to availability on the landscape, including

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interactive models predicting dependence on breeding stage, and study site as an additive term to control for site effects. Model selection results suggest that plover use relative to availability is best explained by a nonlinear relationship with vegetation structure which is also dependent on breeding stage. Specifically, probability of use for nests was highest in areas with shorter vegetation, consistent with previous research, while probability of use for broods had a quadratic relationship with groundcover height and bare ground coverage, with highest use at the extremes of these vegetation features. These results provide further support for investigation of stage-specific habitat use for species with precocial young, particularly species in decline with management strategies that may not consider the full range of needs.

Effects of Parental Care Behavior on Fledging Success in the Endangered Puerto Rican Parrot (*Amazona vittata*)

B Ramos-Guivas, T Wright*Presenting author: Brian Ramos-Guivas, New Mexico State University, brianrg@nmsu.edu*

Parental care is a fundamental aspect of bird behavior that is crucial for offspring survival. For endangered species in captive breeding programs, the impact of captive conditions adds further complexity, and importance, to understanding the dynamics of parental care and their effects on reproduction. Our study examines the relationship between parental care behaviors and reproductive success in the endangered Puerto Rican amazon (*Amazona vittata*), with a specific emphasis on understanding how these behaviors may differ based on sex and population. Using video recordings, we quantified the number of feeding bouts in a nest visit, the average feeding bout duration and duration of a nest visit and examined the relationship of these parental care behaviors to fledgling production. We hypothesized that parental care behaviors would influence reproductive success and we predicted differences based on sex and populations. Our results confirm that the total number of bouts and the bout average duration affects the total number of fledglings produced by pairs. Notably, we found that sex influences parental care behavior, with females exhibiting a greater tendency to spending more time inside the nest compared to males. Additionally, captive birds display lower total feeding bouts than wild birds. We also found that average chick age and pair duration influenced certain aspects of parental care behaviors, suggesting the need for consideration in future studies of parental care. Anticipating potential challenges to bi-parental care through similar programs of video monitoring could contribute to refining captive breeding programs and conservation efforts for other endangered bird populations.

****Physiological consequences of breeding later in a Neotropical migratory bird: implications for behavioral responses to a warmer, greener Autumn**

A Brunner, C Taff, S Kaiser, S Sillett, M Vitousek, M Webster*Presenting author: Alicia Brunner, Cornell University, aliciaaebrunner@gmail.com*

Northern temperate forests are exhibiting a lengthening of the 'green' period with earlier springs and later autumns. For migratory songbirds, autumn marks a critical transition in their annual cycle, in which individuals must physiologically prepare for fall migration. An elongated green period might allow birds to extend their breeding season, however, these birds might then experience an increased overlap in pre-migratory life history stages, such that individuals are forced to feed fledglings, molt their flight feathers, gain muscle and deposit fat simultaneously. The goal of this study was to identify if migratory birds incur physiological costs when extending the breeding season in warmer autumns. We used long-term breeding (e.g. nesting duration, nest success) and physiological (e.g. feather samples) data collected from Black-throated blue warblers (*Setophaga caerulescens*) that bred at Hubbard Brook Experimental Forest, NH from 1989-2023. We assessed individuals' physiological state in the post-breeding period by measuring molt rate, as well as structural quality and integrated corticosterone (CORTf) of tail feather samples collected from all birds. We predicted that individuals who completed their breeding season later would experience greater energetic constraint during this crucial pre-migratory period and would have lower quality feathers and higher concentrations of CORTf. Individuals that bred later molted faster and had lower quality feathers, but this pattern was much more pronounced for females than for males. Females also experienced greater energetic constraint, and this trend was more pronounced in individuals occupying areas with longer green periods.

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Landscape changes influence sage-grouse brood-rearing habitat and survival within the Great Basin region of Nevada and California**B Brussee, P Coates, S O'Neil, M Milligan, J Severson, M Ricca, S Abele, J Boone, E Ammon, S Mathews, S Gardener, M Casazza, D Delehanty***Presenting author: Brianne Brussee, USGS, bbrussee@usgs.gov*

During brood-rearing, Greater Sage-grouse (*Centrocercus urophasianus*; hereafter, sage-grouse) migrate from nesting habitat to heterogeneous upland mesic habitats that retain moisture and support important food resources. Brood-rearing habitat is facing widespread loss and fragmentation across the range due to invasion of annual grasses, wildfire, conifer expansion, and anthropogenic development. Using findings from three separate studies, we describe effects of landscape disturbance on sage-grouse brood habitat, survival, and the implications for population maintenance. First, across the southern Great Basin, brood-rearing sage-grouse selected greater perennial grass cover, higher elevations, and areas closer to wet meadows. Brood survival decreased in burned areas with high annual grass cover, potentially representing monocultures of invasive grasses, which further supports the importance of heterogeneous vegetation communities to sage-grouse broods. Second, within the Bi-State Distinct Population Segment, brood-rearing sage-grouse accessing mesic resources in high elevations demonstrated weakened avoidance of conifers, with consequences to survival. Last, the importance of mesic resources was also evident within the Long Valley population of the Bi-State, where large-scale water diversion influences mesic habitat availability. Here, landscape use by broods tracked mesic resources, especially during dry conditions, and survival was highest at the ecotone of uplands and wet meadows. Taken together, these findings improve understanding of how landscape changes affect the availability and quality of sage-grouse brood-rearing habitat. Information is preliminary and provided for best timely science.

****The Role of Parental Phenotype on Nest Predation in a Facultatively Biparental Species****F Fernandez-Duque, A Stiefvater, S Chikoti, J Chabain, T Benson, M Hauber***Presenting author: Facundo Fernandez-Duque, facundo2@illinois.edu*

Sexual dichromatism has long captivated the attention of evolutionary biologists, with significant impetus from the seminal contributions of Darwin and Wallace. While Darwin's work emphasized the aspects of male ornamentation driven by intrasexual competition and female mate choice, Wallace's perspective shifted towards the role of natural selection and cryptic female ornamentation in reducing predation risk to dependent young. Here, we investigated the role of sexual dichromatism in the nest depredation risk of Red-winged Blackbird (*Agelaius phoeniceus*), a species with facultative parental care by the more ornamented male sex. We experimentally assessed clutch survival as a function of both artificial nest placement (either over water or land) and the presence of a life-like model of either parental sex at the nest. We found that nests placed over water experienced lower depredation rates and that there was a strong effect of sex, as nests with the female models had lower depredation rates over water only. These findings support an interplay between natural and sexual selection in the context of sexual dichromatism and contribute to a fuller understanding of the selective pressures shaping parental care trade-offs.

Investigation of pinyon jay breeding colonies in western Colorado**A Seglund, L Rossi, J Runge***Presenting author: Amy Seglund, Colorado Parks and Wildlife, amy.seglund@state.co.us*

Pinyon jay (*Gymnorhinus cyanocephalus*) populations are thought to be declining range-wide, and the species was recently petitioned to be listed under the Endangered Species Act. The reasons for these apparent declines are unclear, but are thought to be associated with degraded pinyon-juniper woodlands (*Pinus edulis*, *Juniperus osteosperma*, *J. monosperma*, *J. scopulorum*) caused by climate change, extensive beetle kill, fire suppression, and mismanagement. Pinyon jays breed collectively as a group in loose colony sites that are used over multiple years. Breeding colonies encompass a variety of vegetation

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types and topographies and are often characterized by areas with patches of trees for nesting interspersed with sagebrush and grasslands. Since very little was known about breeding colonies in Colorado, with the majority of existing research occurring in Arizona and New Mexico, Colorado Parks and Wildlife began a project in 2020 to investigate 23 breeding colonies across western Colorado. We used nest survival analysis in Program MARK to evaluate hatching success based on 148 active nests for hatching and 130 for fledging outcomes. We identified potential threats to reproductive output, assessed colony site fidelity, and mapped colony extent based on 1414 old nests and 281 active nests. Our colony fidelity and location information will be used to better inform conservation of the species through integrating the pinyon jay into multi-species planning of proposed woodland treatment projects.

Effects of Male Saltmarsh Sparrow Home Range Size and Time Within Breeding Season on Reproductive Success

T Kuras, A Kovach*Presenting author: Talia Kuras, University of New Hampshire, talia.kuras@unh.edu*

Saltmarsh Sparrow (*Ammospiza caudacuta*) is a non-territorial, multiply mating passerine with a polygynandrous mating system where females are synchronously sexually receptive during 3 breeding cycles within the breeding season. In similarly multiply mating species with synchronously receptive females, home range size and time within breeding season have been identified as drivers of male reproductive success. We investigated the relationship between male Saltmarsh Sparrow home range size, location, time within breeding season, and male reproductive success. We performed nest monitoring, mist netting, and collection of genetic samples from banded individuals ($n = 164$ adult females and 226 adult males), at two marshes in the northern part of the species range. We also ran color band resighting surveys to assess the home range sizes and locations of breeding males at each site. We used SNPs identified from restriction-site associated DNA sequencing (RAD-seq) to conduct paternity analysis of 415 nestlings and unhatched eggs from 190 Saltmarsh and Nelson's sparrow nests over the course of two breeding seasons. Male home range varied significantly with the number of nests within home range ($n=28$ males, $p=0.002$). The number of offspring sired by each male and their spatial dispersion will be compared with home range size to test for the relationship between space use and male reproductive success. Temporal patterns of paternity will also be compared among males of different ages to test the hypothesis that sire age will impact the time in breeding season when individuals produce offspring.

**Female space use and plumage color are correlated with extra-pair mating in barn swallows

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Extra-pair mating is a common feature of avian systems and can modulate the strength of sexual selection. Mate searching behavior of female birds may be an important predictor of mating opportunity and extra-pair mating, yet notable gaps in knowledge remain due to lack of fine-scale movement data and a historic focus on male phenotypes. Accordingly, much is still unknown about whether and how female phenotypes contribute to extra-pair mating. Individual movement behavior can influence mate encounters and mating opportunity and is therefore important for understanding the scale of mate choice and the process of sexual selection in natural populations. Here, we examined how female space use and female and social mate plumage color are associated with extra-pair mating outcomes and multiple mating in wild barn swallows (*Hirundo rustica erythrogaster*). We tracked 10 females breeding in Colorado, USA with GPS backpack tags during their fertile period after an experimental nest failure. We then used low-coverage whole-genome sequencing to determine offspring paternity and extra-pair mating. Females who spent more time away from the nest had a higher proportion of extra-pair offspring. Furthermore, this relationship was stronger for females with darker plumage, suggesting that a female's own plumage helps determine whether differences in space use translate to differences in fertilizations. Surprisingly, we found no evidence for an interaction between female space use and her social mate's plumage color to influence extra-pair mating. In contrast to the historic emphasis on male traits, our study highlights female

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movement ecology and phenotype as important predictors of mating outcomes in a natural population.

Eastern Whip-poor-will (*Antrostomus vociferus*) Nesting Ecology in Northern New York

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Antrostomus vociferus (Eastern Whip-poor-will; hereafter Whip-poor-will) is an IUCN Near Threatened species that has declined throughout its range. The cause of this decline is unclear. A leading concern is loss of breeding habitat, so research into Whip-poor-will breeding ecology is essential for conserving their populations. Our research will address nest site selection and nest survival of Whip-poor-wills in northern New York through a telemetry-based study during the 2023 and 2024 breeding seasons. During the 2023 breeding season, we deployed VHF transmitters on 15 adult male Eastern Whip-poor-wills between mid-May and late-June. We located 14 Whip-poor-will nests by carefully monitoring male behavior and movements around dusk when they exchange incubation duties with the females. This is an alternative Whip-poor-will nest searching technique that is effective in study areas where the vegetation structure makes eyesight searches challenging. Future nightjar research may benefit from this alternative method. We monitored each nest every 2-6 days until failure or chicks reached 15 days of age and estimated the overall daily nest survival rate at 98.5%. Our first-year nest site selection analyses suggests Whip-poor-wills in our study area selected for more coniferous tree cover, greater amounts of ground litter cover, and taller shrubs when placing their nests, possibly for protection from predators and nest accessibility. We will complete our field research for this project in 2024 during a second breeding field season, where we plan to track an additional 20 adult males. As Whip-poor-wills are a target species for conservation in New York, our results will inform future forest best management practices on public lands in the state for sustaining and promoting Whip-poor-will breeding populations.

****Assessing within-season dispersal dynamics and breeding pressures for a declining tidal marsh obligate songbird**

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Since the 1990s, the degradation of salt marsh habitat has resulted in a 9% annual population decline for the Saltmarsh Sparrow (*Ammospiza caudacuta*; hereby SALS). Current estimates predict the extinction of the species as early as 2040. Primary threats facing SALS include low reproductive success and the loss of high marsh nesting habitat through increased rates of sea-level rise. From May-July 2023, we began conducting research to determine the breeding status and distribution of SALS in Accomack County, VA USA-the southern end of the breeding range, which is historically understudied. During this period, we documented nest abandonment (8 of a total 45 nests) and low recapture rates of banded females (11% out of 45 banded females, compared to 23% out of 130 banded males) leading us to question whether females were dying or dispersing from the site. Within-season dispersal of this species has not been recorded, but dispersal theory predicts that the prevalence of within-season dispersal is higher in spatially and temporally variable habitats, where predictability of habitat quality is low. Temporal predictability of habitat in this part of the range may have decreased due to shifts in predator communities and increases in tidal flooding accelerated by sea level rise. In this study, we aimed to determine if female SALS exhibit within-season dispersal after a failed nest attempt by leveraging Cellular Tracking Technology. Understanding this unique behavior may be useful for conservation efforts, as marshes with increased variability due to sea level rise may no longer provide suitable breeding habitat for the species.

Long-term Environmental Variation in Nest Survival for the Western Bluebird and Ash-throated Flycatcher

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Nest success and now, nest survival, has been a central question in understanding the limitations and determinants on avian reproduction. Our primary objective was to investigate the long-term environmental determinants of western bluebird and ash-throated flycatcher nest survival in Los Alamos, New Mexico. We focused on understanding general patterns of nest survival and how two nest stages (incubation and nestling) may have responded differently to a range of environmental covariates for the two species. We collected and analyzed 22 years of data obtained from a total of 1,649 bluebird and flycatcher nests between the years 1997 and 2018, including 1,378 bluebird nests and 271 flycatcher nests. For the bluebird, the top nest survival model had an additive linear temporal trend across the nesting season for both nest stages, plus an additive stage-specific effect of nest age (when identified) as well as elevation, with higher elevation breeding birds having higher nest survival. For both species, daily nest survival increased early in the season and leveled off but was lower for incubation when compared to the nestling period. The top model for flycatchers had an additive linear temporal trend across the nesting season for both nest stages. Survival declined with increasing nest age during both the incubation and nestling stages. This bluebird population has also shifted to higher elevations over time. Here, we present how this long-term study of cavity-nesting birds is documenting breeding biology changes alongside changing environmental conditions.

It takes time: Insights from 25 years of Common Tern (*Sterna hirundo*) monitoring in a changing Gulf of Maine

E Craig, A Caldwell

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Reproductive success in seabirds is influenced by a diversity of factors, including environmental conditions and the availability and quality of prey in waters surrounding their breeding colonies. Understanding the response of seabirds to these variables is crucial to conservation efforts, as climate change continues to impact marine food webs through temperature-driven changes in the distribution and phenology of biological communities. In the Gulf of Maine, where waters are warming faster than 99% of the world's oceans, seabirds may be particularly impacted, and can serve as bioindicators of environmental and food web shifts over time. A collaborative group of conservation organizations has monitored the diet and reproductive metrics of Common Terns (*Sterna hirundo*) at a NH breeding colony in the Gulf of Maine for over 25 years, during which time breeding-season sea surface temperatures have increased by nearly 3 degrees C. We constructed Generalized Linear Models including environmental and biological parameters to determine what factors drive variability in Common Tern reproductive success. Sub-models further explored long-term trends in Common Tern diet and reproductive variables. Results indicated changes in environmental conditions and prey community during this 25-year timespan, with consequences for reproductive success in terns. This study highlights factors contributing to seabird reproductive success, providing insights for conservation managers. Additionally, our results suggest possible mechanisms of climate impacts to seabird species of conservation concern.

Species interactions between two cavity-nesting songbirds under the threat of brood parasitism and nest depredation

S Green, K Miller, K O'Neil, R Pell, M Mash, E Bowers

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Nest-site availability is often perceived as a significant competitive pressure between individuals and species, especially in secondary cavity nesters that do not excavate their own nesting sites. However, some individuals may derive benefit by nesting in close proximity to heterospecifics whose presence reduces the risk of nest depredation or brood parasitism, yet the potential benefits of these community interactions are still understudied in wild populations. Our field site in west TN is occupied during the breeding season by sympatric, box-nesting populations of resident Carolina Wrens (*Thryothorus ludovicianus*) and migratory Prothonotary Warblers (*Protonotaria citrea*). These species occupy similar ecological niches on their breeding grounds, and nest densities across their ranges vary inversely with each other in space and time. However, rates of cowbird brood parasitism and nest depredation differ strongly between them despite utilizing the same nestboxes at our site. Because wrens are relatively

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more vocal, territorial, and physically aggressive to novel intruders – and far less likely to experience brood parasitism – we hypothesize that warblers may benefit by establishing nest sites near Carolina Wrens. We examined the occupancy of nestboxes, clutch size, rates of predation and cowbird parasitism, and fledging success of these populations over 8 years. Warblers experienced less brood parasitism when nesting closer to wrens, but wrens experienced more nest depredation with increases in their number of neighbors nesting nearby (within 150 m). These results suggest that selection could act on warbler nest-site selection by reducing brood parasitism, but at a potential cost to wren fitness.

****Thermal, behavioural and fitness responses to warming temperatures in an Arctic-breeding songbird**

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The Arctic is experiencing rapid rates of climate change, where temperatures are increasing faster than the global average. Arctic-breeding birds that have adapted to harsh and cold conditions throughout their annual cycle may not be physiologically prepared for warming conditions, especially during the energetically demanding breeding season. Of specific concern within this group is the Snow Bunting (*Plectrophenax nivalis*), an Arctic-breeding songbird whose populations are declining without clear mechanism. Due to high metabolic rates and correspondingly high body temperatures, effective heat dissipation during chick-rearing is vital to reduce the risk of reaching lethal body temperatures. Thus, when environmental temperatures exceed optimal levels, breeding birds working at an elevated metabolic rate must dissipate heat and adjust behaviorally by reducing chick-rearing behaviours. Recent modelling applying a thermoregulatory polygon approach on high-Arctic breeding Snow Buntings predicts that chick-rearing performance would be impacted at environmental temperatures of only 11.7°C, temperatures the Arctic now regularly experiences. However, these predictions have yet to be field-tested. Furthermore, we do not know whether these predictions apply to low-Arctic sites where temperature fluctuations occur over a daily cycle, potentially offering a break from high consistent temperatures. To determine whether buntings are impacted by increasing temperatures during the breeding season, we tagged birds using Radio-Frequency Identification thermal tags which measure real-time body temperatures and parental foraging responses. Understanding the conditions under which breeding Snow Buntings need to alter reproductive behaviours when exposed to elevated temperatures will improve our understanding of Arctic species' responses to global warming.

****Evidence for winter reproductive seasonality in an opportunistic breeder, the Red Crossbill (*Loxia curvirostra*)**

J Devereaux, J Karr, J Cornelius, T Hahn

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Warmer winter temperatures may impose higher thermoregulatory costs on birds. Evidence suggests that challenging environmental conditions can induce high levels of corticosterone and that chronic stress can impact reproductive investment. Red crossbills (*Loxia curvirostra*) are an opportunistically breeding finch that often breed in winter and summer, however crossbills tend to breed less frequently during winters characterized by cold rain rather than snowier conditions. We used 48 wild-caught captive red crossbills to investigate how temperature, precipitation, and daylength impact energetic and reproductive investments from November to February. Birds were divided into cold (6°C) and warm (21°C) treatment groups that experienced wet (rain 30 min/day) or dry conditions. Cold birds were housed on two different photoperiods (Corvallis, OR, USA; Fort Nelson, BC, Canada). We used gonadal measurements and plasma corticosterone (CORT) and testosterone (males only) to quantify the effects of these treatments on glucocorticoid and reproductive physiology. We found that birds housed in the cold and wet conditions ate more than those in warm and dry conditions. Baseline levels of plasma CORT were higher in rain groups versus dry groups ($p=0.04$). Induced CORT was higher in warm treatment groups than cold ($P = 0.001$). Both baseline ($P = 0.02$) and GnRH-induced ($P = < 0.0001$) levels were impacted by season and both increased from early to late winter, while testis size did not differ across groups. However, ovaries did differ ($P=0.03$). These results suggest that winter rain may be a cost to crossbills, but

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reproductive investment was better described by season in this opportunist.

Chitty Chitty Duck Duck From behavior dynamics to population dynamics and back again in a precocial bird

J Eadie, B Lyon, E Bridge, T Moore, E Berg, N Odell, E Graves, C Thow, T Stair, M Hinton, M Jones, C Wells, A Olson, B Cook, D Scheck, T Russell

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Despite decades of interest dating back to the Chitty hypothesis, there are surprisingly few studies that demonstrate direct links between behavioral dynamics and population dynamics, particularly when populations fluctuate or cycle. We studied population density, reproductive success, and frequency of reproductive tactics of a precocial bird, the Wood Duck (*Aix sponsa*), at 6 sites for 15-26 years near Davis CA. We monitored > 2500 nests, tracked reproductive success of 2100 females, recorded nest use and success at 197 nest sites with RFID readers, and genotyped >1000 females and >5000 ducklings using 19 microsatellites to assess the frequency of alternative reproductive tactics. We present evidence showing that social interactions among females – specifically conspecific brood parasitism – drive population variability, leading to unstable fluctuations or crashes. Simultaneously we show that variation in population density results in different payoffs for female reproductive tactics. Our results demonstrate that behavioral dynamics can drive populations dynamics, and reciprocally, fluctuating population dynamics can maintain divergent behavioral phenotypes.

***Host and brood-parasite nestling mouth coloration and parental care: an experimental test**

K Miller, K O'Neil, R Pell, S Green, M Mash, E Bowers

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Parents can optimize reproductive outcomes by using nestling signals, favoring either young that are most likely to survive or those whose survival depends more strongly on being fed. The colorful tissue surrounding nestlings' mouths (the rictal flange) can signal condition and plays a role in parent-offspring communication. If rictal flange coloration influences parental-care decisions and certain phenotypes receive more care, selection may favor the exploitation of this preference by brood parasites.

Brood-parasitic nestlings receive most of the food brought to the nest by parents and, although this is largely attributed to their greater size and begging intensity relative to host young, it may also be related to their coloration. We discovered differences between Prothonotary Warbler (*Protonotaria citrea*) and Brown-headed Cowbird (*Molothrus ater*) nestlings in yellow and ultraviolet (UV) rictal flange coloration, where cowbirds reflect significantly less yellow and more UV light than warblers. Additionally, UV reflectance was positively condition-dependent. To examine whether UV reflectance influences parental care, we experimentally reduced rictal flange UV reflectance within parasitized and non-parasitized broods. Nestlings were randomly assigned to either a natural (no lip balm), control (non-SPF lip balm), or experimental (SPF 35 lip balm) group, and we subsequently recorded parental provisioning behavior. While controlling for nestling mass and begging, we found significantly reduced parental provisioning toward experimental nestlings. This suggests parents use nestling flange UV reflectance when making feeding decisions, which may contribute to the observed higher feeding rates toward brood-parasitic young.

****Context-dependent fitness benefits of a host-tolerant brood parasite in Prothonotary Warblers (*Protonotaria citrea*)**

R Pell, K O'Neil, K Miller, S Green, M Mash, A Atkins Coleman, E Bowers

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The coevolutionary arms race between hosts and parasites often portrays opposing forces in an ongoing battle of alternating selective advantages, but this framework may fail to capture the full, complex nature of these multispecies interactions. For example, compared with unparasitized conspecifics, hosts of the

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Brown-headed Cowbird (*Molothrus ater*) generally experience greater nestling mortality and nest failure, and worse nestling pre-fledging condition, yet many hosts continue to accept brood-parasitic young. While understanding this singular parasite-host interaction has shed important light on the natural history of these systems, pressures shaping host decisions to accept or reject a brood parasite may be more complicated than we thought. Here, we investigate whether rearing cowbird young confers context-dependent benefits to host nestlings by mitigating the deleterious impacts of an avian ectoparasite: hematophagous blowfly larvae (*Protonotaria citrea*). We experimentally eradicated larvae in Prothonotary Warbler (*Protonotaria citrea*) nests containing or lacking a cowbird nestling and recorded morphometric measurements, hematocrit, and host fledging success. In following seasons, we recaptured adults and documented the recruitment of offspring into the local breeding population. Our data reveal that the strongly negative effects typically attributed to cowbird parasitism only occurred when combined with the presence of blowflies. Furthermore, though cowbird-parasitized nests fledged fewer host young, warbler nestlings raised alongside cowbirds were more likely to recruit and breed as adults in subsequent years, suggesting a benefit of rearing cowbirds on host fitness. Thus, this coevolutionary arms race is complicated by interactions between multiple parasites, which may help explain the evolutionary maintenance of brood-parasite acceptance.

***Limited evidence of biased offspring sex allocation in a cavity-nesting conspecific brood parasite**

C Wells, B Lyon, C Thow, T Stair, M Jones, M Hinton, J Eadie

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Sex allocation theory predicts that mothers should bias investment in offspring toward the sex that yields higher fitness returns; one such bias may be a skewed offspring sex ratio. Sex allocation is well-studied in birds with cooperative breeding systems, with theory on local resource enhancement and production of helpers at the nest, but little theoretical or empirical work has focused on birds with brood parasitic breeding systems. Wood ducks (*Aix sponsa*) are a conspecific brood parasite, and rates of parasitism appear to increase with density. Because female wood ducks show high natal philopatry and nest sites are often limiting, local resource competition (LRC) theory predicts that females should overproduce male offspring-the dispersing sex-when competition (density) is high. However, the unique features of conspecific brood parasitism generate alternative predictions from other sex allocation theory, which we develop and test here. We experimentally manipulated nesting density of female wood ducks in four populations from 2013-2016, and analyzed the resulting sex allocation of >2000 ducklings. In contrast to predictions we did not find overproduction of male offspring by females in high-density populations, females in better condition, or parasitic females; modest support for LRC was found in overproduction of only female parasitic offspring with higher nest box availability. The lack of evidence for sex ratio biases, as expected for LRC and some aspects of brood parasitism, could reflect conflicting selection pressures from nest competition and brood parasitism, or that mechanisms of adaptive sex ratio bias are not possible.

****Differences in black vulture resource selection across core and periphery populations and implications for range expansion**

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Land use alterations and shifting climatic conditions are contributing to novel wildlife-human interactions due to species range contractions, shifts, or expansions. Black vultures (*Coragyps atratus*) have expanded the northern margin of their range significantly in recent decades, accompanied by an increase in human-vulture conflicts, driving a need to better understand current and future occupancy of black vultures. Although the exact drivers of this range expansion are unknown, climate change, anthropogenic food subsidies, or behavioral changes at range margins have been hypothesized to play a role. Thus, our objective was to examine whether patterns of resource selection across core and periphery populations were consistent with land use changes or behavioral changes as the primary driver of range expansion.

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We analyzed seasonal resource selection across core and periphery populations, employing a step selection function (SSF) approach and quantifying selection behaviors related to anthropogenic food subsidies and various landcover types. We found marked differences between populations in core and periphery, but these differences fail to explain range expansion. Black vultures in periphery populations exhibited weaker selection for distance to roads and landfills, and more strongly avoided high proportions of all landcover types. However, core and periphery populations demonstrated consistent selection for increased landscape richness. Their ability to use a variety of landscapes would allow them to closely track a changing climate envelope and changing resource availability. These results have provided important insights to the drivers of black vulture range expansion and management of human-vulture conflicts.

***Range expansion dynamics of Green Jay (*Cyanocorax yncas*) in Texas revealed through population genomics**

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Climate change is rapidly shifting the geographic range of thousands of species, but empirical research has not fully addressed the complexities of this global ecological trend. The goals of this study were to 1.) investigate how the landscape structures gene flow during range expansion and 2.) characterize genetic changes across the newly colonized areas. We use the range expansion of green jay (*Cyanocorax yncas*) in South Texas as a model system to explore the relationship between an expanding population and the landscape. Historically, green jays were found within about 50 km of the Rio Grande in South Texas. Green jays have steadily expanded their northern range limit to about 300 km north of the Rio Grande. Using whole genome sequencing data from green jay (n=65) captured throughout 30 sites in Texas and Mexico covering the range expansion area, we compared measures of genetic variation and heterozygosity with regional landscape and climatic variables. We developed models of land use by green jay and statistically compared these with empirical measures of genetic connectivity to characterize the likely pathways of expansion. Our findings indicate that expansion pathways are likely dependent on resource distribution in time and space. Additionally, we identify some genes which may be linked to climate adaptation at the sub-population level within the newly expanded area.

***Avian annual survival rates heavily influenced by climate cycles on a continental scale**

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Understanding how climate variability influences avian survival at continental scales is essential to predict how populations will respond to climate change. This is especially relevant given recent widespread declines in North American bird populations. Climate cycles like the El Niño-Southern Oscillation (ENSO) and the North-Atlantic Oscillation (NAO) are predicted to become more extreme as the climate changes, but effects of climate cycles on animal populations remain uncertain. Here, we use bird-banding data from the Monitoring Avian Productivity and Survivorship (MAPS) network collected at a continental scale during the breeding seasons of 1992-2018 to estimate changes in annual apparent survival and to test the influence of ENSO and NAO on survival rates for 49 passerine species. We found that ENSO and NAO influenced annual survival in about 60% of species. There are not strong differences in the effects of climate on survival as a function of their migratory status or range. If responses of bird survival to climate cycles are indicative of responses to climate change, our results suggest that climate may strongly impact demographic rates. Climate cycles are likely to influence survival rates by affecting migration efficiency or the quality of habitats encountered during migration or stationary nonbreeding seasons. Responses of migratory and resident birds to climate variability may also include other demographic parameters such as

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reproductive success, calling for more comprehensive studies aimed at understanding links between variation in climate cycles and the demography and population trends for species of conservation concern.

***Birds in a changing climate: A global meta-analysis of weather effects on avian reproduction**

H Todaro, A North, A Galante, C Duchardt, S Loss*Presenting author: Holly Todaro, Oklahoma State University, htodaro@okstate.edu*

Climate change, along with land-use modifications, has been recognized as a key factor driving global changes in biodiversity. Rising temperatures, altered precipitation patterns, and severe weather events pose significant threats for various taxa; however, avian species face unique challenges as many aspects of their life cycles, including breeding, migration, and non-breeding periods are intricately linked to specific ecological conditions. For many species, there is only a short period during the annual cycle when conditions are suitable for reproduction. Stochastic and long-term changes in weather and climate can strongly influence components of reproduction such as laying date, clutch size, nest success, and survival of young. The effects of weather and climate on avian reproduction become more complex when considering species that inhabit diverse biomes and exhibit a range of life history traits. For example, the influence of weather and climate on avian reproduction may vary depending on site or species-specific characteristics. To increase understanding of and make accurate predictions about the influence of climate change on avian reproduction, it is essential to synthesize the complex array of these factors. We expanded on previous research by conducting a global meta-analysis of how weather and climate variables are associated with avian reproduction. We predict that effects of weather and climate on avian reproduction will vary among regions with different climates. In regions with greater weather and climatic variability, we expect a greater range of effects on reproduction. Furthermore, species with open cup nest structures likely experience stronger effects of adverse weather conditions on reproduction compared to species with more protected nest structures (e.g., dome-shaped or cavity nests). Our findings will provide information that helps conserve the large majority of birds whose reproductive output will be affected by climate change.

***Simultaneous shifts in the breeding latitude, elevation, and phenology of North American birds**

M Neate-Clegg, B Tonelli, M Tingley*Presenting author: Monte Neate-Clegg, University of California, Santa Cruz, monteneateclegg@gmail.com*

Terrestrial species have multiple ways to respond to a warming climate, including shifts in space (via latitude or elevation) and time (via phenology). Evidence for these shifts is often assessed independent of other temperature-tracking mechanisms; critically, no study has tested for shifts across all three spatiotemporal dimensions simultaneously. Here, we estimate trends in the breeding latitude (311 species), elevation (251 species), and phenology (111 species) of North American landbirds over 27 years using two continental-scale monitoring databases. We then measure how much species have shifted relative to what would be expected given regional warming. On average, species are shifting polewards (1.1 km/year, mean ratio = 11%) and to higher elevations (1.2 m/year, mean ratio = 17%), while simultaneously shifting their breeding phenology earlier (0.08 days/year, mean ratio = 26%). These overall trends belie substantial variation among species, with some species shifting more than expected, some shifting slowly, and others shifting counter to expectation. Evaluating total shifts across three dimensions, birds are cumulatively tracking temperature at 31% of current warming rates; however, 63% of this tracking is driven by advances in breeding phenology as opposed to shifts in either latitude or elevation. A narrow focus on spatial dimensions of tracking underestimates the response of birds to climate change, while phenological shifts offer an alternative for birds – and likely other organisms – to conserve their thermal niche in a warming world.

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Identifying boreal climate refugia to inform landbird conservation action in a changing landscape**A Drake, F van Oordt La Hoz, D Stralberg, C Mahon, H Cooke, S Haché, C Handel, S Matsuoka***Presenting author: Anna Drake*, University of British Columbia, drake.ae@gmail.com

Boreal ecosystems are especially sensitive to climate change. The Taiga and Boreal Cordillera CEC level 2 ecoregions in northwest Canada and Alaska, USA, are projected to host climate refugia for songbirds at the end of the century due to their position at the cold margins of species' distributions and because of their complex terrain. We developed climate-based, species distribution and abundance models (SDMs) for 47 landbird species that currently breed in the Boreal and Taiga Cordillera. We use these models to: (1) project species' distributions and abundances in the region by 2100 under multiple climate change scenarios, (2) identify climate refugia for these species, using backward velocity/colonization potential of the plant community as a constraint, and (3) identify future 'suitable refugia'. We identify species expected to increase and decrease in the Cordilleras and discuss population traits associated with projected declines. We stack 'suitable refugia' within migratory strategy groupings and within our increaser/decreaser groupings to identify 'high value' areas that are projected to be suitable for multiple species by 2100. We then examine overlap between these areas and currently protected areas in Canada and Alaska. Our findings suggest suitable habitat in the Cordilleras will decline for residents and short-distance migrants and increase for long-distance migrants. Range-restricted and high elevation species are high risk species under future climate scenarios. By 2100, the amount of 'high value' land area within currently protected areas is projected to: increase by 70% for long-distance migrants, remain stable for residents, and decrease by 20% and 96% for short-distance migrants and our decreaser grouping, respectively.

Complex changes in climatic suitability for Cassin's Sparrow (*Peucaea cassinii*) revealed by retrospective ecological niche modeling**J Schnase, M Carroll, P Montesano, V Seamster***Presenting author: John Schnase*, NASA Goddard Space Flight Center, john.l.schnase@nasa.gov

Cassin's Sparrow (*Peucaea cassinii*) is a grassland resident of the southwestern United States and northern Mexico. Despite decades of study, conservation status assessments for the species show considerable variability. In this study, we combined environmental data from NASA's MERRA-2 reanalysis with occurrence records spanning the past 40 years to investigate Cassin's Sparrow's historical response to a changing climate that could help explain this variability. We examined two time- and variable-specific climatic suitability time series using MaxEnt. Bioclimatic predictors provided a seasonal, macroclimatic perspective confirming the previously documented importance of monsoon rainfall. Ecosystem functional attributes provided a localized, microclimatic view that revealed the importance of increasing wind speed and drying land surface conditions. Modeled estimates of climatic suitability in the macroclimatic time series were more favorable than in the microclimatic series, and the differences between the two were more pronounced when considered at the state level. These findings could have important implications for conservation practice, given that many conservation policy decisions and management actions occur at the state level and often rely on models and projections based solely on bioclimatic predictors. Our results also showed that suitability estimates vary widely depending on the temporal frame considered and are a likely consequence of non-constant trends in the drivers themselves. This variability mirrors the inconsistencies we see in the literature regarding this species' conservation status and points to the need for an updated, state-by-state examination of Cassin's Sparrow's regional vulnerabilities.

Genomic variation associated with climate in Yellow Warblers breeding California**W Tsai, R Harrigan, J McCormack, M Alfaro, T Smith, R Bay***Presenting author: John McCormack*, mccormack@oxy.edu

To mitigate the current biodiversity crisis due to climate change, we need to base our conservation decisions on informed predictions of species response to environmental change. Previous work

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integrating environmental and genomic data across the breeding range of Yellow Warblers found that the inability to adapt to climate change might already be playing a role in Yellow Warbler declines in California. However, due to the broad scale of this study, we do not know how climate-associated genetic variation is distributed across smaller environmental gradients in California, which is crucial for conserving the species. Here, we produced a high-quality reference genome and performed low-coverage whole genome sequencing of 137 California breeding Yellow Warblers. We analyzed population genetic diversity and structure and genotype-environmental associations. We found little evidence for population genetic structure in Yellow Warblers breeding in California. Despite this low genetic structure, we identified about 3,000 putatively adaptive SNPs associated with climate with the top environmental variables associated with precipitation and vegetation. When we map these associations across California, we identify populations harboring unique genotype-environment associations that can be prioritized for conservation. This highlights the importance of understanding both neutral and adaptive genetic variation when considering conservation prioritization.

****Long-term body size changes in a dry forest bird population amidst a changing climate****A Wendler, J Walters***Presenting author: Amber Wendler, Virginia Tech, awendler@vt.edu*

Long-term monitoring of bird populations can give us valuable insights into how birds are adapting to climate change over time. In response to changes in temperature and rainfall, birds may exhibit varied morphological shifts. Using almost 50 years of morphometric data from a long-term mist netting study in Guánica Dry Forest, changes in Puerto Rican Tody (*Todus mexicanus*) body size - including mass, tarsus length, wing chord, and bill size - were assessed in response to increases in mean ambient temperature, along with inter-annual variability in rainfall. Based on this analysis, bill size appears to be the feature that has changed the most among Puerto Rican Todies with average bill surface area increasing over time. Previous studies have shown that the bill acts as an important mechanism to dissipate dry heat, thus larger bills may be useful for thermoregulation as the climate gets drier and hotter.

Effects of the climate changes on the migratory shorebirds*J Ferreira, L Diele-Viegas***Presenting author: Juliana Ferreira, Federal University of Bahia, jumoraesf.bio@gmail.com*

Migratory birds face different environmental pressures along their migration routes. Among migratory birds, shorebirds are one of the most diverse and threatened groups, experiencing significant population declines. Climate change can directly or indirectly impact migratory birds, substantially influencing migratory shorebirds. Therefore, this study aims to assess the effects of climate change on migratory shorebirds, using environmental temperature as a metric for climate change. We seek to answer whether the increase in temperature will negatively affect migratory shorebird species. To achieve this, we conducted a systematic review using the search strings "climate change" & temperature & "migratory shorebird*" on the search platforms Google Scholar and Web of Science. We included articles published in scientific journals that evaluated the relationship between environmental temperature and any biological aspect of migratory shorebird species. We excluded theses, dissertations, and studies that did not include migratory shorebirds. After selection, we collected variables from the articles to perform a meta-analysis to analyze the relationship between environmental temperature and migratory shorebirds. We found 940 results on the two platforms. After selection, only 22 articles were included. Preliminary data analysis indicates that the increase in environmental temperature led to earlier laying and hatching dates of the eggs, in addition to negatively affecting food intake in some species. However, no effect was observed on the survival of adult males and females so far.

Climate change effects on forest songbirds breeding in the Appalachian Mountains are mediated by latitude and elevation*H Clipp, C Rota, P Wood**

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Presenting author: **Hannah Clipp**, USDA Forest Service, hannah.clipp@gmail.com

Warming temperatures and shifting precipitation patterns may be contributing to historic and ongoing declines in forest songbird populations that breed in eastern North America, which has prompted recent efforts to forecast the effects of climate change on forest songbird species into the future. However, climate relationships are commonly assumed to be static across latitudinal and elevational gradients. To improve accuracy of predictions and to better inform conservation efforts, it is imperative to evaluate whether the influence of climate is mediated by latitude and elevation, especially in mountainous regions. In this study, we quantified differences in how forest songbirds are affected by climate factors across latitudinal and elevational gradients within the Appalachian Mountains. We used nearly 30 years of bird survey data from 1,733 sites at various elevations in National Forests located within the Northern, Central, and Southern Appalachians to model responses in climate-related guild richness (using a Bayesian hierarchical community model and generalized linear mixed effects models) and focal species abundance (using Bayesian N-mixture models). Our model results indicate that climate effects on forest songbird communities during the breeding season are dynamic along latitudinal and elevational gradients in the Appalachian Mountains. Specifically, guild-specific relationships with temperature and precipitation variables varied in direction and magnitude across latitudes and elevations. In addition, our findings suggest that cold-associated species are at highest risk from warming temperatures and that future climate change could potentially result in the steepest declines in forest songbird species at low elevations in the Southern Appalachians.

****Short-term stabilization of population trends likely belies the future viability of salt marsh birds in eastern North America**

F Gigliotti, G Shriver, A Kovach, J Cohen, B Olsen, E Tymkiw, M Correll, W Beisler, C Elphick

Presenting author: **Franco Gigliotti**, University of Connecticut, frank.gigliotti@uconn.edu

Salt marshes in the northeastern USA support several specialized breeding bird species that are at risk due to sea level rise (SLR) and coastal development, processes that result in habitat change and fragmentation. Past studies suggest rapid, widespread declines in several species, but mechanisms driving population change and whether declines continue remain unclear. We examined the relative influence of phenomena hypothesized to modify breeding bird habitat in salt marshes, including SLR, rates of sediment delivery inferred from satellite imagery, and land use, on the population trajectories of saltmarsh breeding birds. We modelled population trajectories with 12 years of spatially extensive point count surveys collected from Maine to Virginia and found them to be disparate. Between 2011 and 2022, clapper rails continued to decline (- 4.1% / year), willets (+ 2.6% / year) and saltmarsh sparrows (+ 4.1% / year) increased, and seaside sparrows and Nelson's sparrows exhibited no clear change. The estimated increase for saltmarsh sparrow runs counter to observed trends over the previous 25 years but aligns with predictions from demographic modelling. The model results also suggest that increases will be short-lived and followed by further declines. Tidal restrictions and road density near marshes were generally important predictors of abundance, as was habitat composition, while local rates of SLR and sediment delivery were less important. Our results show that, during a period of lower realized SLR, local-scale drivers are relatively more important to the persistence of several salt marsh breeding birds, but conservation practitioners should be attentive to global drivers as rates of SLR accelerate.

****Assessing productivity and abundance trends of North American bird species in response to ongoing abiotic environmental change**

E Moylan, C Francis, S Jennings

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Abrupt population declines and altered distributions of North American birds have been linked to anthropogenic and climate change. Furthermore, changes in avian communities could have dramatic ecological consequences at local and regional scales, yet we currently lack knowledge on which aspects of environmental and anthropogenic change are associated with long-term population trends. This project

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used 2 million bird captures spanning 29 years from the Monitoring Avian Productivity and Survivorship Program to test whether anthropogenic and environmental changes can explain local changes in avian abundance and reproduction for North American landbirds. We found correlations between 11 measures of environmental change and species-specific changes in productivity and abundance for 28 species. Notably, light pollution increased at 55% of banding stations and was correlated with declining abundance and/or productivity for 7 species, while 7 different species had population trends that were associated with changes in airborne particulate matter. The Southeastern United States experienced the greatest increase in nighttime light and had lower air quality than other regions, which may explain the negative population trends we detected for 5 species that breed in this area. However, the degree of environmental change among stations at the local level was highly variable, with the locations that experienced the most change driving species' responses to these pollutants. This study links long-term population trends with environmental change at a fine spatial resolution and highlights the importance of examining local-level species change, providing crucial knowledge for mitigating the impacts of anthropogenic environmental change.

Effects of heat on the forest bird community in National Parks in the National Capital Region

L Rudge, G Shriver*Presenting author: Leah Rudge, rudge.leah@gmail.com*

Eastern forest bird populations are in decline, exacerbated by the dual effects of habitat loss and rising temperatures typical of highly urbanized areas like the greater Washington DC region. The 11 national parks in the National Capital Region (NCR) protect important habitats throughout this region. We used point count data collected between 2007 and 2023 from 411 forested sampling locations in the NCR to calculate a bird community index (BCI) to infer relative estimates of ecological integrity. BCI, a weighted species richness metric, places higher weights on species belonging to specialist behavioral and morphological guilds. Using land surface temperatures derived from Landsat satellite imagery, we determined the mean temperature in the NCR for each bird breeding season (May – August) in the study period. Our objectives were to (1) test for relationships between temperature and BCI, (2) test for relationships between temperature and specialist guilds, (3) and determine if relationships with heat can be attributed to the Urban Heat Island effect. This research can underscore the significance of relatively small national parks in highly metropolitan regions in protecting high quality bird habitats, while also offering insights for making more informed decisions on forest management and urban planning in the region.

Functional traits explain the responses of North American bird populations to environmental and anthropogenic change

S Jennings, E Moylan, C Francis*Presenting author: Sarah Jennings, California Polytechnic State University, sjenni02@calpoly.edu*

Many species of North American birds are in steep decline, yet it remains unclear which aspects of climate and anthropogenic change are driving local-level population trends. To address this knowledge gap, we leveraged three decades of abundance and productivity data collected during the breeding season at banding stations across North America as part of the Monitoring Avian Productivity and Survivorship Program. Our goal was to identify the abiotic and anthropogenic conditions driving species-level changes in productivity and abundance, and ultimately to connect these patterns to variation in species traits. We identified 28 species with long-term population trends that were correlated with at least one aspect of environmental or anthropogenic change. To further clarify the species-specific results, we employed phylogenetically-controlled analyses to determine whether variation in traits can help explain variation among species in their responses to environmental change. We find that birds that see better in dim light conditions exhibited declining abundance in response to increased light pollution. Additionally, species that occupy warmer thermal niches increased in abundance in response to higher temperatures during the breeding season, while those adapted to cooler temperatures experienced abundance declines. And unexpectedly, species with longer lifespans had higher productivity in response

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to greater levels of urbanization. Our study links variation in local, long-term avian population trends to local environmental change across the continent, providing critical insight into how North American bird species are responding to anthropogenic environmental change.

***Modeling western snowy plover (*Charadrius nivosus nivosus*) nest success under future climate conditions across California State Parks**

G Cummins, S Coates, L Salas, D Jongsomjit, K Neuman, S Veloz, H White

Presenting author: George Cummins, Point Blue Conservation Science, gcc321@gmail.com

The Pacific coast population of the western snowy plover (*Charadrius nivosus nivosus*) is likely vulnerable to climate change, primarily because rising sea levels are predicted to greatly alter coastal beaches over the next century. To guide actions that increase the chances of maintaining viable populations of this beach nesting shorebird, we sought to understand how snowy plovers are likely to respond to projected changes in sea level, habitat, and climate. We used long-term nest monitoring datasets from California State Parks across coastal California to investigate relationships between nest success and habitat features (ground cover, distance to water), ecological factors (nesting density, human beach visitation levels), and climate variables (precipitation, temperature). We also considered the use of nest predator exclosures and structural human barriers, which have been shown to increase nest success. We found nest success to be influenced by distance to water (success is lower both close to and farthest from water), amount of vegetation (success is higher in areas of open sand), and nesting density (generally higher success at higher nest densities). Effects of human visitation and climate variables were less clear, but human visitation and spring temperature had generally positive effects whereas precipitation during the previous fall had negative effects on nest success. We then projected nest success under future climate and beach conditions, focusing on the effects of sea level rise altering nesting habitat. The projected loss of habitat could be mitigated by directing management efforts towards areas where inland migration of open beach habitat will not be impeded by geological or human structural barriers.

***Beyond the Edge: Investigating Species Potential for Range Expansion**

W Dorman, M Ward

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While many studies state that they expect birds in North America to shift their ranges north, little attention has been paid to which species will move and the mechanism by which ranges shift. Extralimital occurrences involve individuals occurring outside of their species' core breeding distribution. The probability of extralimital occurrences may be used to infer the potential of a species to expand their range, while the location of extralimital occurrences could indicate potential areas where the range may expand. Using a Bayesian approach combining data from eBird and the Breeding Bird Survey we identified breeding season dates, delimited the breeding range, and modeled occupancy for twenty migrant passerine species. Using pattern analysis, we explored changes in these species' distributions north of the range edge to determine a given species demonstrated range plasticity over time. Range plasticity is the combined result of phenotypic plasticity and the impacts of natural selection and may serve as a proxy for a species' capacity to respond to environmental change. Incorporating plasticity could both overcome a major limitation of Species Distribution Modeling and allow land managers to direct conservation efforts to facilitate range shifts in the face of climate change. I will discuss progress towards constructing a Range Plasticity Index for all birds in North America and the implications for modeling climate change impacts.

***Climate change alters the adaptive landscape of avian morphology and drives evolution**

S Yanco, C Youngflesh, M Tingley, B Weeks

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Climate change is driving widespread morphological changes among birds. Yet, the mechanisms driving this phenomenon, and the potential impacts to population trajectories, remain unknown. Two hypotheses

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have been proposed to explain the phenomenon: developmental plasticity and natural selection. The developmental plasticity hypothesis has mixed support and cannot explain observed patterns across species and contexts. No studies have yet evaluated whether micro-evolutionary processes drive observed morphological changes. Here we leverage a multi-decade, continental-scale monitoring scheme covering over 100 species of North American birds ('Monitoring Avian Productivity and Survivorship; MAPS). We present evidence that climate change-induced natural selection is driving avian morphological change. Using species-specific survival models we show that, in a typical year, temperature and precipitation during the breeding season apply opposing selective pressures on body size resulting in stabilizing selection. However, warm years shift the balance between these two selective pressures and smaller individuals experience greater apparent annual survival. By modeling age-structured abundance we also find that plastic life history trade offs result in higher reproductive success from sites with on-average maladaptive morphologies. Together these findings suggest that climate change is modifying the adaptive landscape to which North American birds are exposed and driving evolutionary change in avian morphology. These changes have important implications for population abundance trajectories and our analyses quantify the degree to which directional selection can buffer populations from climate-driven declines.

***Spatio-temporal community dynamics in a hotspot of trailing-edge population diversity**

H Gaya, R Chandler*Presenting author: Heather Gaya, heather.e.gaya@gmail.com*

Mounting evidence indicates that populations at the warm edge of geographic ranges are declining in response to climate change, but little is known about community-level impacts of trailing-edge population declines. We used ten years (2014--2023) of avian point count data from the southern Appalachian Mountains, USA, to assess changes in abundance and spatial distribution of 9 trailing-edge populations and 16 populations at the core of their range. Three of the nine trailing-edge populations decreased in abundance whereas six species had no change. For species near the core of their ranges, one of 16 populations decreased in abundance, 11 increased, and 4 exhibited no change. Species richness increased at the majority of sites, especially at high elevations. Our results indicate that community composition in a trailing-edge hotspot has become increasingly dominated by warm-adapted species, and increases in species richness may be temporary if declines of cool-adapted species continue.

Evaluating climate disruption on avian species and communities in the southern Rocky Mountains

L Gowens, B Freeman, C Wells*Presenting author: Lily Gowens, Georgia Institute of Technology, ligowens358@gmail.com*

Climate change is altering the phenology and distribution of organisms across taxonomic groups. Natural variation in abiotic factors along elevational gradients may be exacerbated by climate change, especially temperature. At high elevations, temperature can limit species distributions and upward range shifts occur as a response to climate warming. Contemporary and historical survey data can assess such range shifts and identify changes, declines, and extinction risks. This study assessed regional species abundance trends at one elevation in Gothic, Colorado using 23 years of annual survey data and resurveys points along an elevational gradient (2,469-3,421m) in the southern Rocky Mountains to evaluate changes in community composition and shifts in species elevation range compared to 2011 survey data and historical ranges. In addition to climate disruption, human disturbance in Gothic, Colorado has increased over the survey period and may contribute to impacts on avian species. We found a complex relationship between climate disruption and trends in species abundance. Our elevational gradient survey analysis indicates that avian species communities significantly differ in composition between survey sites and years at different elevations. Point-count survey observations suggest that species may be shifting their ranges upwards when compared to historical ranges, however, comparison to 2011 survey observations produced a variety of results and indicates that avian species are not uniformly responding to climate disruption with an upward range shift.

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Avian response to climate and fire history in national parks of the Sierra Nevada
C Ray, R Siegel, R Wilkerson, L Schofield, M Holmgren, L Bryant, M Tingley, S Aronson, S Haultain, S Stock*Presenting author: Lee C Bryant, The Institute for Bird Populations, lbryant@birdpop.org*

National parks must offer refuge for species and ecological processes over the long term. To aid in managing park habitats, baseline inventories and long-term monitoring of avian populations have been supported by the Sierra Nevada Inventory and Monitoring Network. Thousands of avian point-count surveys conducted over more than two decades throughout Yosemite and Sequoia-Kings Canyon national parks provide an opportunity to explore trends in bird species with potentially divergent responses to changes in climate and fire regime. We used these data to investigate temporal trends in breeding season population density for 62 species, and to characterize effects of fire history on density for 42 species. Using hierarchical models to account for effects of habitat and survey conditions on detection probability and abundance, we found that most species were stable or increasing over the monitoring period (2011-2019), when a series of dry winters and warm springs appeared to boost population densities that were otherwise inversely related to year. Effects of fire were examined using data from both the inventory and monitoring periods (1999-2019) to model population densities at each point in a long (1984-2018) history of fire in these parks. Avian responses to fire were dominated by nearly equal numbers of populations that increased rapidly after high-severity burns or slowly after low-severity burns. These results offer a rare perspective on avian response to habitat conditions in some of the few western forests where effects of climate and fire are relatively unconfounded by anthropogenic habitat loss, resource extraction, or related management activities.

The Relative Importance of Safety Cues from Mixed Species Flocks to a Neotropical Bird Community**C Hunts, A Martinez, D Blumstein, E Parra***Presenting author: Chelsey Hunts, chunts@ucsc.edu*

Predation plays a large part in an animal's decision-making process of where to forage and when to flee. Information about potential threats can be acquired through eavesdropping on vocalizations and behaviors of others. Previous research on predation information has largely focused on alarm calls while little is known about other types of calls indicating different levels of risk. Safety cues may provide information created in the absence of a predation threat. Mixed species flocks (MSFs) are a source of information as they vocalize while moving through their territory, potentially alerting birds outside the flock about the safety of the habitat. Here, we investigated how MSF safety cues are used by the avian community within an Amazonian lowland tropical forest in Peru, testing three hypotheses: 1) MSF species provide safety information to the avian community, 2) specific MSF species function as community informants of safety, and 3) the relevance of safety cues is driven by group size. We used playback experiments to contrast responses to MSF and non-flock calls as well as grouped and individual calls. Our results show that MSF species provide more safety information to the avian community, but only when calling alone. Birds were more active after playback of three different individual MSF species, suggesting their role as key safety informants within communities of this system. The lack of response to grouped MSF safety cues suggests a competitive effect that overrides the benefits of individual species safety information. These findings further our understanding of the extent to which the community-wide eavesdropping network uses a variety of information to determine risk levels within their environment.

Examining the light sensitivity and dispersal limitation hypotheses for forest fragmentation sensitivity in Bornean understory birds*W Brooks, N Hasan, D Hanley, H Lim***Presenting author: William Brooks, willbrooks.0@gmail.com*

Extinction has accelerated to >100 times the pre-human rate, driven in part by anthropogenic habitat

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fragmentation and degradation. Understory birds routinely decline in fragmented tropical forests, but mechanisms for their decline remain unknown. Efforts to find drivers of fragmentation sensitivity are hampered by geographic bias in research. The response of understory birds to fragmentation remains virtually unstudied in Asia, despite the dire threat of deforestation in the region. I surveyed birds in Malaysian Borneo with passive acoustics across a gradient of forest disturbance, ranging from highly fragmented forest in an oil palm plantation to primary rainforest. I fit a spatial multi-species occupancy model using local forest cover as a covariate to determine fragmentation sensitivity. I then used model estimates of fragmentation sensitivity in a two-stage linear model to test the influence of traits relating to light sensitivity and dispersal ability. I detected 140 species, two-thirds of which were determined fragmentation sensitive. Proxies for flight ability and light sensitivity failed to predict fragmentation sensitivity, suggesting that more direct measures of these traits are necessary. Mechanisms for forest fragmentation sensitivity must be found to ensure the conservation and greater ecological understanding of these poorly known species.

****Using LiDAR-derived vegetation indices to examine avian community and functional diversity recovery in the highly endangered Chocó Rainforest of Northwest Ecuador**

N Lussier, J Woodlief, C Adams, G Paladines, J Karubian, C Kwit

Presenting author: Nicole Lussier, University of Tennessee, Knoxville, nlussier@vols.utk.edu

In response to global forest loss, the United Nations declared the 'Decade of Restoration' (2021-2030), specifically prioritizing reforestation in tropical regions. The success of such initiatives relies on understanding natural community recovery dynamics. This study aims to examine avian community recovery and its potential determinants along a chronosequential gradient in the severely threatened Chocó Rainforest ecosystem of Northwest Ecuador. We hypothesized that avian functional diversity will increase with time since disturbance and will be driven by forest structural attributes. To address this, we sampled avian communities using mist-netting and point count surveys in six plots within each of four stages of forest recovery: 2, 10, 25, and 50 years post-agricultural abandonment. Functional diversity measures were calculated for each community based on several life-history, morphological, and behavioral traits of each bird species. We then calculated several LiDAR-derived vegetation indices using drone imagery for each plot. Redundancy analysis revealed that avian communities significantly varied across recovery stages, and that canopy cover and height were significant drivers of these differences. Functional divergence and functional evenness significantly increased with restoration time and were significantly positively correlated with canopy attributes. Excitingly, we found that in as little as 25 years of natural recovery, avian communities had similar functional diversity measures to those of 50-year-old forests, indicating rapid recovery and emphasizing the resilience of avian communities within this system. Understanding these dynamics can serve as a valuable indicator of tropical forest recovery, guiding conservation strategies for restoration initiatives within this highly threatened region.

Breeding birds in Upper Mississippi River floodplain forest: 20 years of change

M Wellik, E Kirsch, R Burner

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Forested floodplains along the Upper Mississippi River are important for breeding birds and are shaped by our use of the surrounding lands and the construction of lock and dam system in the 1940's to control water levels. These forests are continuing to change because of higher water levels, maturing forests, and invasive species. We looked at potential changes in the avian community in forests by comparing bird species' relative abundance, species richness, and species' frequency of occurrence between data collected from 1994-1997 and 2015-2019. Point counts were conducted in three stretches of river at sites where there has been no direct forest management since the 1940's. The same sites were sampled in several years during both time periods, using point counts with the same spatial scale and duration. The sites in the 1990's were sampled once per year by a single observer, whereas in the 2010's they were sampled multiple times by multiple observers each year. To account for this difference in yearly sampling effort we bootstrapped the 2010's data, creating a distribution to compare to the yearly one-survey

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one-observer method used in the 1990's. We then calculated z-scores to examine changes in the bird communities over 20 years. In this timeframe there was a slight decline in species richness for each of the three stretches. Across all three stretches some species have declined in frequency of occurrence, such as American Redstarts, whereas others, increased, like the Prothonotary warbler. Examining bird community trends over decades, even with slightly different sampling methods, may benefit avian and habitat management.

Bird communities in a selectively logged tropical montane forest are dominated by small, low-elevation species

R Chanda, S Rai, B Tamang, B Munda, D Pradhan, M Rai, A Biswakarma, U Srinivasan

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Tropical montane forests are critical centers of terrestrial biodiversity and endemism, and face a range of threats, including selective logging and climate change. However, few studies have explored the joint influence of these threats, particularly in tropical mountains, despite how crucial it is to understand the cumulative impact of forest loss and climate change on biodiversity. We used mist-netting and bird ringing data from a long-term (10-year) community and population monitoring program to examine how the composition of the mid-elevation Eastern Himalayan understorey bird community changed in primary and selectively logged forest. Because logged forest is warmer than primary forest, we predicted that the bird community would gradually shift towards lower elevation species, and the transition would occur faster in the logged forest. Additionally, we predicted that the bird community in primary forest would have larger species as compared to the logged forest community. We recorded 9036 captures of 6189 individuals from 130 species in our mist nets across all years and all sampling plots. We finally analyzed 6926 captures of 4801 individuals of 61 understorey insectivorous species upon curating the data. We found that the bird community in the logged forest shifted faster towards lower-elevation species than in the primary forest. We also found that smaller species were better able to colonize warmer logged forest, whereas larger species reached higher densities in primary forest. These trends are likely to be driven by climate change causing upslope range shifts and logged forest selecting for species that are likely to tolerate the consequently altered abiotic (higher temperatures) and biotic (lower resources) environment. These findings have significant implications for understanding the impacts of forest loss and climate change on biodiversity, particularly in tropical montane forests.

An overlooked species loss event in bird communities of the highly threatened seasonal forests of central Brazil

E Santos

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South American seasonally dry tropical forests were formerly connected, linking Atlantic and Amazonian rainforests through corridors across central Brazil. They have acted as important routes for forest birds' range expansions prior to recent deforestation. Despite their uniqueness, these forests were reduced to near extinction in this region even before their bird assemblages could be investigated. To determine how large-scale fragmentation has impacted the composition of bird communities of central-Brazilian seasonal forests, museum-housed specimens of 12 historical collections were examined and compared with present-day avifauna in two remaining woodlots that were monthly surveyed for 2 years. Significant differences, including patterns of species loss and decline, were noted between the past and present communities. Twenty-eight species recorded in the last century were not found in the same areas between 2021 and 2023. Species loss was related to fragment conservation and size, thus in older and larger fragments, some vanished species elsewhere were still present. The more diverse original community has been replaced by a more generalist one, with some species that were uncommon or absent in the last century. Declining or lost birds show specialized ecological requirements or are at the limit of their distributional range. These results reveal that an overlooked species loss event has taken place in this heavily endangered habitat of central Brazil, being one of the few studies about historical changes in bird communities in this tropical ecosystem.

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Testing long-standing assumptions about army ant swarms: how prey biomass and dominance alter space use of birds**E Howard, J Kelley, M De Aquino, B Agenbrod, M Castaño Diaz, C Tarwater***Presenting author: Elizabeth Howard, ejhoward812@gmail.com*

Animals try to make foraging choices that maximize energy intake, while minimizing energy spent. One type of foraging decision animals make is their use of space. However, competition among individuals may result in some individuals occupying suboptimal foraging patches. Ant-following birds in the Neotropics provide a unique opportunity to evaluate how food resources and dominance impact space use. The army ant species, *Eciton burchelli*, create mass swarming events that flush out prey from the forest floor. This, in turn, attracts many bird species that take advantage of the prey being flushed. In 1978, Willis and Oniki drew a graph that is often used to depict how competition structures ant-followers. The graph included three untested assumptions. First, the most dominant species is ocellated antbirds, followed by bicolor antbirds, and then spotted antbirds. Second, the most dominant bird species will occupy the area of highest prey biomass. Third, the center of the swarm is the best place to be (has the highest prey biomass) and prey biomass decreases as one moves away from the center. In 2023, we used insect biomass surveys, point counts, and behavioral observations to examine what area of the swarm has the highest prey biomass, how different bird species use space, and which species is dominant. Our results are congruent with Willis and Oniki in terms of which species is dominant and that birds occupy areas with higher prey biomass. Contrary to previous assumptions, prey biomass is highest at the edge of the swarm, not the center. This study provides a test of optimal foraging theory and of the underlying assumptions of how prey biomass and dominance structure birds following army ant swarms.

Multi-decadal changes in seabird and forage fish distributions in the Northwest Atlantic**E Adams, J Gulka, C Goetsch, K Friedland, A Gilbert, H Goyert, I Stenhouse, K Williams***Presenting author: Evan Adams, Biodiversity Research Institute, evan.adams@briwildlife.org*

Forage fish availability influences the demographic rates of seabird populations through breeding season productivity and year-round survival. Offshore wind development is expected to change forage fish distributions and productivity in the Northwest Atlantic, which could alter seabird behaviors and distributions in the region. Using two long-term survey datasets, we explored the spatiotemporal changes in Northwest Atlantic forage fish and seabird populations and how these changes interrelate across groups. Joint species distribution modeling frameworks were used to predict seasonal spatiotemporal changes in occupancy and relative density for forage fishes and seabirds, respectively. Across the study area in the U.S. Atlantic, most seabird species decreased in relative density over the study period (2002–2019), while forage fish species exhibited more variable trends. Declining forage fishes, like northern sand lance, exhibited strong correlations with declining seabird densities across seasons. The centroids of seabird and forage fish distributions shifted over the study period, with more substantial range shifts among seabirds, though this pattern varied across seasons and species. These distribution shifts affected the spatial overlap between predator and prey distributions, especially for seabirds whose distributions tended towards nearshore areas during the non-breeding period. Our results suggest widespread regional relative density declines in the seabird community of the Northwest Atlantic, as well as declines in the occupancy of several forage fish species that are important prey for seabirds in the region (e.g., sand lance). Range shifts are occurring in both forage fishes and seabirds, albeit at different rates. These different rates of distribution change likely reflect species-level traits like mobility and strength of response to ecological change. These findings reinforce the importance of considering predator-prey dynamics for conservation planning.

The impacts of quaking aspen on avian community composition following wildfire in montane, mixed-conifer forests**C Lane, H Specht, T Riecke, W Wehtje, J Millspaugh***Presenting author: Cody Lane, University of Montana, codyqlane@gmail.com*

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Following widespread fire suppression during the 20th century, land managers are now actively trying to emulate natural fire regimes to reduce wildfire risk to communities and benefit biodiversity. Therefore, it is important to understand how avian species respond to wildfire in different ecological contexts. Quaking aspen is unique within mixed-conifer forests for its ability to regenerate following wildfire via vegetative resprouting. This response is mediated by fire severity and can lead to different successional trajectories compared to conifer-dominated stands. To investigate the interacting effects of fire severity, time since fire, and pre-fire forest composition on avian communities, we conducted Integrated Monitoring in Bird Conservation Regions (IMBCR) protocol point counts at 93 stations within the perimeter of the 2018 Roosevelt Fire from 2019 to 2023. We are utilizing a multi-species occupancy model to understand mechanisms underlying patterns of avian occupancy, species richness, and turnover with pre-fire forest composition, fire severity, time since fire, and post-fire habitat structure. The results of this analysis will provide a more mechanistic understanding of avian responses to disturbance and resulting habitat structure to inform future management practices.

How the environment alters network structure in mixed-species groups of army-ant-following birds

M De Aquino, J Vizentin-Bugoni, J Wolter, H Pollock, J Kelley, M Castaño Diaz, C Tarwater

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Species interactions shape patterns of biodiversity and community structure, and alterations to them can have cascading impacts on populations and communities. However, how environmental variables influence interactions, and the processes modulating impacts across spatial and temporal scales, is not well understood. We examined species interactions in one type of mixed-species animal group – army-ant-following birds – to assess the impacts of environmental variability on network structure. We performed point counts to record species associations at ant swarms and used these to construct species interaction networks. We examined the influence of precipitation, temperature, and different metrics of land cover on network metrics across space, time, and the interactive effects of spatial and temporal variation in environmental variables. Higher precipitation resulted in fewer species interacting at swarms and greater network clustering, which held true across both spatial and temporal (dry versus wet season) scales. The number of species attending swarms increased with decreasing precipitation, while interaction frequency and consistency in interacting species were greatest at moderate precipitation levels. These patterns likely reflect variation in the profitability of attending ant swarms in different environmental conditions and changes in the local bird community across sites. Examining how species interactions are impacted by environmental conditions is critical for understanding the processes modulating species interactions and how interactions will be impacted by anthropogenic change.

***Closing the research-implementation gap for landbird stopover habitat conservation in U.S. State Wildlife Action Plans**

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Conserving stopover habitat is essential for conservation and recovery of migratory bird populations. In the U.S., State Wildlife Action Plans (SWAPs) are one of the primary tools that practitioners use to guide conservation of species and habitats within their states, yet SWAPs often focus mainly on protecting breeding habitat of migratory species, without explicit consideration of the migratory period. Furthermore, information on migration generated by academic researchers may not reach or be relevant to conservation practitioners, contributing to the well-established research-implementation gap. To address this problem, we brought together university researchers, state wildlife biologists, and other conservation managers to co-develop data needs and evidence summaries to incorporate into Maryland's 2025 SWAP. We used weather radar data to identify and map spring and fall stopover hotspots and compiled complementary data sources to identify species composition and distributions during migration within these regions, highlighting species of greatest conservation need (SGCNs) and other taxa of particular interest at management-relevant scales. We identified the current or potential threats to migrating landbirds across Maryland and developed specific recommendations for conservation practitioners to

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promote quality stopover habitat and reduce hazards, tailored to the species, habitats, and stopover hotspots in each region of the state. By co-developing objectives, information needs, and outcomes relevant to state agencies and conservation groups, we provide a case study for how migration can effectively be incorporated into widely used frameworks like the SWAP that have often overlooked this critical period of the annual cycle.

***Forest governance and biodiversity: How community forest management affects avian diversity in the imperiled lowland forests of Cambodia**

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Decentralized forest management has increased over the last 40 years, with governments ceding forest governance back to local communities. While studies have investigated the socio-economic benefits of community forest management (CFM), few have assessed the effect of CFM on biodiversity. CFM may protect biodiversity when the local community, equipped with local ecological knowledge, is invested in preserving a community resource, thus reducing forest degradation and wildlife poaching. Conversely, CFM may result in increased resource exploitation, with increased forest degradation and wildlife harvest. We investigated the influence of forest governance on biodiversity, specifically the impact of CFM on avian diversity in lowland forests of Cambodia, a region undergoing rapid forest loss. We surveyed avian communities using point counts and acoustic recording units in 8 community and 5 state managed forest sites. We quantified forest structure using field measurements and remote sensing. We modeled species occupancy and detection probabilities across sites and analyzed the influence of forest governance and structure on species diversity and occupancy. We also assessed the occupancy of high market value species in relation to forest governance. Our results show differences in avian communities related to forest governance and structure and highlight the variability of CFM and its impact on avian diversity, where some community forests maintained higher diversity than others. Future work should focus on determining how community and NGO investment in forest protection influences biodiversity under CFM. However, community forests could provide a promising alternative to state protected areas for biodiversity conservation.

***Island Forest Bird Health in the Face of Multiple Stressors**

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Hawaiian forest birds-like other island endemic species-experience multiple stressors, such as habitat loss and degradation, climate change, disease, and predation by invasive animals. Our aim was to determine which stressors were most strongly associated with the physiological condition of Kaua'i Island forest birds to prioritize management actions to conserve them. We examined the body condition of four Hawaiian forest bird species in Kaua'i's Alaka'i Wilderness Preserve. We mistnetted and banded 570 individuals between 2021 and 2023, collected blood samples to determine malarial infection status, and recorded metrics related to body condition. We then statistically assessed body condition in relation to habitat, climate, disease, and predation risk. Specifically, we quantified habitat with canopy density and the topographic wetness index (TWI) and climate with temperature and precipitation as predictors of mosquito populations and malarial status. We quantified the density of rat traps in the area where the bird was caught to test the effectiveness of ongoing rodent suppression and measured disease by malarial infection status. Predation and disease are significant causes of Hawaiian forest bird declines, with malaria primarily affecting individuals from the group of birds known as honeycreepers. Initial results suggest that for three of the four focal species, there was a negative correlation between mean temperature during the mosquito breeding season prior to when the bird was caught and body condition. The fourth focal species was a honeycreeper, and for this species, malarial infection status significantly predicted lower body condition. These findings will inform management actions to protect Kaua'i's montane bird populations and contribute to a deeper understanding of multiple stressors on forest bird health and demography.

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Achieving strategic focus for migratory bird conservation in the face of limited resources; the case of the Atlantic Coast Joint Venture**M Correll, A Weldon, M Hartley, D Reynolds, K Luke, C Faulhaber***Presenting author: Maureen Correll, USFWS, maureen_correll@fws.gov*

The Atlantic Coast Joint Venture (ACJV) is one of 22 habitat joint ventures that work to conserve migratory birds across North American landscapes. The ACJV spans the Atlantic Flyway from Maine to Florida, and making a measurable impact to birds at that scale with limited staff and budget is challenging. To address this challenge the ACJV management board and staff embarked on a multi-stage decision-making process in 2016 to focus resources and make a measurable impact within the 17-state geography. We used a combination of expert elicitation, weighted criteria assessment, and post-hoc surveys and interviews to select an ecosystem and suite of species on which to focus where a Joint Venture partnership would be the most value added. The result of this 1-year endeavor was a coastal marsh focus through a suite of 'flagship species' associated with tidal marsh habitat: Saltmarsh Sparrow, American Black Duck, and eastern Black Rail. Since this process of strategic focus was completed the ACJV has had used the resources of six staff to 1) collaboratively write and published conservation plans for each species and coastal marsh as an ecosystem, 2) identify priority areas in which to work to benefit each species, 3) develop partnerships and focus groups to help address known bottlenecks to marsh conservation, 4) develop a database to track marsh project progress over time, and 5) recruit resources through grant application support and ghost-writing. The ACJV has accomplished these goals by providing coordination capacity, science development/integration, and funding support exclusively focused on coastal marsh restoration efforts. We will share details from the decision-making process, discuss lessons learned, and celebrate conservation successes achieved after 8 years of strategic focus by the ACJV.

Strategic restoration planning for land birds in the Colorado River Delta, Mexico**J Grand, T Meehan, B DeLuca, J Morton, J Pitt, A Calvo-Fonseca, C Dodge, M Gómez-Sapiens, E González-Sargas, O Hinojosa-Huerta, P Nagler, C Restrepo-Giraldo, P Shafroth, S Villagomez-Palma, C Wilsey***Presenting author: Joanna Grand, National Audubon Society, joanna.grand@audubon.org*

Ecological restoration is an essential strategy for mitigating the current biodiversity crisis, yet active restoration is costly. We designed an approach that prioritizes restoration sites for birds and tested it with a riparian forest restoration program in the Colorado River Delta. Restoration goals were to maximize the abundance and diversity of 15 priority birds with a variety of habitat preferences. We built relative abundance models for priority birds based on the current landscape and predicted abundances under a scenario of complete riparian forest restoration throughout the study area. We used Zonation conservation planning software to rank the restored landscape based on core areas for all priority birds. The locations with the highest ranks represented the highest priorities for restoration and were located throughout the river reach. We optimized how much of the available landscape to restore by simulating restoration of the top 10 to 90% of ranked sites in 10% intervals. We found that total diversity was maximized when 40% of the landscape was restored, and mean relative abundance was maximized when 80% of the landscape was restored. The results suggest that complete restoration is not optimal for this community of priority birds and restoration of approximately 60% of the landscape would provide a balance between maximum relative abundance and diversity. Subsequent planning efforts will combine our results with an assessment of restoration costs to provide further decision support for the restoration-siting process. This approach can be applied to any landscape-scale restoration effort to improve the return on investment of limited resources for restoration.

Patterns of Vulnerability in Partners in Flights assessment of North American bird species**A Panjabi, K Rosenberg, A Shaw, M Gahbauer, W Easton, P Blancher, A Smith, J**

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Hostetler, D Demarest, L Sandoval, T Will, R Dettmers, V Ruiz-Gutierrez, B Bateman, B Stewart, M Wells, A Roberts, H Berlanga, V Rodriguez*Presenting author: Allison Shaw*, Bird Conservancy of the Rockies, allison.shaw@birdconservancy.org

The Avian Conservation Assessment Database (ACAD) was developed by Partners in Flight (PIF) to evaluate vulnerability and regional responsibility of U.S. and Canadian landbirds to help prioritize science and conservation action. Since its launch in 2000, PIF has continually refined and improved its assessment methodology and has expanded and adapted it to address all birds from Canada to Panama, including during the non-breeding seasons. PIF has regularly updated ACAD to make use of novel data sets and analyses, and recently added a climate vulnerability assessment for 604 species. Using ACAD, we demonstrate geographic and ecological patterns of vulnerability for resident and migratory species, including higher diversity and vulnerability in the south and greater breeding abundance in the north. Island and oceanic species had a higher proportion of vulnerable species and the highest total number of vulnerable species was in tropical evergreen forests. We compare the PIF Watch List derived from ACAD with the IUCN Red List and illustrate how the PIF assessment proactively targets conservation action by weaving together species and ecosystems approaches at various scales before endangerment. We discuss future directions in ACAD, including how eBird data and models can be used to improve population estimates and trends, and expansion of climate vulnerability models.

Cape May (*Setophaga tigrina*) and Bay-breasted Warblers (*Setophaga castanea*) exhibit different dietary responses to reduced prey availability**F Maika, J Nocera, R Johns***Presenting author: Fawn Maika*, University of New Brunswick, fmaika@unb.ca

Insectivorous songbirds are generally known to consume large quantities of Lepidopteran prey throughout the breeding season due to their nutritional quality. During outbreaks, the spruce budworm (*Choristoneura fumiferana*, hereafter SBW) (Lepidoptera: Tortricidae) is a common prey for a variety of predators and can constitute up to 90% of wood-warbler diets. Nevertheless, the cyclic nature of SBW outbreaks can result in severe defoliation of valuable tree species, frequently targeted for harvesting. In response, Lepidoptera-specific insecticides such as *Bacillus thuringiensis* var. *kurstaki* (Btk) are used to suppress their populations and associated impact. My study sought to examine the indirect effects of Btk on the dietary habits of two species of wood-warblers that specialize in foraging on SBW, namely the bay-breasted warbler (*Setophaga castanea*) and Cape May warbler (*Setophaga tigrina*). By utilizing stable isotope analysis of their fecal samples, I assessed dietary patterns in untreated and Btk treated sites pre- and post-insecticide application. My findings suggest that the consumption ratio of Lepidoptera in SBW specialists is comparatively insignificant among treatments. However, estimates of the proportional contribution of Lepidoptera to the overall diet increased for both bird species in Btk sites post-treatment. Therefore, individuals residing in Btk-treated sites may need to intensify their search activity and behaviour, highlighting potential ecological implications of decreased reproductive success and overall fitness.

Isotopic analysis in feathers of the Least Tern (*Sternula antillarum*) to infer its trophic ecology*A Morales Flores, G Busquets-Vass, E Palacios, E Solana Arellano, T Ryan, G Heckel Dziendzielewski***Presenting author: Andehui Morales Flores*, Centro de Investigación Científica y de Educación Superior de Ensenada, CICESE, biodanay@gmail.com

Little is known about the behavior and movement of Least Terns (*Sternula antillarum*) that breed on the Pacific Coast and the Gulf of California. Adult Least Terns molt their primary feathers during the non-breeding season, making it practical to investigate diet and geographic location by analyzing stable carbon and nitrogen isotopes in their primary feathers. We expect similar diets and feeding strategies among adults during non-reproductive and reproductive seasons. In 2022, we collected samples of primary feathers from adults and fledgling Least Terns at nesting colonies in Southern California and

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Northwestern Mexico. Analysis of the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ isotopic ratios in primary feathers estimated adult and fledgling Least Terns trophic niche breadth and overlap. We used the Standard Ellipse Area (SEAB) to estimate niche breadth using Bayesian methods. We analyzed the variability of these isotopic signatures during the sequential growth of primary feathers through generalized additive models. We assessed the variability between the primary feathers using anomalies related to local media. The study found variations in trophic niche between adult and fledgling birds. Adult SEAB values ranged from 16.3‰ to 28.4‰, while fledglings ranged from 44.8‰ to 75.5‰. Fledglings exhibited larger niche breadth compared to adults, potentially due to variations in feeding strategies. Alternatively, adults from certain colonies could share a wintering site during the primary feather molt period, with different feeding strategies of individual Least Terns. The bibliographic review of $\delta^{13}\text{C}$ isotopic gradient maps suggests a potential wintering site in the Tropical Eastern Pacific Ocean.

The effects of human interaction on Canada jay (*Perisoreus canadensis*) behavior and nest predation

J Long, M Postava-Davignon

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Humans have a long history of feeding birds, either to help them survive by supplementing their diets, or simply to enjoy interacting with them. Canada jays are charismatic birds that have become accustomed to these interactions to varying degrees. To survive the winter, they need to cache numerous food morsels throughout their territory. Their diverse diets include insects, berries, carrion, human offerings, and the eggs and nestlings of other birds. Concern has been expressed in recent years that Canada jays attracted to wilderness recreationists might increase predation pressure on nesting songbirds. To address this concern, we compared jay behavior and nest predation levels in New Hampshire and Maine between sites where little human interaction has been documented, and sites located at popular recreation areas where feeding has been well documented. During May and June 2022-2024, we captured and banded Canada jays to track individuals, recorded their behavioral responses to people in their territory, and used artificial nests with game cameras to document nest predation. Results show that in areas of high human interaction, jays approach closer to humans, usually landing on someone's hand to take food, spend much more time near people, find decoy nests in less time and find more nests compared to low interaction areas. In areas with fewer human interactions, they rarely approach people, showing no interest in human food. These results suggest that feeding jays may have an impact on breeding songbirds, which could have important conservation implications.

Conservation implications of breeding Eastern Whip-poor-will prey preferences assessed via comparison of fecal DNA metabarcoding and UV light insect trap samples

G Witynski, O Moline, M Ward, S Tomczyk, J Gillece, J Foster, T Benson

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An understanding of how dietary requirements and preferences shape the ecology of declining species is one of the most fundamental components of planning for their conservation. Nightjars are highly susceptible to dietary constraints on breeding success because they are active only during crepuscular or nocturnal periods and rely on flying nocturnal insects—many of which are in steep decline—as their primary prey. Likely due in part to these restrictions on their foraging capacity, many nightjars have experienced rapid range contractions and population declines in recent decades, including the Eastern Whip-poor-will (*Antrostomus vociferus*), whose call was once near-ubiquitous across nighttime soundscapes in eastern North American woodlands. Although recent studies have confirmed whip-poor-will's reliance on moths as their primary food source, very limited information is available on their prey preferences below the order level. To better understand whip-poor-will dietary preferences and requirements, we are conducting DNA metabarcoding on fecal samples collected from whip-poor-wills on breeding territories in central Illinois, USA from 2021 to 2024. We are comparing these sequences with prey availability measured through ultraviolet light insect trapping that was conducted concurrently at our sites across three habitat classifications: forest, edge, and grassland. We present our preliminary

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analyses of these data investigating the taxonomic, size, and habitat affinities of prey consumed by breeding whip-poor-wills as well as the host plant requirements of preferred prey species. These dietary requirements have far-reaching implications for the conservation of moths and whip-poor-wills alike, and we hope our methods will provide roadmap for conservation research on aerial insectivores and their prey beyond our study system.

Five years of seabird diet monitoring in the Gulf of Maine using dietary DNA*G Clucas, L Welch, D Lyons, P Shannon, W Kennerley, E McGourty, S Kress, E Craig***Presenting author:* **Gemma Clucas**, Cornell Lab of Ornithology, Gemma.Clucas@cornell.edu

Seabirds have long been recognized as sentinels of marine ecosystem health, and monitoring their diets can yield insights into forage fish availability that underpins seabird breeding success. Traditional methods to monitor seabird diets can be labor intensive in the field and/or suffer from low taxonomic resolution. However, dietary DNA gathered from fecal samples does not suffer from these limitations. Here, I show how dietary DNA can be used to gather high-resolution, quantitative information on prey proportions in seabird diets and delve into five years of tern and alcid diet monitoring in the Gulf of Maine. I show how inter-annual changes in the prevalence of preferred prey, such as Atlantic herring, lead to increases in dietary diversity and how these patterns relate to the prevalence of marine heatwaves. I also determine the extent to which adult and chick diets differ and place this in the context of optimal foraging theory. Gathering this type of high-resolution data on changes in seabird diets, combined with efforts to scale-up diet monitoring across populations, represents a key pathway to advance our understanding of worldwide seabird declines and work to effectively address the challenges posed by fisheries management and global change.

Syntopic diet divergence inferred from meta-barcoding in parulid warblers**D Toews, M Baiz, A Dale, R Fleischer, A Benavides Castaño, L Phung, S Szarmach, A Wood, A Welch, E Miller***Presenting author:* **David Toews**, toews@psu.edu

The parulid warblers of North America are a well-known avian radiation with a rich legacy of study. This includes early works by Robert MacArthur in the 1950s, which remain a cornerstone of modern community ecology. MacArthur's studies focused on possible niche differences of co-occurring species within the family, with a particular emphasis on fine-scale foraging variation. Understanding the exact types of forest insects these warblers are eating, however, has been difficult to quantify. Here, using inferences from COI fecal metabarcoding, we combine a broad-scale phylogenetic analysis of diet across 13 species of warbler ($n = 336$ fecal samples) with a fine-scale, paired analysis of two species, black-throated green warblers (*Setophaga virens*, $n = 60$) and ovenbirds (*Seiurus aurocapilla*, $n = 59$), captured at the same time and place. We show that while there is broad overlap in the diets of parulid warblers, a significant portion of that variation is phylogenetically conserved. From the two species with highly syntopic sampling-and spanning the breadth of the warbler diet space-we also show strong differences are maintained at a very fine scale. Both studies also highlight the use of fecal meta-barcoding approaches to quantify and monitor the spread of invasive arthropods, such as spongy moths.

Linking climatic variability, tree masting in coniferous forests, bird irruptions, and disease outbreaks in the United States**B Tonelli, C Youngflesh, M Tingley***Presenting author:* **Ben Tonelli**, btonelli@ucla.edu

Outbreaks of Salmonellosis are often detected in wild birds leading to substantial morbidity and mortality. One recent and severe outbreak in the winter of 2020-2021 demonstrated the risk for spillover from birds to human hosts through contact with wild bird feeders. Understanding the mechanisms driving the risk of these events could help forecast risks to wildlife and human health. Here, we test the hypothesis that Salmonellosis outbreaks are associated with irruptions – irregular winter migrations – of the Pine Siskin.

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Simultaneously, we test the previously suggested hypotheses that irruptions of this and other species are associated with food availability – conifer seeds – in high-latitude and high-altitude forests, and that conifer seed production is in turn related to climatic cues. Using a multi-level Bayesian model, we find strong evidence for a mechanistic link between climate in boreal and western forests on cone production, bird irruptions, and disease outbreaks. We demonstrate how our predictive model can be used to probabilistically forecast future irruptions and disease outbreaks using contemporary climate information. These predictions have the potential to help inform wildlife and public health agencies to take preemptive steps to mitigate avian and human health impacts, such as encouraging the public to take down bird feeders in anticipation of high-risk irruption years.

****First confirmation of birds hosting ticks with tick-borne pathogens in eastern redcedar-encroached grasslands of the Great Plains**

T Taylor, S Loss, B Noden

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Eastern redcedar (ERC), a native tree with invasive properties, is rapidly encroaching into grasslands across the U.S. Great Plains. Its spread, mainly due to fire suppression, affects entire ecosystems, including bird communities and the ecology of vector-borne disease. ERC encroachment is known to increase abundance of tick species that carry pathogens, but the role birds play in hosting these ticks and pathogens in these communities is unknown. In areas of Oklahoma representing successive stages of ERC encroachment, we sampled birds for ticks from May-October 2023 and evaluated tick infestation of birds and presence of tick-borne pathogens in ticks sampled. We identified ticks to species and tested for pathogens that cause Spotted Fever Group Rickettsiosis, Ehrlichiosis, and Lyme Disease. Among 144 birds sampled, 35 had at least one tick (24% infestation prevalence); Northern Cardinal (*Cardinalis cardinalis*) made up 71% of tick-infested birds with Carolina Wren (*Thryothorus ludovicianus*) and Painted Bunting (*Passerina ciris*) at 9% and 5% respectively. On average, infested birds carried 2.5 ticks. Among ticks sampled from birds, we identified 5 black-legged ticks (*Ixodes scapularis*), 56 lone star ticks (*Amblyomma americanum*), 1 Gulf Coast tick (*A. maculatum*), and 29 rabbit ticks (*Haemaphysalis leporispalustris*). We found at least 1 pathogen in 32% of ticks tested; while most were well-known species such as *Ehrlichia chaffeensis*, one *Rickettsia* sp. had been only recorded twice. This study provides the first evidence that birds in ERC encroached grasslands carry ticks and tick-borne pathogens that infect humans and wildlife, further clarifying the implications of encroachment for the ecology of vector-borne diseases.

***Immunogenomics of susceptibility to avian tuberculosis (*Mycobacterium avium*) in the Endangered White-winged Duck (*Asarcornis scutulata*)**

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Captive breeding in zoos can be an important reservoir for preserving genetic diversity in endangered species. The White-winged Duck (*Asarcornis scutulata*) is an Endangered species from the sub-continent and southeast Asia, whose captive breeding population in North America is managed by Sylvan Heights Bird Park (NC). However, captive breeding efforts for this species have been hindered due to high losses of young birds to avian tuberculosis (*Mycobacterium avium* complex). This pathogen does not cause clinical symptoms in closely related duck species at the same rate, even when housed in the same enclosures as the White-winged Duck. This suggests an immunogenetic component to their susceptibility. The major histocompatibility complex is a gene family involved in antigen recognition in the immune system, and could be an important component mediating susceptibility. To understand the basis of susceptibility to this pathogen, we characterized diversity in the major histocompatibility complex of captive and wild ducks using whole genome sequences. We found a significant loss of diversity in the major histocompatibility complex of the captive ducks. Then, we used RNAseq on whole-blood of symptomatic and a-symptomatic individuals and compared these with a similar sample in the less-susceptible Redhead Duck (*Aythya americana*). We characterize differences in the transcriptomic response to infection, and compare the complement of immune gene expression between the two

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species. Our results are the first to examine the components of immunity to *Mycobacterium* in a species of conservation concern .

***Variation in body size and telomeres in a Hawaiian passerine across a disease gradient**

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Since avian malaria was introduced to Hawaii a century ago, it has become prevalent in warmer, low elevation habitats but remains absent from cooler, high elevation areas. The Hawaii Amakihi (*Hemignathus virens*) is an endemic Hawaiian passerine that spans a broad elevational gradient. Low elevation Amakihi have evolved increased resilience to avian malaria, which may be related to stronger innate immunity. Immunity helps defend against infection but it can also be energetically costly, thereby reducing the resources available for other processes, like growth and development. Telomere length is a metric of physiological aging that can provide information about an individual's developmental conditions and be predictive of longevity. The goal of this study was to determine how variation in disease pressures across elevation have influenced Amakihi development by measuring body size and telomeres in juveniles (hatch year and second year birds). Since challenging developmental conditions (e.g., increased infection risk) can impair growth and accelerate telomere attrition, we predicted that body size and telomere length would be lower in low compared to high elevation juveniles. As predicted, body size as measured by tarsus was significantly smaller in low compared to high elevation juveniles ($p = 0.0029$). Also as predicted, telomere length was significantly shorter in low compared to high elevation hatch year birds ($p = 0.034$), but it was longer (though not significantly, $p = 0.19$) in low compared to high elevation second year birds. Our results suggest that increased disease pressures may be related to lower growth and, in some cases, higher telomere attrition, but additional studies will be necessary to determine causation.

***Recent effects of West Nile virus on Pennsylvania breeding bird populations**

B Geary, L Williams, S Murphy, R Gagne*Presenting author: Brock Geary*, Wildlife Futures Program, brock.j.geary@gmail.com

Understanding pathogen effects on wildlife populations requires comparable and contemporaneous data on both the pathogen and host populations, which are often challenging to obtain. Wildlife population trends are also influenced by many other ecological factors, potentially weakening causative inferences regarding disease. West Nile virus (WNV) has driven declines in many avian populations since arriving in the United States, but its more recent impacts are less well-understood. At a community level, bird responses to WNV in the United States have not been broadly assessed in over 15 years, and a more thorough understanding of its persistent effects from a landscape perspective is needed to improve future health outcomes for wildlife and humans. We used Pennsylvania's mosquito surveillance database to model the incidence of WNV at a fine spatiotemporal scale, and Breeding Bird Survey records to obtain similarly fine-scaled abundance estimates. WNV incidence varied substantially over space and time, and was also correlated with factors such as temperature, elevation, forest cover, day length, and a tendency to collect standing water (but not open water). By bringing these two outputs together, we found variable impacts of WNV on bird population trends, and are now conducting community-scale analyses to assess the potential ecological or genetic correlates of WNV vulnerability. Future work will supplement model-based inferences with field-based data, address species- and habitat-related knowledge gaps on the Pennsylvania landscape, and better understand how disease shapes population trends relative to habitat loss and other threats.

***Moving towards a holistic assessment of the food-safety risks imposed by wild birds**

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Wild birds pose a unique food-safety risk to agriculture as they carry multiple zoonotic pathogens, are difficult to exclude, and most are federally protected. As a result, farmers have few strategies for reducing bird fecal contamination. Here, we evaluate the food-safety risks of wild birds, from the point of entering farms through harvest via three complementary approaches. First, we collected feces from 38 under-sampled species and assayed them for *Salmonella*, Shiga toxin-producing *E. coli*, and *Campylobacter*. Second, for crop contamination to occur, infected birds must be present on agricultural fields and defecate on the crops. We conducted bird surveys on 28 leafy-green farms across the Central Coast of California during the harvest season. Finally, we conducted laboratory and field experiments examining *E. coli* survival in feces from diverse set of bird species, which were then placed on lettuce, soil, and plastic. Our results indicate pathogen prevalence in birds in this region is very low, with all three pathogens found in less than 2% of the ~1,200 samples tested. Additionally, our work suggests food-safety risks from birds change across the growing season. Twice as many individuals and nearly quadruple the number of bird flocks were observed in the fall. Importantly, not all species carried the same risk in terms of pathogen survival. Fecal mass was the strongest predictor for how long *E. coli* survives, with increased survival in larger fecal samples. Larger birds thus carry greater food-safety risks. By investigating which birds are more likely to harbor pathogens, which birds occupy agricultural habitat, and how long pathogens survive in feces after bird defecation, our work contributes to a more holistic understanding of the risk wild birds pose to food safety. These results will better inform farmers and policy makers on how to co-manage agricultural lands for both conservation and human health.

A nationwide surveillance program for monitoring highly pathogenic avian influenza in wild migratory birds

K Dilione, J Lenocho, S Bevins, J Ringenberg, K Weir

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In January 2022, the clade 2.3.4.4b H5N1 highly pathogenic avian influenza (HPAI) was reported in a wild bird sample from Colleton County, South Carolina, and heralded what has become the largest avian influenza outbreak in United States history. This sample was collected from an apparently healthy hunter harvested bird as part of the U.S. National Surveillance Plan for Highly Pathogenic Avian Influenza in Wild Birds, which was initiated in 2006 to serve as a unified national system for the early detection and monitoring of HPAI and other avian influenza viruses in migratory birds. We will give an overview of the Surveillance Plan, which focuses on sampling apparently healthy waterfowl from areas with extensive mixing of wild bird populations and a history of avian influenza virus detection. We will also share results of the past three years (Fall 2021 – present) of targeted surveillance efforts, wherein APHIS Wildlife Services and its partners tested >85,000 wild birds across all four North American Flyways. Since the initial H5N1 HPAI detection in 2022, targeted surveillance efforts have led to >4,500 detections of H5N1 HPAI in at least 65 species of wild birds from 48 States. Unlike the 2014-2015 HPAI outbreak in the U.S., the primary driver for the spatial extent of spread of the 2022-2024 HPAI event has been migratory wild bird movements. Going forward, continued targeted surveillance of wild migratory birds will be a critical component for understanding transmission dynamics and disease risk to wild birds, domestic birds, and people.

Avian Malaria in the migratory White-Crowned Sparrow (*Zonotrichia leucophrys*), and its impact on the immune system and gut microbiome.

A Valenzuela

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Malaria is a global disease that infects a variety of organisms, from small rodents and reptiles to mammals. Avian malaria has been of interest to researchers due to the potential effects on migratory birds. Studies have shown negative consequences on birds infected with haemosporidians (blood parasites) and their fitness, such as body condition, fat score, and plumage quality. However, the effects of malaria on the immune system and gut microflora on migratory birds are not well understood. We investigated the action for haemosporidians to impact the immune system and gut microflora using the migratory white-crowned sparrow (*Zonotrichia leucophrys*; WCSP) as a model. In our experiment, blood

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and fecal samples were obtained from 122 WCSP wintering at the San Joaquin Experimental range. Fixed blood smears were observed to determine relationship between parasite load and stress levels via quantities of infected red blood cells and heterophil-to-lymphocyte (H:L) ratios. Blood parasites and gut microbiome lineages were determined from sequenced DNA extractions obtained from WCSP blood and fecal samples, respectively. We observed that infected birds displayed elevated H:L and changes in the quantity of microorganism compared to non-infected birds. These results suggest infection with haemosporidians decreases heterophil cells in peripheral blood and alters gut microbial abundance, proposing a correlation with malaria infection, the innate immune system and gut microflora. In addition to infection rates and expansion of malaria, this study aids in understanding the influence haemosporidians have on the immune system and gut microbiome in WCSP during their wintering ground stopover.

Virus sequencing and bioinformatics of avian influenza viruses among wild birds in Arizona

M Scotch, T Faleye, P Jones, S Kraberger, B Bermudez Rivera, J Custer, B Hampton, N Kaiser, J Lacson, M Lund, D Olivo, S Swaminathan, J Vargas, C Wheeler, K McGraw, A Varsani

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Arizona is mostly within the North American Pacific flyway that has long been an area of concern for both low and highly pathogenic avian influenza viruses (AIV) due to the number of species in the flyway and the vast, northern breeding grounds in Alaska and Canada. Although statistics related to the number of confirmed AIV cases by species and state are important for outbreak monitoring, they do not provide context for the diversity and evolution of the virus which can only be studied through virus sequencing and genomic epidemiology. Here, we can use bioinformatics methods for subtyping, clade assignment, and identification of single nucleotide variants (SNV) within specific influenza A gene segments. As part of ongoing research and surveillance, we used Oxford Nanopore MinION technology for long-read sequencing of AIVs from cloacal swab samples from birds in Arizona in 2021 and 2022. We used the Centers for Disease Control and Prevention's Iterative Refinement Meta-Assembler (IRMA) to assemble the raw sequencing reads. We selected the hemagglutinin and neuraminidase assembled contigs as input into the National Center for Biotechnology Information's (NCBI) BLASTn tool to identify the most similar sequences in the NCBI GenBank database. The results suggested that two of the samples were positive for AIV including one highly pathogenic A/H5N1 virus in a mallard (*Anas platyrhynchos*) in December 2022 in Maricopa County and one low pathogenic A/H12N5 virus in a mallard in December 2021 in Cochise County. The A/H5N1 sequence matched with the current circulating clade of 2.3.4.4b viruses and included ten SNVs in the H5 gene and seven in the N1 gene. The A/H12N5 sequence matched most closely with an A/H12N5 virus found in a mallard in Ohio in 2018 and included seven SNVs in the H12 gene and one variant in the N5 gene. As AIVs continue to circulate, monitoring and sequencing of both low and highly pathogenic subtypes is critical for monitoring diversity and evolution.

Unraveling avian parasites diversification: Phylogenomics of the louse genus *Myrsidea

J Soto Patiño, J Dona, K Johnson

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Birds harbor an astonishing diversity of parasites and pathogens. Avian lice, with over 4,000 described species, and many more undescribed, are ectoparasites that spend their entire life cycle on the host. The louse genus *Myrsidea* (Phthiraptera: Menoponidae) is the most diverse among avian lice. Due to its high species diversity, host-specificity, and patterns of host association (primarily songbirds of the order Passeriformes and some non-passerines from the order Piciformes), this genus provides an excellent system for investigating patterns of codiversification and biogeography in avian parasites. This study aims to uncover a high-resolution picture of the phylogenetic relationships within the genus *Myrsidea* by leveraging whole-genome sequence data. To achieve this, we sequenced genomes for 104 avian louse species, representing lice in the genus *Myrsidea* from five host species of Piciformes, 98 species of

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Passeriformes, across 37 families, and the first confirm record from one hummingbird species. Using the bioinformatic software aTRAM, we assembled 2,395 single copy gene orthologs from louse genomic reads and aligned the resulting sequences. To estimate the phylogeny, we used both concatenated and coalescent gene tree estimation methods under a maximum likelihood framework. Our results suggest strong support for the monophyly of the genus *Myrsidea*, with species from non-passerines phylogenetically embedded within those from passerines. These phylogenies provide a basis for reconstructing the cophylogenetic and biogeographic patterns between these lice and their hosts, as well as delving into the mechanisms that shape parasite diversification, such as cospeciation and host-switching.

When did avian malaria arrive in Hawaii?

R Fleischer, N VanTassel, A Henschen, M Ochirbat, M Campana

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Infection by avian malaria (*Plasmodium relictum*; lineage GRW4) has greatly impacted the Hawaiian avifauna, causing high mortality, severe population declines and limiting the distribution of most native Hawaiian birds to higher elevations. The historical record indicates that its mosquito vector *Culex quinquefasciatus* was introduced to Hawai'i in the 1820s, but it has not been easy to identify when *Plasmodium relictum* arrived. We initially evaluated the infection status of museum specimens of native Hawaiian birds from the 1830s to 1949 using classic PCR and sequencing methods. For a subset, we also used library preparation, oligo capture and high-throughput sequencing methods to obtain nuclear SNPs. We also assessed non-Hawaiian specimens from a similar timeframe as a control to document the ability of our methods to detect malarial infection in older museum specimens from areas in which avian malaria normally occurs. We obtained sequences of *Plasmodium* and related haemosporidian taxa in control specimens collected back to the 1870s. Except for one Hawai'i amakihi (*Chlorodrepanis virens*) specimen collected from the Hilo area in 1903 (that we carefully replicated) we found no confirmed positives for *Plasmodium relictum* in hundreds of Hawaiian specimens prior to 1948. In addition to confirming that the 1903 specimen had GRW4 malaria sequence, we also were able to place it in the context of samples from after 1948-1949 via SNP analyses. We discuss the likelihood that GRW4 malaria was present in Hawai'i as far back as 1903, whether it may have only occurred locally in the Hilo area, and what this means for understanding the impacts the parasite has had, and continues to have, on the native avifauna.

*Cassowary casques are lightning rods for functional speculation: Assessing potential visual display roles via developmental anatomy and morphometric shape variation

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The cranial casques of extant cassowaries (*Casuarus*) have long intrigued researchers; yet, in-depth studies regarding their morphological variation are scarce. Despite numerous functional hypotheses for these bony and keratinous ornaments (e.g., physical ramming, vocal resonance, audition, thermoregulation, sociosexual visual display), few empirical studies exist to lend support. In order to test this longstanding question, thorough investigations of casque anatomy must be completed. Through gross inspection it has been recognized that ornament variability exists between species (*C. bennetti*, *C. casuarus*, *C. unappendiculatus*) and between conspecifics. Although hypothesized to be targeted by natural selection, intra- and interspecific casque variation has not been quantified previously. Using a large sample of *C. casuarus* (n = 103) we compared casque shapes (lateral and rostral views) between sexes and geographic regions via a 2D geometric morphometrics approach. We also compared casque shape across the genus (n = 166). In *C. casuarus* we found no significant differences between the casque shape of females and males and few substantial shape differences between geographic areas. Much of the intraspecific variation within *C. casuarus* is due to casque asymmetries (77.5% rightward, 20.7% leftward, and 1.8% non-deviating from the midline). Although our casque morphospace across the

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genus had some areas of overlap, casque morphologies between species are significantly different from one another. Casque shapes of *C. bennetti* (relatively short, trigonal pyramids) and *C. casuarius* (vertically tall, laterally-compressed keels) were particularly unique, while casques of *C. unappendiculatus* exhibited some intermediate features. These findings provide important context for better interpretations of cassowary biology, casque display function(s), and cranial ornament evolution in this unique group of birds.

***Investigating the Z:A ratio, a genomic index of sexual selection strength, in manakins (Pipridae)**

H Anderson, K Bennett, E Shogren, K Long, J Brawn, A Boyle, C Balakrishnan, J Karubian, M Braun

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When males are subject to strong sexual selection, population genetic variation on male-biased sex chromosomes is expected to be disproportionately depleted relative to autosomes. In birds, males are the homogametic sex (ZZ) and females are heterogametic (ZW); therefore, a genomic metric that should relate to the strength of sexual selection is the ratio of genetic diversity on the male-biased Z chromosome relative to the autosomes (hereafter, the Z:A ratio), with reductions below the neutral expectation of 0.75 being indicative of stronger sexual selection on males. However, these straightforward theoretical predictions have received mixed empirical support, and factors other than sexual selection (e.g., sex-biased mortality, migration, or mutation; exposure of Z-linked recessives to selection in females) also have the potential to influence Z:A ratios. Here, we investigate Z:A ratios in manakins (Aves: Pipridae), a predominantly lekking clade of Neotropical birds known for having elaborate sexually selected traits in males. Manakins have the potential to serve as a compelling test case for the utility of the Z:A ratio, as the family is expected to have evolved under strong sexual selection, and a well-resolved phylogeny offers the potential to examine the Z:A ratio in relation to mating system, display complexity, and multiple transitions to and from sexual dichromatism. In several genera of lekking manakins, we find evidence of reduced Z:A ratios that are consistent with strong sexual selection on males. We also examine the variation in Z:A ratios within species over space and time, providing insight into the degree to which this genomic index varies within and across populations. Ultimately, this work aims to elucidate the influence of sexual selection on patterns of genetic diversity on sex chromosomes, as well as the circumstances under which the Z:A ratio can serve as an informative measure of the strength of sexual selection in avian lineages.

****Analyzing the interaction between song and color complexity in finches at different taxonomic scales**

A Casale, D Lijtmaer, P Tubaro

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The interaction between simultaneously expressed secondary sexual characters in an organism is among the least understood aspects of sexual selection. Different interpretations predict that the correlation of the complexity of these simultaneous signals should be positive, negative, or non-existent. These three possibilities have been supported by studies of different bird groups. In this context, we examined the relationship between color complexity and vocal elaboration in the passerine family Fringillidae. The analyses were performed at two scales: at the family level and within the genera *Crithagra* and *Spinus*. *Crithagra* was chosen for its gradual color variation among species, and *Spinus* because it includes some of the most elaborate avian songs, such as those of the Hooded Siskin (*Spinus magellanicus*). At the family level, a total of 916 songs belonging to 105 species were evaluated, while at the genus level, 555 songs from 57 species were analyzed. The results revealed a lack of association at both scales of analysis between color complexity and three measures that evaluated different aspects of vocal elaboration. In addition, we confirmed that finches exhibit a notably high vocal performance compared to other bird groups. The lack of correlation found in this study suggests that visual and acoustic signals may have evolved independently in Fringillidae, having different functions in communication and being under

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different pressures of sexual selection. This analysis adds to a growing list of studies that have found this lack of correlation in different groups of birds and evaluating various types of signals.

***Conflicting patterns of introgression: incompatibilities and gene flow in hybridizing honeyeaters with neo-sex chromosomes**

E Shogren, C Muirhead, E Martí, D Presgraves, J Uy*Presenting author: Elsie Shogren, elsie.shogren@gmail.com*

Hybridization can shed light on the genomic features which act as barriers to introgression. Regions of the genome which have experienced divergent selection or have limited recombination may be refractory to gene flow if sexual, ecological, or genetic incompatibilities reduce fitness of hybrid individuals. Conversely, regions which confer an adaptive advantage or have lower mutational loads may introgress freely or asymmetrically between species. Changes in genomic structure or transmission can also influence gene flow between taxa. For example, neo-sex chromosomes— former autosomes which have recently become sex-specific— may be particularly important as rapidly diverging regions of the genome could lead to the formation of reproductive barriers. The *Myzomela* honeyeaters of the Solomon Islands provide an unusual opportunity to identify genomic factors that limit or facilitate introgression following hybridization of two species which both carry neo-sex chromosomes and have recently come into secondary contact. Previous work shows limited gene flow on Z/neo-Z and strongly asymmetric introgression of W/neo-W and mitochondria. Building on these findings, we infer local ancestry across whole-genome sequence data for 132 birds sampled in sympatry. Using these fine scale patterns of introgression, we investigate how the interaction of admixture and natural selection shapes gene flow across regions of the genome which vary in divergence, recombination, and inheritance.

Patterns of genomic divergence in the Philippine swiftlet species complex

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The swiftlet species complex *Collocalia esculenta* has a wide geographic distribution from southeastern Asia through Indonesia and into the Pacific Ocean, with two recognized endemic species in the Philippines (*C. marginata* and *C. isonota*). These species have a long history of taxonomic instability due to their conserved phenotype and complex biogeographic pattern. Throughout the islands, the two species occur in either allopatry or sympatry with apparent elevational displacement and, due to the phenotypic similarities, these patterns are poorly understood. We will explore the genetic patterns of divergence within and between these two swiftlet species in the Philippines using reduced-representation genome-wide genetic data (RAD-seq). Samples analyzed were collected throughout the Philippines and include areas where the two species occur in sympatry. Our research uncovers genomic patterns of differentiation both among allopatric populations of each species and deeper differentiation between species. We also analyze gene flow between species and among populations, given the historical suggestion of intergradation between species where they occur in sympatry. Key findings illuminate genetic differentiation, evolutionary history, and elevation divergence between *C. marginata* and *C. isonota*.

****Body mass, colony size, and survival in Cliff Swallows**

A West, C Brown*Presenting author: Amy West, University of Tulsa, acw1471@utulsa.edu*

An optimal body mass can promote greater rates of survival in birds. However, body mass can fluctuate over the course of a year to reflect energetic requirements of different stages of the life cycle. Additionally, the optimal body mass may change from year to year depending on environmental conditions resulting in either fluctuating or stabilizing selection on body mass within a population. We examined the effects of body mass on survival in a colonially nesting bird, the Cliff Swallow (*Petrochelidon pyrrhonota*), over the course of 20 years to see 1) if there is an optimal body mass and how it may have changed over time and 2) if colony size and weather interacts with body mass to influence survival. Over the course of the 20

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years, we found that with the exception of a few years with atypical weather, Cliff Swallows of varying body mass had similar survival outcomes, unless their weight was extremely high or low. In general, body mass seemed to be under stabilizing selection. Birds in small colonies tended to have lower survival rates regardless of body mass. Years with a higher rainfall in June tended to result in lower survival with birds of intermediate masses doing better, suggesting that annual weather conditions can be a driver of variation in body mass of birds.

****Fluctuating selection maintains variation in colony size of Cliff Swallows
(*Petrochelidon pyrrhonota*)**

O Pletcher*Presenting author: Olivia Pletcher, oplech1211@gmail.com*

Avian breeding colonies provide benefits such as improved group foraging and avoidance of predators. However, in most species both the costs and benefits are known to vary with group size and has led to the question of why a single group size that maximizes fitness does not exist. It has been hypothesized that fixation does not occur because fitness of group sizes varies due to spatial and temporal differences in their shared selective pressures that favor certain group sizes one year and other sizes during other years. Addressing this requires determining whether fluctuating selection really occurs, which at present remains a controversial question in evolutionary ecology, and few studies have shown this convincingly. Coloniality is common in the Cliff Swallow (*Petrochelidon pyrrhonota*) where colony size is heritable, yet colony sizes vary greatly. Using fecundity as a proxy of fitness, I compared selection on colony size across 40 years for a population in western Nebraska. Changes in the direction of selection occurred in some years, in others there was no significant selection on colony size, and in still others stabilizing or disruptive selection around an intermediate colony size was apparent. Date also interacted with colony size to lead to fluctuations in selection on colony size within the same year. Our work supports the idea that fluctuations in the direction, form, and/or magnitude of selection allows the persistent variation of colony sizes in Cliff Swallows.

***Evolution of visual signals associated with aggressive displays in leaf warblers
(*Phylloscopus*)**

K Fialko*Presenting author: Kristina Fialko, fialko@uchicago.edu*

Aggressive interactions between conspecifics are commonly associated with stereotyped display movements, which serve to efficiently inform receivers of motivation. Consequently, once an effective aggressive display has evolved, it is unclear why it should be altered through subsequent speciation events. Here, we evaluate the evolution of an aggressive signal across 10 leaf warbler (*Phylloscopus*) species. Using high-speed videography and methods borrowed from geometric morphometrics, we quantify differences in wing motion. We find that the form of the display remains similar across species, which we attribute to an effective signal being maintained through multiple speciation events. Modifications arise through additions of discrete displays to the behavioral repertoire (two lineages) and the loss of display (one species). While part of this variation can be related to habitat, some differences may result from appearance of a feature that is simply more effective in eliciting responses. We conclude that display evolution proceeds largely in a modular fashion. The basic conventional signal is maintained across species, enabling modifications to appear without loss of efficacy.

***The genomic landscape of gene flow in wood-warblers (Parulidae)**

K Bennett, A Wood, M Baiz, L Phung, D Toews*Presenting author: Kevin Bennett, Pennsylvania State University, kevinfbennett@gmail.com*

Modern sequencing and analysis methods have sparked new insights into how species evolve and diversify. Gene flow, in particular, has been identified as a key process, both in the trajectory of individual species' evolution and in the radiation of entire families. We generated a whole-genome sequencing (WGS) dataset for 103 species in an avian radiation, the Parulidae warblers, to investigate the role of

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gene flow in the diversification and evolution of the group. First, we used ultra-conserved elements (UCEs) extracted from the WGS data to make a new phylogeny for the family. Next, we examined signatures of gene tree/species tree discordance and allele frequency measures of introgression across the genome to identify regions that have experienced the most gene flow. Finally, we focused on a gene, BCO2, known to have introgressed among warblers and traced the history of its spread between species and genera. With these data, we can begin to reveal the genomic landscape of gene flow in a group of birds where plumage differences evolved rapidly and reproductive isolating barriers are incomplete.

***Impacts of hybridization between cactus and ground finches (Geospiza) on Isla San Cristóbal, Galápagos Islands**

E Enbody, L Keller, S Lamichhaney, K Petren, C Rubin, C Sprehn, C Valle, R Grant, P Grant, L Andersson

Presenting author: **Erik Enbody**, erik.enbody@gmail.com

Hybridization has shaped evolutionary history by reinforcing species barriers and by diversifying phenotypes available to selection when hybrid fitness is high. Genetic and genomic data has implicated widespread historical hybridization across the radiation of finches in the Galápagos islands. Long-term population monitoring of ground-finches (Geospiza) on the small island of Daphne Major has demonstrated how introgressive hybridization has affected short-term outcomes of natural selection, but its impact on modern populations on larger islands is not well understood. Here, we use genomic data to examine an unusual population of cactus finches (Geospiza scandens) on San Cristóbal, one of the largest in the archipelago. Here, cactus finches have unusually small beaks, compared with cactus finches on other islands. We hypothesized that their small size is due to recent hybridization with small ground finches (Geospiza fuliginosa). To investigate this possibility, we used global admixture and local ancestry analysis. Our results support the hypothesis that hybridization has resulted in unidirectional introgression from the small ground finch to the cactus finch. We use a combination of local ancestry analysis and genome association data to identify genes involved in this phenotypic change. These results show that introgressive hybridization is not restricted to small islands like Daphne. We place these results in a broader context of species composition and island history by discussing how they may have contributed to patterns of hybridization across the Galápagos.

****Genomic basis of the avian 'saltmarsh syndrome' in coastal sparrow species**

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Tidal saltmarshes are an ecotone where terrestrial habitats transition to marine, presenting several unique challenges for animal species, including limited freshwater, variable salinity, and regular tidal flooding. Accordingly, few avian species are adapted to saltmarshes. Nevertheless, several North American sparrow species have adapted to saltmarshes and independently evolved a suite of similar phenotypes, known as the 'saltmarsh syndrome': larger bills, darker plumage, and the ability to ingest saline water. These species enable investigating the processes of parallel evolution to a harsh environment in an avian system. We used low-coverage whole-genome sequencing (~2X), and high-quality reference genomes, to determine the genetic basis of the saltmarsh syndrome across six saltmarsh-breeding sparrow species found in the eastern US, which span a gradient of adaptation. We used ANGSD to generate genotype likelihood data for millions of SNPs per species. Phenotype data for each trait of the saltmarsh syndrome (bill size, plumage melanism, and salt excretion) were collected for each sparrow ($n \hat{=} 1,100$) to use for genotype-phenotype associations via genome-wide association methods. We also collected environmental data at each capture location for genotype-environment associations. We then assessed whether the genes underlying saltmarsh adaptation were shared across species or were species-specific. This work (1) furthers our understanding of the genetic basis of avian phenotypes across several passerine species and (2) answers whether parallel evolution to saltmarshes is driven by independent genetic mechanisms across North American sparrows.

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Evolution of Hemisphere-Shifting Barn Swallows*V Gómez-Bahamón, Z Szpiech, F Gandoy, J Areta, D Toews**Presenting author: **Valentina Gómez-Bahamón**, vgbahamon@gmail.com

The Barn Swallow (*Hirundo rustica erythrogaster*) breeds in North America and overwinters in South America, involving a migratory journey of many thousands of kilometers. About 40 years ago, a population began breeding in the wintering grounds in Argentina. Remarkably, the newly established breeding population has evolved an inverse migratory pattern (and a significant reduction in migratory distance), breeding in Argentina during the austral summer and migrating to northern South America during the austral winter. Did behavioral divergence precede genetic divergence? Or, instead, did genetic mutations trigger these behavioral responses? Moreover, how is reproductive isolation brought about, given the regular presence of migratory individuals? We analyzed whole-genome resequencing data generated from birds captured in the breeding colonies in Argentina and from museum tissues of birds breeding in North America. We find substantial genetic differentiation scattered across the genome in the Argentinean population compared to eastern and western North American populations. This widespread pattern of differentiation across the genome suggests that demographic events are likely playing an important role in the evolution of the Argentinean population. We also find that the newly established population in Argentina has individuals with long runs of homozygosity resembling an inbred population, whereas the parental North American populations resemble the expectations of an admixed population. Although the Argentinean population of Barn Swallows is ecologically successful—it is now abundant and has expanded rapidly in geographic range—it might lack resilience to future environmental challenges due to its inbred genetic pool.

Genetics of spatial learning and memory in birds: insights from food-caching chickadees**G Semenov, A Rice, M McQuillan, J Spinelli, A Russell, N Martinez, A Van Huynh, M Robbins, H Kenyon, B Sonnenberg, C Branch, V Heinen, J Welklin, S Padula, A Patel, E Bridge, V Pravosudov, S Taylor**Presenting author: **Georgy Semenov**, University of Colorado, Boulder, georgesemenov7@gmail.com

While substantial progress has been made in dissecting the genetic architecture of phenotypes involved in a variety of evolutionary processes, behavioral genetics remains among the least understood. Our recent studies have uncovered genes associated with food-caching-related spatial cognitive abilities in Mountain chickadees and identified potential evolutionary mechanisms maintaining natural variation in associated phenotypes. Here, we expand upon these findings by examining parallelisms in genetics of spatial learning and memory in Mountain chickadees and in two other closely related species, Black-capped and Carolina chickadees. Black-capped and Carolina chickadees hybridize in a narrow but geographically extensive hybrid zone spanning nearly half of North America. Among several mechanisms of selection against hybrids, previous studies identified reduced spatial cognitive performance in hybrids compared to both parental species, most likely due to genetic incompatibilities affecting the development and function of central nervous system. We use a combination of behavioral experiments and whole-genome sequencing to uncover genes associated with spatial memory and learning in a set of 90 captive-raised individuals representing a spectrum of genetic ancestry. We discuss our findings in light of broader patterns of behavioral genetics in food-caching species and highlight future avenues of research to better understand the genetics of avian food caching behavior and cognition.

Sex-biased sampling has variable impacts on primary research questions about functional trait diversity and evolution*T Imfeld, B Wu, I Hemmes**Presenting author: **Tyler Imfeld**, Regis University, timfeld@regis.edu

Avian functional traits are widely studied in the fields of ecology and evolutionary biology, and these traits are often quantified from museum study skins. Across such studies, the sex ratio of sampled specimens is highly variable or often unreported, despite knowledge that many avian species are sexually dimorphic

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in size and shape and that museum collections themselves tend to be sex-biased toward males. Our study explicitly quantified whether sex-biased specimen sampling may influence the answers to primary research questions about avian functional trait diversity and evolution. We focused on the songbird clade Emberizoidea and used an existing phylogenetic tree for this clade and a large male-specific dataset for 10 functional traits. After inter-measurer calibration, we collected a matching female-specific dataset for 408 species to assess the degree of size and shape dimorphism across the clade based on these functional traits. We found that emberizoids are significantly dimorphic in both size and shape. We then quantified 3 metrics of functional trait diversity, and found that estimated functional diversity differs significantly between male, female, and pooled datasets for 2 of the metrics. We also modeled branch specific rates of functional trait evolution and found these inferences to be more nuanced. Rates of size evolution were strongly correlated when inferred with male, female, and pooled datasets, but rate shift configurations differed between datasets. We found the opposite for shape, where each dataset inferred identical rate shift configurations but these rates themselves were more weakly correlated. Thus, we found that sex-biased sampling can indeed influence the answers to primary research questions in ecology and evolutionary biology. Our findings suggest that these issues can be avoided by sampling sex ratios consistently across taxa in these studies, and we suggest that these ratios should be explicitly reported.

Artificial light at night as a source of selection of dim light vision among urban birds

M Mackinlay, C Francis*Presenting author: Clinton Francis, cdfrenci@calpoly.edu*

Variation among avian species in their responses to light pollution was recently linked to differences in dim light vision, but whether dim light vision is under selection from human-caused night lighting is unexplored. Here, we approximated dim light vision using eye geometries from museum specimens of six urban-adapted species collected across 100+ years and sought to determine whether proxies for light pollution were related to within-species variation in dim light vision. We hypothesized that exposure to light pollution could select for improved dim light vision because some species can exploit artificial light and night by extending their temporal activity. Alternatively, because of evidence for physiological dysregulation in response to light pollution, light pollution could select for worse dim light vision to protect the visual system from photostimulation at night. We found that dim light vision improved with proxies of light pollution for two species while another two species showed the opposite; however, two of these four species showed support for both hypotheses, suggesting that light pollution intensity and ecological context are relevant to the direction of selection. More broadly, our findings underscore that quantifying animal perceptual abilities will be key to understanding animal responses to an increasingly bright world.

The multigenerational impacts of gene flow

J Summers, F Romero, J Schmidt, D Seidman, E Cosgrove, R Bowman, J Fitzpatrick, N Chen*Presenting author: Nancy Chen, University of Rochester, nancy.chen@rochester.edu*

The movement of individuals (and the alleles they carry) among populations is an important source of evolutionary change. Gene flow can provide a source of novel genetic variation to populations or constrain local adaptation by homogenizing populations. In populations that experience inbreeding depression, gene flow can increase levels of genetic variation and average fitness. However, this response is neither guaranteed nor is it known how long any genetic or fitness changes would last. Our understanding of the importance of gene flow in governing allele frequency dynamics is limited by our inability to directly measure dispersal distances and the reproductive success of immigrants over time, except in a few special study systems. Here, we quantify the multigenerational impacts of gene flow using a 22-year genomic, phenotypic, and pedigree dataset in the Federally Threatened Florida Scrub-Jay (*Aphelocoma coerulescens*). A population of Florida Scrub-Jays at Archbold Biological Station has been studied since 1969, resulting in lifetime fitness measures for thousands of individuals on a 14-generation pedigree. We have identified all immigrant individuals into the study population since 1990, providing a

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unique opportunity to precisely measure the impact of immigration on levels of genetic variation and fitness over time. We performed whole genome sequencing for all individuals in our study population from 1999-2021 (~4000 jays). We test how levels of genetic diversity and fitness change in admixed lineages by comparing heterozygosity and individual fitness in different generations of immigrant descendants. This study provides a detailed look at the importance of immigrants to population genetic diversity over time. Our results have important implications for the potential success of genetic rescue or other assisted translocation strategies in conservation management.

Gene flow in avian endemics of the Philippines

M Lynn, K Winker, T Glenn*Presenting author: Morgan Lynn*, University of Alaska Museum of the North, mlynn47780@gmail.com

The Philippines possess a high degree of avian endemism. The archipelago hosts 258 endemic bird species, including numerous subspecies. Endemic Philippine birds are anticipated to have limited gene flow between island populations, contributing to their endemism. We used ultraconserved elements (UCEs), and Diffusion Approximation for Demographic Inference (DADI) to estimate gene flow between populations of 10 different species level taxa from 10 genera. We predicted that intraspecific gene flow between sister taxa will increase as distance between islands decreases. The Philippine archipelago is made up of multiple Pleistocene Aggregate Island Complexes (PAICs). We predict that gene flow levels will be higher within PAICs than between them. Our analyses reveal metrics on the divergence and speciation processes that are affected by island characteristics and degree of allopatry, and might also inform species delimitations in this region of cryptic diversity.

***Ecological Niche Conservatism in a Widespread Geographic Radiation: The Todiramphus Kingfishers**

F Machado-Stredel, J McCullough, C Eliason, S Hackett, M Andersen, C Myers*Presenting author: Fernando Machado-Stredel*, f.machado.stredel@gmail.com

Abiotic conditions play a key role in determining the geographic distribution of species, due to the limitations set by their fundamental niches (NF). Insular lineages represent challenging systems to estimate NF since they only experience the reduced set of conditions existing within islands. In this study, we explore the extent of ecological niche conservatism in Todiramphus kingfishers, one of the most specious radiations in the Indo-Pacific, while accounting for NF estimation uncertainty and incorporating estimates of historical dispersal. Using distributional data from museum specimens, literature records, and eBird occurrences for all described subspecies, as well as climatic layers of temperature and precipitation (10' spatial resolution, WorldClim), we estimated NF ranges and reconstructed ancestral states throughout the radiation using the R package nichevol. Our findings suggest widespread ecological niche conservatism among Todiramphus taxa, an expected pattern in short evolutionary time scales since allopatric speciation can occur across islands that exhibit analogous abiotic conditions. However, we detected niche shifts in which several lineages show expansions to drier and retractions from wetter environments in Eurasia and Australia (e.g., *T. chloris kalbaensis*, *T. sordidus pilbara*). Through these analyses, we contribute to the understanding of the climatic conditions that these lineages tolerate across geographic space while illuminating aspects of the differentiation and speciation processes of this geographic radiation.

Rapid plumage color evolution across a clade of island-dwelling kingfishers (Alcedinidae:Todiramphus)

J McCullough, C Eliason, S Hackett, M Andersen*Presenting author: Jenna McCullough*, University of New Mexico, mccullough.jenna@gmail.com

Phenotypic traits are related to and can affect diversification rates. Under pressure of sexual selection, avian plumage patterns can evolve rapidly. Recent work on phenotypic evolution across kingfishers has highlighted that the island-dwelling Todiramphus genus displays both immensely variable plumages and rapidly evolving brain shapes in regions related to cognition and vision. The ecological impacts of rapid

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change in these brain regions can be tied to within-species signaling and reproductive isolation, thus promoting speciation. Distributed from the Red Sea to French Polynesia, *Todiramphus* kingfishers have diversified rapidly into 28 species and 93 described taxa, boasting a high speciation rate that rivals other widely celebrated avian radiations. Here, we investigate fine scale patterns of the tempo and mode of color evolution across the genus with a detailed spectral reflectance dataset (>1,000 specimens and 51,000+ spectra). Using a new time calibrated phylogeny comprising all 93 *Todiramphus* taxa, we test whether rapidly diversifying clades also exhibit faster rates of plumage coloration and whether sexual dichromatism is stronger in island endemic taxa.

Allometric scaling of bones and feathers explains migration-associated variation in wing morphology in Song Sparrows (*Melospiza melodia*)

A Sivakumar, S Shakya, S EdwardsPresenting author: **Ashwin Sivakumar**, ahs.birder@gmail.com

The association of migration with wing lengthening and narrowing, as quantified by hand-wing index, is among the most robust relationships in avian ecomorphology. Despite this, the specific integumentary and osteological components of the wing that drive this relationship remain unknown. In this study, we investigate how differential variation in the components of the wing contributes to overall variation in wing morphology across the many phylogenetically independent migratory and sedentary populations of the Song Sparrow (*Melospiza melodia*). We integrate traditional hand measurement with micro-CT scanning, including a novel method for extracting feather lengths from these scans, to analyze ~300 museum study skins and skeletal specimens and characterize hand-wing index, primary and secondary feather lengths, and the morphology of the carpometacarpus and phalanges. We find that the dramatic intraspecific variation in the hand-wing index across the range of the species associated with migratory behavior is disproportionately driven by variation in outer primary feather lengths, while relative bone lengths are relatively conserved. Furthermore, despite average differences, the distribution of hand-wing indices overlaps heavily between all migratory and sedentary populations. These results indicate that the rapid evolution of wing morphology on short timescales is driven by allometric scaling across the components of the wing as well as extensive standing variation in wing morphology, potentially explaining the high evolvability of migration despite the scope of morphological sophistication involved in migration.

The "Inferred Attractiveness" hypothesis and its prospects for providing a new perspective on sexual selection

E DuVal, C Fitzpatrick, E Hobson, M ServedioPresenting author: **Emily DuVal**, Florida State University, ehduval@gmail.com

Sexual selection by mate choice is a powerful evolutionary force, and models of why females choose particular mates are central to understanding its effects. Predominant mate choice theories assume preferences are genetically determined, an assumption still lacking widespread support. Moreover, preferences often vary among individuals or populations, fail to correspond with conspicuous traits, or change with context, patterns not predicted by dominant models. Here, we propose a new model that explains this mate choice complexity, 'Inferred Attractiveness.' In this model, females acquire mating preferences by observing others' choices and use context-dependent information to infer which traits are attractive. They learn to prefer features that most distinguish the chosen male from other available males. We developed a phenogenotypic model to explore the effects over generations, and found this produces repeated population-level switches in preference and maintains male trait variation. When viability selection is strong, Inferred Attractiveness produces population-wide adaptive preferences superficially resembling 'good genes.' However, it results in widespread preference variation or nonadaptive preferences under other predictable circumstances. This talk first explains this new perspective on sexual selection, highlights study systems that might allow further tests of the Inferred Attractiveness hypotheses, and explores the prospects for this idea to explain long-term patterns of variable opportunity for selection over time in an empirical system, the lance-tailed manakin (*Chiroxiphia lanceolata*).

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Urban-Related Introgression and Parallel Evolution in Two Closely Related Desert Songbirds*D Jackson, S Taylor, K McGraw**Presenting author: **Danny Jackson**, University of Arizona, dannyjackson@arizona.edu

Urbanization has reshaped ecosystems globally and has created new selective regimes to which wild animals must adapt if they are to persist in the new urban ecosystem. Urban selection on genes involved in behavior, cognition, and immune function has been demonstrated in several avian species, but urbanization also presents a variety of additional novel challenges (e.g. artificial light at night, noise pollution, novel resource distributions, etc.) that may differently shape gene flow and architecture. Studies of closely-related, sympatric species may shed new light on how organisms experience genetic change in urban settings. We analyzed whole genome sequences of northern cardinals (*Cardinalis cardinalis*) and pyrrhuloxia (*C. sinuatus*) from urban and rural areas of Arizona, USA to test for the presence of urban-related parallel evolution and introgression. We identified 9 genes that appear to have undergone urban selection. 2 of the genes experienced parallel selection in both species, and 4 show evidence of introgression from urban northern cardinals into urban pyrrhuloxia. Our findings emphasize the role of introgression in evolutionary responses to rapid environmental change, and identify light at night, energetic challenges, and pollution as driving stressors for urban adaptation.

****Comparative phylogeography of the Solomon Islands, a model archipelago****E Gyllenhaal, L DeCicco, D DeRaad, L Klicka, R Moyle, M Andersen**Presenting author: **Ethan Gyllenhaal**, University of New Mexico, ethanofthegulls@gmail.com

The Solomon Islands have served as a model for allopatric speciation since the Modern Synthesis. Their intermediate distance from continents and complex geography lend them to testing both how populations diverge in allopatry and how they can achieve secondary sympatry, often better matching continental systems than island adaptive radiations. The Solomons have an arrangement of islands that allow one to test both how connectivity during times of low sea levels and long-term isolation have shaped the patterns of genetic diversity and community assembly across the archipelago. One island, Makira, is both the furthest from the primary source of colonization and the most isolated from long-term inter-island gene flow. This leads to two contrasting predictions for inferred phylogenies, one where Makira is nested within other island populations, and another where it is sister to the rest due to gene flow pulling those taxa together. To evaluate these two hypotheses, we conducted a comparative phylogeographic study with reduced-representation genomic data of a dozen taxa spanning a range of ecological niches and patterns of geographic variation (i.e., from a single subspecies to multiple species-level taxa). Genetic diversity was often similar across islands within a species, matching a model where post-colonization gene flow mitigates founder effects. We also found a wide range of population structure regimes, including both nearly panmictic and well-diverged taxa, including some not generally recognized as 'great speciators'. In most cases where there was strong phylogenetic structure among islands, Makira was sister to all other taxa. The consistency of this finding suggests that inferring biogeographic history from phylogenetic patterns alone in this and similar geographic contexts is fraught.

Whole genome sequencing reveals limited population structure across the King Rail range**C Gause, P Bolton, E Elizondo, D Brewer, J Schmit, C Balakrishnan, S McRae**Presenting author: **Susan McRae**, East Carolina University, mcraes@ecu.edu

King Rail *Rallus elegans* populations have been in decline due to range-wide loss of freshwater marsh habitat. Most remaining populations spend at least part of their lives in coastal marshes of the southeastern U.S., where they encounter additional threats of sea level rise, marsh salination, and more frequent and severe storms due to climate change. Populations that breed inland and migrate toward the Gulf coast have possibly declined the most. Localized resident populations in the southeast are sparsely distributed in pockets of suitable habitat principally on refuge lands. However, it is unclear whether contact occurs along the Central or Atlantic migration routes. It is essential to assess the extent of movement and

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admixture among populations to develop appropriate management plans for this threatened species. Here, we present a first attempt to assess genetic structure using samples collected from migrant and resident populations across the King Rail range. Breeding adults were captured and sampled at sites in Ohio, Arkansas, and North and South Carolina. Whole genomes were generated for 10-23 individuals per population using the Illumina NovaSeq platform and a minimum 10X read depth. Sequences were aligned to a high-quality Clapper Rail *Rallus crepitans* reference genome. Our analyses revealed substantial gene flow among populations and only weak support for geographic population structure. Though surprising given the distances between sites and residency status of individuals, recent studies suggest that King Rails are capable of long-distance movements.

Evidence for recent inbreeding and historical bottlenecks in multiple threatened California Savannah Sparrow subspecies

E Kirsch, A Shultz, S Edmands, P Benham, C Cicero Studley, J Walsh, R Bowie

Presenting author: **Eliza Kirsch**, ekirsch@oxy.edu

Three of the five Savannah Sparrow (*Passerculus sandwichensis*) subspecies that live in California are considered to be of conservation concern. These three subspecies (*P. s. beldingi*, *P.s. rostratus* and *P.s. alaudinus*), along with *P. s. brooksi*, live in coastal saltmarshes, habitat that has suffered declines of up to 90% due to urbanization. We aim to investigate whether habitat loss and fragmentation has led to inbreeding depression in these subspecies, knowledge of which can help inform conservation management strategies. Runs of homozygosity (ROH) provide precise estimates of individual-level inbreeding, which causes a loss of genetic diversity and potentially threatens a population's long term viability. Historical bottlenecks and long-term small population size or recent inbreeding can create short or long ROH, respectively, in the genome. To investigate this question, we analyzed 150 whole genome sequences from all Savannah Sparrow populations created as part of the California Conservation Genomics Project. We show that *P.s. beldingi*, which represents a small population found in Southern California, has the longest tracts of ROH, indicative of recent inbreeding. However, Northern Californian subspecies have intermediate levels of ROH, indicative of historic bottlenecks, and the Eastern California subspecies, which has not experienced nearly as much habitat loss, has the least amount of ROH. To further investigate variation in inbreeding across subspecies, we will assess the genetic load to ascertain if genetic purging has mitigated the effects of inbreeding, or if an accumulation of deleterious mutations poses an additional threat to their survival.

***Genetic differentiation across biogeographic barriers in peninsular India - Comparing a physical barrier to a climatic barrier**

N Goyal, V KL, V Kher, V Joshi, A Warudkar, A Sharma, M Natesh, V CK, R VV

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Biogeographic barriers play an important role in structuring communities and populations within a region. Several potential barriers have been identified across peninsular India. However, much of our understanding of impacts of barriers on gene flow and genetic differentiation in birds is limited to the Palghat Gap; a major physical barrier in the southern Western Ghats with similar climatic regimes north and south of it. Goa Gap, on the other hand, is a major climatic transition zone with high climate variability in the north and relatively stable climate in the south. Many bird subspecies are known to replace each other over this. Here, we test and compare the Goa Gap (a climatic barrier) to the Palghat Gap (a physical barrier) for 5 species of birds that are common across these two barriers in the Western Ghats. We hypothesize that the Palghat Gap would be a stronger barrier to gene flow than the Goa Gap as it would strongly limit dispersal. We expect to find lower genetic differentiation across the Goa gap when compared to the Palghat gap. We collected blood samples of 97 individuals from 5 species of birds across the 2 barriers. We generated genomic datasets using ddRAD Next Generation Sequencing, and investigated the genetic differentiation and population structure across these 2 barriers. We find that populations across the Goa gap show high admixture and low genetic differentiation when compared to the populations across the Palghat gap. However, our results also indicate that the level of genetic differentiation varies between species, potentially owing to their ecological differences. Our study

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highlights the importance of type of a barrier in promoting genetic differentiation.

Variation in European Goldfinches (*Carduelis carduelis*) in their Native Range**L Bodt, J Bates, S Hackett**

Presenting author: Louise Bodt, Field Museum of Natural History / University of Chicago, lbodt@fieldmuseum.org

Species introductions are unintentional and repeated experiments that present an opportunity to investigate evolutionary change within species. Such instances of repeated experiments generate data about adaptation and plasticity in response to novel environments and climate change. Native through Europe and into western Asia, European goldfinches (*Carduelis carduelis*) are introduced to several countries around the world, including Bermuda, Australia, and New Zealand. I assess the population structure and demography of the European goldfinch across its native distribution with data on genetic structure and phenotypic variation. I test whether in the native range, genomic structure exhibits similar patterns to phenotypic differentiation, with a primary focus on a major split into the *caniceps*/*carduelis* groups. I present analyses of phenotypic measurements (bill dimensions, wing chord, tail length, and tarsus length) from approximately 700 study skins at the Field Museum of Natural History and the American Museum of Natural History. I also present on genome resequencing of 50 individuals from throughout the native range. This project leverages widespread and historical specimens to characterize the genomic and phenotypic diversity of goldfinches. These native range data also contribute a necessary comparative baseline for how introduced populations adapt to new environments through time adding to the body of literature on what we can learn from these unintended experiments.

****Genetic structure of Atlantic Puffins (*Fratercula arctica*) breeding in Atlantic Canada****Q Carvey, S Pavey, A Diamond, G Davoren, R Lavoie, M Legard, G Robertson, E Runnells, C Petalas, H Major**

Presenting author: Quinn Carvey, University of New Brunswick, quinn.carvey@unb.ca

The Atlantic Puffin (*Fratercula arctica*; hereafter 'puffin') breeds at the southern limit of its range in the Gulf of Maine (GOM), where waters are warming faster than most of the world's oceans. Puffin productivity and survival have decreased in the GOM with warming, but population-level declines have not been detected. Understanding the connectivity between GOM breeding colonies and colonies to the north has become a priority to determine the demographic importance of immigration, but mark-recapture and tracking studies have yet to resolve this question. In this study, we used ddRADseq to quantify neutral genetic differentiation among five breeding colonies in Atlantic Canada, identify outlier SNPs, and determine if puffins can be reliably assigned to their breeding colony. We identified a new genetic cluster of puffins, represented by Machias Seal Island (MSI), and recommend that this colony be considered separately from Newfoundland and Québec for management. We found three outlier SNPs, with the rare alleles predominantly present in MSI puffins, and recommend further research to determine the extent that selection may be contributing to the differentiation of MSI. Puffins could be reliably assigned to the MSI or the northern-colony genetic cluster, including with a subset of the 200 highest-F_{st} SNPs. Finally, we did not identify evidence of inbreeding at any colony, suggesting that effective population sizes are large enough to buffer against these negative effects.

Mutations in ASIP associated with plumage divergence in Northern Jacana (*Jacana spinosa*) and Wattled Jacana (*Jacana jacana*)*I Gates, S Lipshutz**

Presenting author: Isabella Gates, isabella.gates@northwestern.edu

Phenotypic traits such as differences in coloration can help species avoid hybridizing and can promote reproductive isolation. Two jacana species, Northern Jacana (*Jacana spinosa*) and Wattled Jacana (*Jacana jacana*), hybridize in western Panama. Outside of the hybrid zone, in Central and South America,

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both jacana species have brown plumage. In Panama, however, the Wattled Jacana has black plumage. Differences in feather coloration may contribute to reproductive isolation between these two species. We used PCR to investigate nucleotide differences in the gene ASIP, a well-known candidate in the melanogenesis pathway regulating feather coloration. We hypothesized that there would be genetic divergence between *J. jacana* and *J. spinosa*, and that hybrids would be more genotypically similar to *J. spinosa*. We found six SNPs in ASIP between the two species. Three SNPs were plumage-specific, whereas the other three were species-specific. Additionally, hybrid genotypes were most similar to *J. spinosa* genotypes. Connecting genotype to phenotype can help us understand the mechanisms that influence divergence and reproductive isolation in the speciation process.

***Unraveling the Demography of Bird Extinction in the Most threatened Neotropical Area**

F Bocalini, L Silveira

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The Pernambuco Center of Endemism (PCE) in northeastern Brazil represents the most threatened area within the Atlantic Forest biodiversity hotspot. Extensive deforestation and habitat fragmentation have led to alarming species losses, placing numerous bird species on the brink of extinction. The role of historical demography in rendering populations particularly vulnerable to extinction remains unexplored in Atlantic Forest birds. Genomic sequencing of historical specimens from biological collections has enabled the use of genetic data from taxa presently endangered or extinct. Here we used SNP data from 12 PCE endemic populations to: i) analyze population size variation over time, distinguishing between the impacts of late Pleistocene/Holocene climate change and postcolonial anthropogenic actions on PCE bird population decline, and ii) compare current and historical data to assess the extent of genetic diversity loss over the past century. Our analysis, using Stairway plot, revealed a significant decline in effective population size across 10 of the 12 sampled populations, predating the colonial era. Notable declines coincided with the Last Glacial Maximum (~21 Ka) and the Holocene (~11 Ka), with synchronized decreases observed between 8 and 4 Ka and between 2 and 1 Ka. Post-colonial anthropogenic activities, such as deforestation, fragmentation, and poaching, have further exacerbated this scenario, amplifying a trend that was already underway. Comparisons of genetic diversity indices between present-day and 70-year-old populations showed a tendency towards reducing genetic diversity and effective population size. This highlights the necessity for conservation efforts to prevent the extinction of numerous other species.

Life in the cold: Adaptation to the Arctic in Alaska galliforms

S Sonsthagen, R Wilson, R Harrigan, R Cornman, S Talbot

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Alaska resident species are specialized for life in the cool summer and extremely cold winter environments characteristic of the Arctic. The ability of these species to thrive in Arctic landscapes likely requires novel adaptations at genes underlying response to environmental signaling. Given their year-round occupancy and specialization to sub-Arctic and Arctic ecosystems, resident species may be more (or differentially) impacted by the challenges faced with environmental change than are migratory species. We assayed three species of ptarmigan and spruce grouse along a latitudinal gradient (60–70°N) from temperate to sub-arctic to Arctic Alaska at genes identified in other species to be adaptive to the Arctic and double digest restriction-site associated DNA (ddRAD). Our goal was to identify gene variants that may have arisen as a result of adaptation to the Arctic as well and to determine the strength of environmental selection and the ability of Arctic populations of gallinaceous birds to respond to a changing Arctic conditions. Patterns of neutral and functional genomic structure coincide with physiographic features (e.g., mountain ranges) and highlight the importance of physical and ecological barriers in shaping how genomic diversity is arrayed across the landscape. However, there was a general lack of concordance in spatial patterns across species indicating that species behavior and habitat affinities play key roles in driving the contrasting patterns of genomic structure. As such, using a

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multi-species approach provides a much-needed perspective on the ability of these species to respond to changing environmental conditions, and ultimately persistence and health.

Using telomere length to better understand local adaptation in a wild songbird*M Rodriguez, C Bossu, K Ruegg***Presenting author: Marina Rodriguez, Colorado State University, mdrodriguez10@gmail.com*

To fully understand local adaptation, it is essential to identify potentially adaptive genetic variants, determine their environment specificity, and ascertain the type of genes involved. Although numerous studies have conducted genome scans and have identified candidate loci with high levels of environmental variation, few studies have associated natural fitness variation in a species to genetic variation. Outside of reciprocal transplant studies, demonstrating that certain alleles are beneficial to fitness in certain environments can be a daunting undertaking, and as a result, linking all three parts of the genotype-phenotype-fitness continuum continues to be a challenge. A biomarker that captures individual fitness is telomere length. The correlation between telomere length and survival across species has made telomere length an ideal fitness proxy across numerous studies. Using telomere length as a fitness proxy in studies of local adaptation is a novel approach that could allow researchers to determine the fitness relevance of putatively adaptive loci in species for which this was once unfeasible. In this study, we use a genome-wide association study to identify adaptive variants associated with fitness (i.e. telomere length) and to test the hypothesis that genes associated with bill morphology are mediating local adaptation in the yellow warbler. We also test whether alleles associated with telomere length are associated with certain climate conditions, which is expected if climate variation has strongly contributed to adaptation. Results of this study can provide insight into potential for phenotypic evolution and can improve understanding of the potential for adaptation to environmental change. In addition, this study highlights the use of telomere length in studies of local adaptation.

Whole genome phylogeography of the Wrentit (*Chamaea fasciata*)*M Tofflemire, P Benham, C Cicero Studley, M Davila, L Smith, M Nachman, R Bowie, K Burns***Presenting author: Michael Tofflemire, San Diego State University, mtofflemire@gmail.com*

The Wrentit (*Chamaea fasciata*) is an endemic songbird of the California Floristic Province, a global biodiversity hotspot. The species varies morphologically across climatically distinct ecoregions, with five subspecies described. We used whole genome data of 159 Wrentit individuals to assess fine-scale landscape genomic patterns and test the hypothesis that phenotypic differentiation correlates closely with underlying genomic structure and local adaptation. Overall, our results did not identify a strong correlation with previously described subspecies boundaries; however, we identified two major clades spatially oriented in a north-south division across the California Floristic Province and with limited geographic overlap in the San Francisco Bay region. This division has also been recovered in other co-distributed vertebrate species. We found evidence of introgression from the northern clade into the southern clade occurring primarily along the central California coast. Nucleotide diversity is highest among individuals of the southern clade, but considerably lower for northern populations. Landscape connectivity and gene flow between clades generally occurs along the California coast rather than between the Sierra Nevada and southern California mountain ranges. During our genome-wide analysis, we discovered a structural variant in the form of a chromosomal inversion based on a more inclusive SNP dataset. We found considerably higher nucleotide diversity and linkage disequilibrium occurring at the location of the putative inversion, as well as significant F_{st} values over this same region between heterokaryotypes and homokaryotypes, indicating the importance of structural variants in shaping genome-wide patterns in the Wrentit.

****Characterizing a female-specific growth gene and its relationship to reverse sexual size dimorphism****S Rasband**

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Birds are often sexually dimorphic in size, with larger males being the most common, followed by equally-sized sexes. Rarest of all are species with larger females. While multiple selective forces have been proposed to maintain larger female body size in these clades, the molecular mechanisms allowing larger female growth remain completely uncharacterized. The growth hormone receptor (GHR) is a Z-linked gene with a male-biased expression, and is a known factor in sex-specific development. In addition to the Z-linked GHR found in all birds, I identified a female-specific W-linked GHR gene (GHR-W) and characterize its limited presence across the avian phylogeny by searching hundreds of avian genomes. Using tree-building and parsimony-based methods, I found that GHR-W was ancestral in all birds, but has fallen victim to W-chromosome degradation, leading to deletion or pseudogenization in most birds. In some avian lineages, though, GHR-W is retained, such as in Accipitriformes (hawks, eagles, vultures, etc.) and Strigiformes (barn owls, true owls). Many of these lineages display a marked reverse sexual dimorphism in size, making the female-limited GHR-W an intriguing potential contributor to exceptional female growth. Despite advanced W-chromosome degradation, GHR-W retains an intact gene structure in these birds and is expressed in RNA-seq data from Accipitriformes. Using molecular evolutionary tests and protein modeling, I examine two hypotheses linking GHR-W to reverse sexual dimorphism: 1) if GHR-W could increase the overall GHR gene dosage, compensating for the otherwise haploid GHR-Z and 2) if mutations to the GHR-W coding sequence could enhance GH binding affinity, and therefore the GH growth signal in female birds.

Genetic and Vocal Diversity in Barred Owls and Spotted Owls

N Panora*Presenting author:* **Nathali Panora**, npanora20@gmail.com

The case of the Barred Owl (*Strix Varia*) and Spotted Owl (*Strix Occidentalis*) is a noteworthy example of the impact an invasive species can have on native species. The Barred Owl is a part of the Strigidae family and their most notable features are their vertical brown streaks that run down their chest. Historically, Barred Owls inhabited the woodlands of the eastern United States. However due to deforestation and urbanization they began to expand westward, right into the Spotted Owl's habitat. The Spotted Owl is also a part of the Strigidae family, compared to the Barred Owl, the Spotted Owl is smaller. Its most notable features are its white oval spots on its chest and the white X shape between its eyes. They reside in the old-growth forests of the western side of the United States. Due to their overlapping ecological niches, direct competition between the Barred and Spotted Owl caused for the already endangered Spotted Owl population to decline immensely. Barred Owl calls have the most notable call that is known as 'who cooks for you', which is an 8-9 note hoot. This specific call is used to claim territory and attract mates. Spotted Owls also have a very important call that allows them to communicate and find mates along with territory marking, the four-note call. It has been found that the presence of Barred Owls has impacted the calling behavior of Spotted Owls (Crozier et al, 2006). A study done in 2006 experimented with Spotted Owl call backs in California and Washington. Spotted Owls responded less frequently to Spotted Owl calls after hearing Barred Owl calls in the area. This becomes an issue because Spotted Owls are less likely to find mates if Barred Owls are around. This in turn hurts their population and forces them to expand even more into the west to areas they do not normally inhabit. Barred Owl's expansion also led to hybridization, the hybrid's genetics has yet to be fully researched however their mating behavior has led to significant detail.

Genome-wide patterns of divergence and introgression in three groups of Indian Ocean Muscicapid species

H Lim, S Shakya, F Sheldon*Presenting author:* **Haw Chuan Lim**, George Mason University, hlim22@gmu.edu

Patterns of genome-wide divergence and introgression shed light on the genomic architecture and functional bases of evolutionary processes such as speciation and adaptive introgression. Using whole genome sequence data, we investigate genetic interactions between lineages that come into secondary contact. We study secondary contact in three groups of Muscicapid species, which are found in Borneo

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(*C. saularis* and *C. malabaricus*-*C. stricklandii*) and Madagascar (*C. albospectularis*). Lineages of each group have different divergence times and are characterized by melanin-based plumage colors differences. We estimated demographic history and population structure of each group, and conducted genomic-window based analyses. The three groups show distinct differences in genomic patterns of divergence and introgression, which suggest underlying differences in the strength of pre- and post-mating reproductive isolation.

Gene flow and divergence in Beringian birds

C Oliver Brown, T Glenn, B Faircloth, K Winker

Presenting author: **Caitlyn Oliver Brown**, caitlyn.brown@gmail.com

Historically, allopatry was thought to be the primary driver of speciation between populations. However, speciation with gene flow has been identified in an increasing number of cases, especially in birds. Perhaps nowhere is this more apparent than in Beringia, a region at the top of the North Pacific Ocean that has a history of dramatic landscape alteration through glacial cycles. These cycles repeatedly split and connected the Eurasian and North American continents through the Pleistocene, separating and reconnecting avian populations. We examined gene flow between avian sister taxa from multiple orders in Beringia. Prior work suggests that speciation with gene flow is the predominant mode of avian speciation in Beringia. We add to this literature by identifying gene flow and divergence in 10 Beringian lineages among five orders (Anseriformes, Gaviiformes, Charadriiformes, Piciformes, and Passeriformes) using population-, subspecies-, and species-level pairwise comparisons. We sequenced an average of 3650 ultraconserved elements (UCEs) from these taxa and tested for models of divergence using diffusion analysis for demographic inference (dadi). All the best-fit models of divergence included gene flow, providing further evidence of the importance of speciation with gene flow in Beringian birds.

**Whole genome sequences corroborate deep split and cryptic variation in Steller's Jays (*Cyanocitta stelleri*)

M Laubstein, C Cicero Studley, P Benham, L Smith, M Davila, E Enbody, R Bowie

Presenting author: **Max Laubstein**, maxlaubstein@gmail.com

The global range of the Steller's Jay (*Cyanocitta stelleri*) stretches from southern Alaska through western North America to northern Nicaragua. Across its wide distribution, this species exhibits considerable morphological diversity and occupies a variety of forest and woodland habitat types. Combined, these factors make the Steller's Jay an exemplary system for analyzing the genomics underlying ecological and morphological divergence, and the role of landscapes in driving biotic diversification. A prior study of 1,080 individuals using mtDNA and microsatellites revealed deep divergence and cryptic genetic variation among populations from the Pacific Ocean to the Rocky Mountains. Genetic variation was largely congruent with three morphotypes (Coastal, Interior, Rocky Mountains) and models of ecological niche diversification. Here, we expand on that work by sequencing whole genomes for 310 individuals representing the same populations and morphotypes, with particularly dense sampling at the contact zone between the Interior and Rocky Mountain morphotypes in the Utah-Wyoming-Idaho border region. Whole genome sequences corroborate the deep split and narrow contact zone between Interior and Rocky Mountain morphotypes, as well as divergence of Middle American Steller's Jays. Further, whole genomes and microsatellites reveal cryptic genomic variation in central coastal California that provides evidence for past isolation. Using this genomic dataset, we characterize current and historical states of introgression and hybridization across the contact zone and present candidate genomic regions underlying plumage, morphological, and ecological variation.

*Population genomics and adaptive potential of kittiwakes (genus *Rissa*), northern seabirds vulnerable to climate change

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Anthropogenic climate change is disproportionately affecting polar regions. Determining the potential of

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northern species to adapt to projected future climate conditions is therefore of critical importance. We are assessing the adaptive potential of a representative northern seabird genus: kittiwakes, small gulls that nest colonially along rocky coastlines. The two recognized species, the wide-ranging black-legged kittiwake (*Rissa tridactyla*) found in both Pacific and Atlantic basins, and the range-restricted red-legged kittiwake (*R. brevirostris*), which nests predominantly in the Aleutians and Pribilof Islands, are both listed as Vulnerable by the IUCN primarily because of projected climate change impacts. To assess kittiwake population genomics and prospects for persistence in a warming world, we generated 280 low coverage whole genome sequences covering all major breeding regions of both species. We processed the sequences using a standard pipeline, and are currently calculating genomic offsets, the distance between current genetic/environment relationships and future relationships based on climate-linked loci. Our results confirm previous population genetic findings: little structure within *R. brevirostris* or either *R. tridactyla* subspecies (Atlantic *tridactyla* and Pacific *pollicaris* respectively) but strong genetic differentiation between these subspecies. We did not observe any admixed individuals, even though our data set included a colony (Novaya Zemlya) with bidirectional migrants where some individuals winter in the Atlantic and others in the Pacific. Genomic vulnerability analyses are in progress; we will present which colonies are most at risk given contemporary allelic frequencies and future predicted climate conditions.

***Geo-genomic predictors of phylogeographic and introgression history in an Amazonian bird**

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Selection, drift, recombination, and gene flow interact to produce a genomic landscape of divergence wherein patterns of differentiation and genealogy vary nonrandomly across the genomes of diverging populations. For instance, genealogical patterns that arise due to gene flow should be more likely to occur on smaller chromosomes, which experience high recombination, whereas those tracking histories of geographic isolation (reduced gene flow caused by a barrier) and divergence should be more likely to occur on larger and sex chromosomes. In Amazonia, populations of many bird species diverge and introgress across rivers, resulting in reticulated genomic signals. Herein, we used reduced representation genomic data to disentangle the evolutionary history of four populations of an Amazonian antbird, *Thamnophilus aethiops*, whose biogeographic history was associated with the dynamic evolution of the Madeira River Basin. Specifically, we evaluate whether a large river capture event ca. 200 Ka, gave rise to reticulated genealogies in the genome by making spatially explicit predictions about isolation and gene flow based on knowledge about genomic processes. We modeled levels of divergence, introgression, and genealogical patterns as functions of chromosome length and used this information to reconstruct the complex biogeographic history of this species. Our results suggest that a significant portion of genomic heterogeneity arises due to extrinsic biogeographic processes such as river capture interacting with intrinsic processes associated with genome architecture. Future phylogeographic studies would benefit from accounting for genomic processes, as different parts of the genome reveal contrasting, albeit complementary histories, all of which are relevant for disentangling the intricate geogenomic mechanisms of biotic diversification.

***Comparative karyotypic differences between macrochromosomes and microchromosomes in three genera of parrots (*Ara*, *Pyrrhura*, and *Cacatua*)**

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Chromosomal rearrangements are pivotal in shaping genome architecture and evolutionary trajectories. In birds, these rearrangements have garnered interest due to their potential implications for speciation, adaptation, and phenotypic diversity. Additionally, bird chromosomes are categorized based on size, repeat content, GC content, and recombination rates, into macrochromosomes and microchromosomes. Through the analysis of chromosome-level assemblies generated from Nanopore long reads and Hi-C

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data across three genera of parrots-Ara macaws, Pyrrhura parakeets, and Cacatua cockatoos-we examine the role of the categorization of avian chromosomes into macrochromosomes and microchromosomes and how the accumulation of rearrangements impacts genetic diversity and speciation. Our findings suggest that variation in diploid number among closely related taxonomic groups is primarily driven by fission and fusion in the microchromosomes, whereas post-zygotic barriers to reproductive isolation are potentially primarily associated with the degree of rearrangements in the macrochromosomes. Elucidating patterns and processes of chromosomal rearrangements across avian genomes holds promise for enhancing our understanding of avian evolution, biodiversity, and conservation.

Comparative and population genomics reveals shared patterns of selection associated with convergent phenotypes in birds

T Sackton*Presenting author: Tim Sackton, Harvard University, tsackton@g.harvard.edu*

Convergent evolution, where a similar trait evolves independently in unrelated lineages, provides a powerful natural experiment to study adaptation and evolution by comparing signatures of rapid evolution across diverse lineages that share a convergent trait. Birds have emerged as an excellent system in which to study convergent evolution, given the wealth of phenotypic information available and the rapidly growing genomic resources available. Here, I contrast signatures of positive selection in the genomes of species with two different convergent phenotypes: nectar-taking species (hummingbirds, sunbirds, parrots, and honeyeaters), and species with reduced relative tarsus length (penguins, swallows, kingfishers, and bulbuls). In each case, we can identify signatures of selection in both genes and putative regulatory regions of the genome by comparing genomes across species with and without the convergent phenotype. Among nectar-taking birds, we see evidence for widespread positive selection in both genes and regulatory elements associated with heart function, carbohydrate and lipid metabolism, glycolysis, and blood pressure regulation, and identify a key regulatory transcription factor, MLXIPL, that shows evidence for positive selection in all nectar-taking lineages. Among species with reduced relative tarsus length, we see little evidence for convergent signals of positive selection among protein coding genes, but uncover strong convergent signals of selective shifts associated with putative regulatory elements near key developmental genes involved in hindlimb and skeletal system development. Overall, these results point towards a better understanding of the targets of selection associated with evolution of diverse phenotypes in birds.

***Evolution and functional characterization of olfactory receptors in birds**

R Driver, P Meesa, R Li, N Mantha, M Brewer, M Marie, H Matsunami, C Balakrishnan*Presenting author: Robert Driver, driverr16@students.ecu.edu*

Vertebrates detect odor molecules with olfactory receptors (ORs), a gene family expressed in the olfactory epithelium. Among species, OR diversity is associated with reliance on smell, with some mammals exceeding 2,000 OR genes. Birds are the most speciose class of terrestrial vertebrates, inhabiting nearly all land environments and with diverse social structures and foraging strategies, yet were long thought to make limited use of olfactory signals. Recent behavioral work in birds has shown important roles for olfaction in foraging and species recognition, among other behaviors. Contributing to this surge of interest in avian olfaction, our recent work has shown that birds have hundreds more OR genes in their genomes than previously realized. We have examined the genomic OR repertoire of over 150 high quality long-read bird genomes spanning the avian phylogeny, revealing between 7 and 3,800 intact ORs in all species surveyed. To discern the functional roles of ORs, we found that the ORs are expressed in the bird olfactory epithelium of four species and that bird ORs specifically localize to the olfactory sensory neurons of the posterior turbinate within the chicken maxilla. To confirm the ability of bird ORs to detect odors, we expressed chicken ORs in mammalian cell culture, bombarded ORs with multiple odors, and measured OR activation in response to each odor. We found that chicken ORs respond to several types of pyrazines, a group of chemicals that are found in the scent of green peppers. Additionally, we show that ORs orthologous between mammals and birds bind the same odors, illustrating

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a conservation of OR binding properties through 320 million years of vertebrate evolution. Together, these results show that bird ORs are diverse, evolve dynamically, are expressed in olfactory sensory neurons, and are capable of functionally detecting odors. This work provides the foundation for future functional characterization of bird ORs across a variety of bird species.

Complex genomic patterns underlie subspecific differentiation in the House Wren (*Troglodytes aedon*)

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The House Wren is a morphologically cryptic species that exists across the majority of North and South America. The only two migratory subspecies, *Troglodytes aedon aedon* (eastern) and *T. a. parkmanii* (western), occur in the United States and Canada during the breeding season. We have identified a previously undocumented hybrid zone between the two subspecies along the Front Range of the Colorado Rockies, which constitutes a significant shift in the range estimates for the subspecies. We have also investigated the underlying genetic architecture of differentiation between the eastern and western House Wren, and have identified a large putative inversion (~26mb) on the Z chromosome within the western population. Genes within this inverted region are overrepresented for metabolic functions, including a gene previously linked to migration in warblers, which is particularly fascinating because these subspecies are the only migratory house wrens. We are now investigating whether there is evidence of a migratory divide between the subspecies.

***The genetics of sex color difference: Seeking answers from a female-polymorphic hummingbird**

J Falk, G Semenov, S Taylor

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Little is known about the genetic mechanisms that produce plumage differences between the sexes. Identifying the genetic basis of sexual dichromatism is a challenge because in dichromatic species, coloration is tightly correlated with sex, making it difficult to identify genes that specifically regulate color differences. In this project, we study a fascinating species that is uniquely able to address these questions, the white-necked jacobin hummingbird (*Florisuga mellivora*). White-necked jacobins females are polymorphic – most females have very different coloration from most males (heterochromic), yet 20% of females are male-like in coloration (androchromic). Thus, dramatic sex-difference and sex-similarity are both expressed, allowing the study of genetic factors underlying sex difference while controlling for other factors. We sequenced and aligned whole genomes from 10 males, 23 heterochromic females, and 17 androchromic females. Our results show that a very small region on a single gene (*BNC2*) likely controls color differences in the two female morphs of this species. This gene is a transcription factor associated with melanogenesis in diverse vertebrate taxa, including birds, mammals, and fish. We compared the variation in females with males and discuss how genetic differences may evolve between sexes in hummingbirds. We conclude by discussing how hummingbirds provide a fascinating model for understanding the evolution and development of sexual phenotypes in avian taxa.

***Habitat-associated dispersal predicts genetic connectivity in Amazonian floodplain birds**

L Luna, C Ribas, A Aleixo

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The impact of habitat association on genetic variation patterns in tropical organisms, especially in dynamic floodplain systems, can shed light on the processes shaping population divergence. We compared genomic variation within multiple populations of 12 Amazonian co-distributed floodplain bird species with varying habitat affinity and dispersal strategies. These dispersal strategies are related to the seasonal inundation cycle: during the high-water season, forest birds migrate vertically to the upper

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stratum, while shrub birds migrate horizontally in search of suitable habitat. We aimed to assess if species with different habitat preferences and from different forest strata exhibit varying patterns of gene flow and isolation-by-distance (IBD). Forest species displayed lower gene flow and greater population genetic structure related to geographical distance compared to shrub species. Our findings support the hypothesis that species with different habitat affinities experience contrasting rates of genetic connectivity, probably due to divergent dispersal strategies in response to the flooding cycles, leading to predictable genetic structure mediated by ecological traits within the Amazonian floodplains. However, species with genetic structure exhibited no shared phylogeographic break, indicating that even species with similar habitat affinity may have different divergence histories. These results highlight that continuous processes such as IBD, which may shape genetic variation within populations, do not always result in shared discontinuities of population connectivity.

***Prevalence and implications of adaptive introgression among Amazonian bird populations**

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The accumulation of genetic differentiation between isolated populations produces phenotypic divergence, ecological differentiation, and eventually the buildup of reproductive barriers that limit the prevalence of gene flow. Although the neutral mechanism promoting the accumulation of differentiation between lineages has been the focus of many studies, how natural selection speeds up or slows down the speciation process is far less known. In this study, we focused on multiple populations of two Amazonian bird species, *Xiphorhynchus spixii* and *Phlegopsis nigromaculata*, to investigate genome-wide patterns of selective sweeps. We used a suite of genomic analyses based on Ancestral Recombination Graphs and window-based summary statistics to further identify any selective sweeps with signatures of adaptive introgression. We found that some selective sweeps have a signature of adaptive introgression, indicating that introgression among neighboring populations may be an important part of the adaptive process in Amazonia. We suggest that this finding supports an Amazonian biogeographic model involving cycles of isolation with genomic sweeps accumulating within populations and regular secondary contact across dynamic river barriers, with adaptive alleles diffusing among neighboring populations.

***Signatures of Environmental Adaptation Detected Across a Narrow Range of Environmental Variation in Black-throated Blue Warbler (*Setophaga caerulescens*)**

M Ore, C Rayne, C Bossu, K Ruegg, G Graves, S Sillett, M WebsterPresenting author: **Madelyn Ore**, Cornell University, madelynore@gmail.com

Climate warming trends are driving rapid environmental changes, presenting a pressing need to understand how species will adapt to these altering environments. Environmental adaptation is frequently driven by polygenic traits, which are characterized by subtle allele frequency shifts. High-throughput sequencing advances allow us to detect these subtle changes to explore associations between genetic and environmental variation across a species' range, in virtually any system. These Genotype-Environment Association studies have mostly been used for widespread generalist species and species with major population declines. We test how this framework works in detecting genomic adaptation to environment in a species with a more restricted ecological niche and no major population patterns, the Black-throated Blue Warbler (*Setophaga caerulescens*). We conducted whole genome sequencing on 200 individuals from 12 breeding populations and mapped genetic variation across the landscape. We used gradient forest to determine which environmental factors are most closely associated with genetic variation. Then, we used outlier analyses to determine which regions of genome are most highly associated with environmental variation. Results show there are narrow regions of the genome that are highly associated with environmental variables such as elevation, summer temperature, and measures of greenness across the landscape. This suggests there may be local adaptation to environmental conditions within breeding populations, despite occupying a relatively narrow environmental niche.

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The capuchino pangenome reveals the landscape of structural variation*M Recuerda, C Kopuchian, A Di Giacomo, L Campagna**Presenting author: **María Recuerda**, Cornell University, mariarecuerdacarrasco@gmail.com

Research on genotype/phenotype associations in non-model organisms has traditionally focused on single nucleotide polymorphisms (SNPs), overlooking the potential significance of structural variants (SVs). SVs, including insertions, deletions, inversions, duplications, and Transposable Elements (TEs), significantly influence gene structure and function, but their detection is hindered by the need for long-read sequencing and high-quality reference genomes. Moreover, traditional reference-based genome studies often miss SVs, as sequences containing SVs may not align with reference genomes lacking them. Pangenomes address this limitation by integrating data from multiple genomes to reveal a comprehensive landscape of genetic diversity, including SVs. Our study applies this emerging method to the capuchino seed-eater radiation (Sporophila), comprising twelve species with distinct coloration patterns and songs, to comprehensively characterize genomic variation. Previous SNP-based studies identified a small number of divergent genomic regions among the species of the group. To explore the role of SVs in driving species differentiation, we generated a 32 haplotype capuchino pangenome by sequencing 16 genomes of seven species using Pacific Biosciences (PacBio) HiFi long reads, including *S. hypoxantha* (3), *S. iberaensis* (4), *S. pileata* (1), *S. hypochroma* (1), *S. ruficollis* (2), *S. palustris* (3), and *S. cinnamomea* (2). This approach revealed a variety of highly differentiated SVs across the genome, likely involved in generating species differences. This pangenomic approach enables a deeper understanding and characterization of the genetic architecture underlying species differentiation in the capuchino seed-eater radiation.

Evaluating Genetic Diversity and Population Structure of an Endangered Shorebird**Y Tan, F Cuthbert, S Reddy**Presenting author: **Yi Fang Tan**, University of Minnesota, tan00025@umn.edu

Genetic variation is essential to the long-term persistence of populations to adapt to changing environments. Reductions in population size are associated with decreased survival, fitness and evolutionary potential. Small populations have inherently lower genetic variation and face elevated extinction risk due to inbreeding and genetic drift. The Great Lakes Piping Plover (GLPIPL) is an endangered shorebird that underwent a severe bottleneck which reduced the population from approximately 800 to 12 breeding pairs. Over the past thirty years, intense population management has increased the population to 60-80 breeding pairs. In this study, we aimed to assess genetic diversity and population structure of GLPIPL and investigate the possibility of gene flow between other Piping Plover populations. We used DNA samples from non-invasive sampling (i.e. fecal and buccal), blood samples and a modified RADseq (3RAD) protocol to generate single nucleotide polymorphisms. We calculated estimated heterozygosity and Wright's inbreeding coefficient, FIS. We evaluated population structure and gene flow by generating FST values and STRUCTURE plots. We found the GLPIPL population to have relatively little genetic variation, given their historical bottleneck and low population numbers. We also detected gene flow into the Great Lakes population from the other two PIPL populations. By evaluating the impact of the population bottleneck on genetic diversity and assessing the presence of gene flow in the GLPIPL population, results from this study will provide a clearer picture of potential genetic vulnerabilities faced by the GLPIPL population.

****Multi-scale assessment of Henslow's Sparrow (*Centronyx henslowii*) habitat use in a fire-managed grassland****E Nastase, N Hostetter, K Pacifici, A McKerrow, J Collazo**Presenting author: **Emily Nastase**, North Carolina State University, eanastas@ncsu.edu

Henslow's Sparrows (*Centronyx henslowii*) are migratory, grassland-specialist songbirds experiencing substantial declines throughout their range. We studied habitat requirements and space use of the population at the Voice of America Game Land, a State, fire-managed site in North Carolina. We

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assessed sparrow response to a three-year burn rotation at multiple scales (2016–2023), identifying habitat features associated with density and breeding activity distribution using survey, spot mapping, nest monitoring, and telemetry data. The average density of sparrows in the Game Land (1,200 ha) was highest in areas burned two years prior. The probability of sparrows exhibiting breeding behaviors was associated with decreasing percent of dead standing stems (correlated with open, grassy areas). Average home range size was 2.63 ha and did not vary by location or time-since-last-burn. Nest sites were characterized by higher-than-average percent graminoids when compared to Game Land average value. At a finer level, differences in vegetation between nest and random sites (within 50 m of a nest) were not discernable, suggesting sparrows have multiple options to place nests, perhaps beneficial to mitigate nest predation. We could not discern differences in vegetation between successful and unsuccessful nests, likely an artifact high nest success (24/27) and poor discriminatory power. Our study suggests a three-year fire rotation is adequate to maintain a growing sparrow population, with highest benefits two-years post-burn, and sparrows are making selections based on broad-level patterns in landscape and vegetation structure, e.g., exhibiting an affinity for patches increasingly devoid of woody vegetation for nest placement.

Spatial association between a grassland shorebird (Long-billed Curlew) and a keystone herbivore revealed by GPS tracking data

A Boyce, P Cimprich, J Kelly, A Dreelin

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Keystone species interactions can be key components of an organism's habitat and have important consequences for fitness. In grassland landscapes, native keystone herbivores have largely been eliminated from the landscape to maximize the efficiency and productivity of working lands. Because of the speed and ubiquity of this loss, ecological relationships between keystone herbivores and grassland obligate birds remain largely unknown or undocumented. Here, we use high-resolution movement data and continuous time resource selection functions to test whether a grassland obligate shorebird, Long-billed Curlew (LBCU; *Numenius americanus*) preferentially forage in areas occupied by black-tailed prairie dogs (*Cynomys ludovicianus*). Based on data from 5 individuals over two years we found that LBCU preferentially forage in areas of active prairie-dog colonies after accounting for landcover, water resources and topography. Analysis of additional individuals and years are underway. Our study system lends itself to particularly strong inference given the highly dynamic nature of prairie-dog colonies in the presence of sylvatic plague combined with a multi-year tracking dataset. Our results suggest the presence of strong ecological links between birds and keystone herbivores in temperate grassland systems. Further, it points to a need to quantify and mitigate components of grassland bird habitat loss beyond simple changes to landcover and land use. Our results set up testable questions regarding the mechanism attracting curlews to prairie-dog towns and invite parallel investigations across continents in other grassland ecosystems where colonial burrowing rodents act as ecosystem engineers at large scales.

****Prescribed fire, invertebrate prey abundance, and use of burned grasslands by migratory birds**

L Bobay, S Loss, T Hovick, S Fuhlendorf

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While fire is a well-known driver of structural changes in avian habitat, its short-term effects on bird communities, particularly communities of migrating birds, are understudied. We examined how recently burned patches of tallgrass prairie are used by birds during migration, with a focus on American Golden-Plover, a declining species that migrates through the Great Plains and is known to frequently occur in recently burned landscapes. Additionally, we investigated a potential mechanistic link between fire and prey availability by measuring post-fire occurrence of earthworms in the uppermost levels of soil. Our study took place at the Tallgrass Prairie Preserve in north-central Oklahoma, one of the largest intact tallgrass prairies on Earth that is managed with intensive prescribed fire. We conducted bird and earthworm surveys from March-May of 2022 and 2023, periods aligning with northbound bird migration

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and high fire frequency in the region. We examined relationships between time-since-fire and both earthworm depth and avian habitat use, and whether plover use of burned patches varies in tandem with numbers of earthworms near the surface. Our results offer compelling evidence that earthworms occur near the surface more frequently immediately after fire, suggesting that plovers and other predators may be capitalizing on this fire-mediated food resource. Our work can inform management for migratory birds in prairies and provides unique insights into links between fire, avian predators, and prey.

Estimating the impact of hay harvest on nesting grassland birds*A Binley, S Wilson, K Reed, J Lawrence, J Proctor, S Barker, J Waddell, A Johnson, B Rigley, D Nydham, A Rodewald***Presenting author: Allison Binley, Cornell Lab of Ornithology, allisondbinley@gmail.com*

Grassland birds are facing precipitous declines, largely due to habitat loss and threats posed by agricultural activities such as spring hay harvest. Our objective was to estimate the impacts of hay harvest on nesting grassland birds over time and across their breeding ranges. We predicted nesting dates for grassland birds across North America using data from community science projects, breeding bird atlases and published literature, as well as climate variables including monthly precipitation and temperature. The estimated probability that nests are active on a given date and in a given region were combined with the species' relative abundance to quantify the nest destruction estimated if harvest were to occur on that date. We then compared these active dates in each region and year with harvest schedules to estimate nest mortality. The impact of hay harvest on grassland birds was highly species-specific. For some species, nesting dates varied substantially from year to year, and thus the estimated impact of hay harvest varied as well. Other species remained more consistent over time. Interestingly, in some regions we found that the average first hay harvest date was changing over time. For example, in New York State, we found that the average first harvest date was almost two weeks earlier compared to a decade ago. Thus, even species with relatively consistent nesting dates over time were subject to changing harvest impact over time. Our analysis uncovers the dynamics of a major threat to declining grassland birds, while also providing tools to aid with conservation planning in agricultural landscapes moving forward.

****Bison grazing and restoration treatments influence nest-site selection and nesting success in a tallgrass prairie****A Chávez Treviño, S Lerman, L Sullivan, K Gutknecht, M Byrne***Presenting author: Alejandro Chávez Treviño, School of Natural Resources - University of Missouri, acxgd@umsystem.edu*

Tallgrass prairie restoration is an important tool for grassland bird conservation. Agriculture, invasive plants, and homogenizing landscape practices, such as mowing, have negatively impacted grassland bird breeding success. Disturbances like bison (*Bison bison*) grazing and fire are integral to the tallgrass prairie ecosystem but the effect on grassland bird nesting success is not fully understood. We quantified nest-site selection and success within different restoration treatments (control, fire, mowing, and herbicide) on bison-grazed and ungrazed pastures at Midewin National Tallgrass Prairie (Wilmington, IL). We quantified microhabitat at nest sites and used movement data from 7 GPS collared bison (out of a herd of 60) to quantify intensity and distribution of grazing. We used logistic regression to quantify nest-site selection, and logistic exposure regression to estimate daily survival probability as a function of habitat for four species of grassland birds ($n = 371$ nests). We identified species-specific patterns of nest-site selection. Dickcissel (*Spiza americana*) favored greater shrub cover, while Eastern Meadowlark (*Sturnella magna*) and Grasshopper Sparrow (*Ammodramus saviarum*) preferred lower shrub density, all exhibiting a preference for bison-grazed vegetation. Conversely, Red-winged Blackbirds (*Agelaius phoeniceus*), preferred taller, ungrazed vegetation. Nesting success was greater in taller vegetation with minimal disturbance. The study's key insight suggests that while grassland birds select grazed habitats, nesting success is greatest in undisturbed areas. This implies that larger tracts or lower bison stock density may create nesting habitat with less disturbance, enhancing overall success. Our findings contribute to effective restoration strategies for grassland bird species in the tallgrass prairie.

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****Keystone effects of prairie dogs (*Cynomys* spp.) on grassland birds: current knowledge and future directions****A Dreelin, A Boyce, H Jones***Presenting author: Andrew Dreelin*, Northern Illinois University, randrew899@gmail.com

Prairie dogs (*Cynomys* sp.) are colonial keystone species that modify bird community composition via ecological disturbance, but this topic has not been reviewed despite many studies on grassland bird associations with prairie dogs. We conducted a systematic literature review ($n = 111$ studies) where we assessed three hypotheses and found consistent support for each: 1) prairie dogs increase abundance of early-successional grassland birds, 2) prairie dogs increase avian beta diversity via increased heterogeneity in vegetation structure, and 3) prairie dogs increase raptor abundance by serving as a prey base. Due to rapid declines of grassland birds, we suggest conserving prairie dog towns as vital sources of early successional grassland and habitat heterogeneity. However, significant gaps in our understanding of the effects of prairie dog on birds remain. Most research was conducted on Black-tailed Prairie Dogs, during the bird breeding season, and focused on how prairie dogs modify occurrence and abundance of birds. Research is needed on the effects of other prairie dog species, effects on birds during the non-breeding or migratory seasons, and effects on demography, particularly for songbirds. Continued work on this topic can increase our understanding of grassland bird ecology and inform conservation for the most rapidly declining group of birds in North America.

****Cascading effects of management on an obligate grassland bird****J Clarke, T Hovick, K Sedivec, B Geaumont, J Harmon***Presenting author: Justin Clarke*, justin@clarke-home.com

Conventional grazing regimes have contributed to widespread grassland bird declines by reducing vegetation structure and composition variability, which decreases avian niche diversity. Recoupling fire and grazing can restore heterogeneity, but regional limitations in knowledge and prescribed fire tools prevent widespread application. This suggests a need for innovative grazing regimes that utilize existing infrastructure to restore heterogeneity. We examined the impacts of one conventional and two heterogeneity-based grazing regimes on territory size, a proxy for territory quality, of an obligate grassland passerine. We delineated avian territories from mid-May to early June and characterized vegetation structure and composition in early July. We assessed 38 territories from 2022 to 2023 and analyzed the direct and indirect impacts of grazing regime on territory quality using structural equation modeling. Kentucky bluegrass and standing litter positively influenced territory quality (standardized $\hat{\beta}^2 = 0.10$ and 0.06 , respectively). Territory quality was negatively impacted by vegetation density and the percent cover of litter, smooth brome, and western snowberry were associated with larger territories (standardized $\hat{\beta}^2 = -0.05$, -0.09 , -0.01 , and -0.11 , respectively). Grazing regime did not directly impact territory quality, but patch-burn grazing exhibited reduced cover of the vegetation variables that negatively impacted territory quality. Our research suggests that rangeland management decisions have cascading and compounding effects on wildlife. Indirect and cascading consequences of management decisions can complicate incorporating conservation into working lands. However, understanding the complex interaction between grazing regimes, vegetation structure, and habitat quality will allow land managers to tailor management to avian conservation goals.

Grassland bird trends from the National Bobwhite and Grassland Initiative (NBGI) Coordinated Implementation Program (CIP): Densities and response to habitat, management, and weather.*M Zimmerman, J Morgan, J Elmore***Presenting author: Marisa Zimmerman*, Clemson University, marisaz@clemson.edu

Grasslands and grassland birds have declined globally, leading to an increase in time and resource investments to implement prescribed grassland management supporting grassland bird species such as Northern Bobwhite. It is necessary to monitor and evaluate how specific management practices and habitat characteristics influence target species populations to most efficiently allocate limited resources to

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best manage grasslands at broad spatial and temporal scales. The National Bobwhite and Grassland Initiative utilizes a Coordinated Implementation Program, which is an adaptive management framework that follows standardized protocols to collect avian abundance and presence-absence data at focus and reference areas, including using fall covey counts for Northern Bobwhite and breeding bird point-counts for target grassland bird species. Within this program, covariate data is collected for habitat management, habitat characteristics, and weather. We hypothesized that bird densities would be higher on focus areas versus reference areas and that densities would increase in response to favorable management, habitat characteristics, and weather (e.g., mild winters). We estimated bird densities at focus and reference areas and evaluated bird response to management, habitat characteristics, and weather while accounting for effort, daily weather, and regional and site variation. Our results were varied, but in general we found that bird densities increased with intensive management and habitat improvement, and that densities were higher on focus areas than reference areas. These results can help inform stakeholders of the most successful adaptive management practices for grassland restoration and grassland bird conservation.

Virtual fences as a tool for grassland bird conservation

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We tested the effectiveness of Virtual Fence to achieve conservation goals by conducting a replicated before-after-control-impact experiment in the Flint Hills of eastern Kansas. We excluded cattle from 11 4-ha patches, each paired with a control area, all located in prime nesting locations for threatened species in this tallgrass prairie ecosystem. During 2022, cattle wore collars but allowed free movement. In 2023 and 2024, collars restricted access to treatment plots. We surveyed vegetation height and composition, Greater Prairie-Chicken lek counts, and breeding bird diversity and abundance. Due to the newness of this technology, we experienced several problems with collars due to water damage and detachment. Despite these challenges and drought post-treatment, vegetation in treatment plots more closely resembled ideal conditions for prairie chickens and Henslow's Sparrows; they had taller vegetation, less litter, and a greater proportion of live grass near the center (vs. edge) of plots. Grassland bird richness and abundance were slower to respond to the treatment, but preliminary data indicate that abundances of a few species were altered by the experiment in the ways we predicted. Virtual fence technology may be a promising management tool for grassland bird conservation, but imperfect exclusion and the high inter-annual variability in climate in this region mean that interventions must last for several years.

***Little Brown Birds In Peril: How the Grasslands Outcomes Tool for Birds (GOT Birds) is on the frontline, modeling non-breeding season grassland bird abundance related to woody vegetation encroachment in the Chihuahuan Desert and surrounding areas**

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Grassland bird populations are rapidly decreasing across the globe and throughout North America, with some of the steepest declines observed in species dependent on the Chihuahuan Desert during the non-breeding portion of their life cycles. One of the main factors contributing to dwindling populations is woody plant encroachment, which decreases the quality and quantity of the grasslands that birds use. Many organizations and universities are collaborating to model how woody plant encroachment, among other variables, are directly influencing breeding bird abundance across the grasslands of North America. However, few efforts have attempted to model how these grassland threats will influence bird species abundance within the non-breeding season of their ranges, especially in Mexico. The Grasslands Outcomes Tool for Birds (GOT Birds) is on the frontline attempting such a feat. Using boosted regression tree analyses with geospatial data available in both Mexico and the United States, GOT Birds is assessing the variables with the greatest influence on target grassland bird species abundances. Early results indicate that birds within the Chihuahuan Desert respond strongly to weather and climate covariates, which is expected given the nomadic nature of the species in the non-breeding season. Additionally, GOT Birds is creating 'heat maps' of predicted bird species densities that will guide

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landowners and practitioners with locations on where to focus conservation-related projects.

****Modeling high-elevation spruce-fir forest patch dynamics to improve forestry practices and Bicknell's Thrush breeding habitat models****J Longo, A Roth, P Thomas***Presenting author: James Longo, James.Longo.birds@gmail.com*

The Bicknell's Thrush (*Catharus bicknelli*) is a migratory songbird species with breeding habitat consisting of stunted, high-elevation, coniferous forest in northeastern North America. Bicknell's Thrushes inhabit areas where timber harvesting of spruce-fir forest produces vigorous regeneration. These harvested areas tend to be at relatively lower elevations and presumably resemble their naturally occurring breeding habitat on mountain tops. While some breeding habitat characteristics, particularly tree composition and forest structure, are well described, the patch dynamics of the greater habitat mosaic are poorly understood. This study combines remotely-sensed data and citizen science point count surveys to model the relationship between patch dynamics and Bicknell's Thrush breeding habitat selection. A better understanding of patch dynamics in non-harvested areas can inform forestry practices in harvested areas which can aid forest managers in their management of Bicknell's Thrush breeding habitat.

****Assessing the factors driving American Oystercatcher nest and chick survival at a site with declining productivity in the U.S. Mid-Atlantic****M Call, A Wilke, K Lapenta, S Karpanty, P Denmon, J Fraser, C Wails***Presenting author: Mikayla Call, Virginia Tech, mncall@vt.edu*

The American Oystercatcher (*Haematopus palliatus*) undergoes intense management across its range. Conservation efforts target reproductive success to increase the population, and monitoring often focuses on identifying key threats to the survival of nests and pre-fledged chicks. However, threats may vary spatiotemporally, especially in a dynamic coastal landscape. In Virginia, which supports a large oystercatcher breeding population, a decline in productivity since 2016 may indicate changing drivers of nest and chick survival. We monitored the reproductive success of 76 total pairs of oystercatchers in Virginia on Metompkin Island in 2021–2022 and Fisherman Island in 2023. Additionally, we used radio telemetry to track one chick per brood ($n = 44$ chicks) and improve our chances of identifying fate. We found that hatch success was high, indicating low chick survival was driving low productivity. Median survival time for nests was 31 days, greater than average age at hatching (29 days; range 26–39 days). In contrast, median survival time for chicks was 14 days, less than minimum fledging age at 35 days. We also found that despite ongoing management actions, such as removal of mammalian predators, nest and chick survival continue to be affected by a complex set of environmental and biotic factors. Primary causes of nest loss included weather (14.5%) and predation (10% total; 3.6% by mammals; 2.7% by ghost crabs *Ocypode quadrata*; 3.6% by unknown predators). Predation was the primary source of mortality for radio-tagged chicks (28.9% total; 13.3% by ghost crabs; 15.7% by avian species). Our results inform oystercatcher management in Virginia, but also have implications for the conservation of other beach-nesting bird species.

Effect of Habitat Characteristics and Wetland Management on Least Bittern Occupancy in Missouri**R McGinty, K Malone, L Webb, A Messerman, J Haslerig, D Mengel***Presenting author: Ryan McGinty, SUNY Brockport, RyanMcGinty1999@gmail.com*

The Least Bittern (*Ixobrychus exilis*) is a species of secretive marsh bird that depends on wetland habitat throughout its life cycle. They are a species of conservation concern in several U.S. states where their populations are declining, likely due to habitat loss. The purpose of this project is to determine the effect of habitat characteristics and wetland management practices on Least Bittern distribution in a portion of their breeding range. To accomplish this, we conducted call-playback surveys at 84 survey points placed in 43 emergent wetland pools. We collected both habitat data at every survey point and data on the

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management practices at each wetland pool. Least Bittern site occupancy was positively associated with percent cover of both tall emergent vegetation ($\hat{I}^2 = 0.619$, 85% CI = 0.143 – 1.123) and open water ($\hat{I}^2 = 1.092$, CI = 0.509 – 1.789). Increasing water depth was positively associated with Least Bittern occupancy ($\hat{I}^2 = 1.363$, CI = 0.689 – 2.198). Points with greater interspersed were more likely to be occupied by Least Bittern (mean occupancy = 0.582, CI = 0.369 – 0.808) than points with less interspersed (mean occupancy = 0.214, CI = 0.087 – 0.375). Wetland pools that were permanently inundated with water were more likely to be occupied by Least Bittern (mean occupancy = 0.685, CI = 0.415 – 0.923) than sites that were drawn down every other year (mean occupancy = 0.474, CI 0.201 – 0.767) or every year (mean occupancy = 0.200, CI = 0.102 – 0.314). Least Bittern occupancy was also positively associated with a later initiation of spring drawdowns (effect size = 1.234, CI = 0.509 – 2.036). The decrease in wetland habitat in the United States coupled with the decline in least bittern populations in portions of their breeding range suggest that the few remaining wetlands are crucial for the persistence of Least Bittern in these areas. The results of this project may help inform best management practices for Least Bittern populations.

****The habitat and behavior of the Belding's Savannah Sparrow (*Passerculus sandwichensis beldingi*)**

D Boehmer, C Whitcraft

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The Belding's Savannah Sparrow (*Passerculus sandwichensis beldingi*; BSSP) is a salt marsh endemic bird that has been listed as an endangered subspecies in California since 1974. Despite its listing status, there are few recent studies that have examined how these birds interact with their urbanized environment. To examine this, we looked at how the BSSP populations, nest locations, and behavior differs at four southern California salt marshes during the BSSP's nesting season. After nesting season, habitat parameters, including vegetation community metrics, inundation levels, and urbanization of the watershed, were measured. We found vegetation community metrics such as total percent cover and percent cover of invasive plants to be the strongest predictors of BSSP population numbers, while abiotic parameters like inundation level and distance to edge were the strongest predictors of nest occupancy. In terms of the behavior of the BSSP, we found that time activity budgets differed by sampling station and site, and these differences were driven primarily by the differences in time spent perching, taking cover, and foraging. Differences in behavior were correlated with distance to edge, weather, and substrate used. This variation in behavior could be benefit BSSP as its habitat changes in the future. Under sea-level rise scenarios, the rising waters will change the vegetation community, increase inundation, and push BSSP closer to the edge of their habitat. Future salt marsh restoration projects should incorporate habitat features that maximize nesting habitat, so that the populations of this endangered species can persist and grow.

****Spatial partitioning of Cassin's Sparrows (*Peucaea cassinii*) breeding territories**

E Landi, E Landi, C Ramos

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North American grasslands are one of the most threatened ecosystems in the world, and grassland birds have experienced the largest declines. Grassland species like Cassin's Sparrows (*Peucaea cassinii*) have lost almost half of their population in the past 50 years. Cassin's Sparrow breed in high densities which may lead to fitness costs incurred by intrasexual competition between males. Spatial partitioning of territories may be used to reduce competition between males. Cassin's Sparrows may be more competitive over nesting sites and areas of high-quality habitat. To test this hypothesis, we deployed 26 LifeTags in an automatic telemetry network from Cellular Tracking Technologies on male Cassin's Sparrows during the summers of 2021 and 2022. Location data from the LifeTags was used to calculate Automated Kernel Density Estimates (AKDE). A resource selection function was conducted to measure which vegetation resources like cover type and Normalized Difference Vegetation Index (NDVI) could cause competition. Cover type was classified across the entire study site by using Object Based Imagery Analysis on satellite imagery. Results show Cassin's Sparrows are significantly more likely to select tree

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cholla (*Cylindropuntia imbricata*) and shrubs (Family: Asteraceae; $p < 0.05$) compared to grass. NDVI was shown to have a negative quadratic relationship with probability of use ($p < 0.001$). As the percentage of cholla cover on 50% AKDE territories increases, size and percent overlap on these territories decreased significantly ($p < 0.001$). These results show modern-day land conversions of shortgrass prairie for cattle grazing, agriculture, and urban development are not ideal for Cassin's Sparrows and could cause a range-wide decline.

Applying avian species-centered models to quantify landscape change in both a natural and managed forest disturbance

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A key management objective in western forests is to achieve desired ecological conditions associated with fire-adapted forests across landscape scales, including providing bird habitat. Yet the effect of fuels treatments across large landscapes on bird habitat remains poorly understood. We apply a species-centered distribution modeling (SDM) approach that uses Landsat imagery instead of classified layers to examine bird habitat change in a landscape-level forest restoration project. Using values extracted from SDMs, we use NMS ordination to measure bird community change following disturbances. Using data from before and 9-years after the Quartz wildfire, we test the SDM approach for measuring bird habitat change following a disturbance that had already been quantified using field data in a published study. We then use the same SDM approach to examine bird habitat change before and after treatments that occurred as part of the 9000 acre Ashland Watershed Forest Resiliency Stewardship project from 2005-2019. We found that the bird community composition following the Quartz Fire showed a similar pattern to the results from the original analysis, supporting the model approach to evaluating temporal change in bird habitat following disturbance. Bird habitat in the Ashland Watershed Forest Resiliency Stewardship project differed pre and post treatment in density management treated units. Indicator species associated with shrub and mid-story cover were representative of pre-treatment conditions. Our results demonstrate that SDMs are sensitive enough to detect changes in coniferous forests following a disturbance, and that bird habitat suitability can provide a complex indicator of forest restoration success at landscape scales.

****Painting the bunting: Linking resource use to plant communities using emerging space-use and genetic surveillance technologies**

D Klement, C Rushing*Presenting author: Diane Klement, University of Georgia, djk34130@uga.edu*

To halt the rapid decline of many migratory birds, conservationists must understand which plants provide high-quality avian habitats and actively target those plants in conservation efforts. We used emerging automated tracking and genetic technologies to quantify resource- and space-use across the breeding season to determine the specific plant resources that provide high-quality habitat for a declining neotropical migratory bird, the Painted Bunting (*Passerina ciris*). I aimed to address this critical gap in our understanding of avian conservation by 1) cataloging seasonal variation in resource abundance provided by plant communities, 2) quantifying resource use through fecal DNA metabarcoding analysis, and 3) quantifying fine-scale bird space use in relation to plant communities/ food abundance using automated radio telemetry units. This work strengthens conservation efforts by identifying the highest-value plant communities for birds, informing both coastal ecological managers and homeowners of which plant species provide preferred bunting habitat. By identifying which plant species provide preferred bunting habitat throughout the entire breeding season, this research fills an important knowledge gap regarding how ecological restoration efforts can utilize fine-scale space use data to restore specific plants associated with habitat quality for other bird species. Furthermore, by leveraging novel tracking technology to quantify specific individual habitat use, this work demonstrates how emerging technologies can decrease the cost- and labor-intensity often associated with habitat-quality studies.

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Using structural and floristic microhabitat associations in Southwestern pinyon-juniper woodlands to understand effects of thinning and tree mortality on bird habitat suitability*H Jones, B Merriell, M Swan, M Johnson, R Siegel***Presenting author:* **Harrison Jones**, The Institute for Bird Populations, hjones@birdpop.org

Drought-induced tree die-off and die-back in the southwestern United States is changing the structure and floristics of pinyon-juniper woodland, a widespread middle-elevation community with high bird endemism. Amid increasing risk of high-severity wildfires in this habitat, managers have turned to mechanical thinning to reduce fuel loads, yet the effects of this practice and tree mortality on bird habitat suitability are poorly understood. In this study, we fit Bayesian N-mixture models to eight years of bird monitoring data collected at three national parks on the Colorado Plateau to relate microhabitat-scale floristic composition and vegetation structure to breeding-season bird densities. We found numerous supported responses to microhabitat variables across 17 of 19 bird species modelled, with vegetation structure generally more important than floristic composition in explaining densities. Birds showed limited preference for pinyon pine over juniper or for specific understory shrub species, though cavity-nesters preferred more pinyon pine. From a structural perspective, both canopy and understory species preferred greater foliage cover in the shrub layer and subcanopy; shrubs are often the only deciduous vegetation in pinyon-juniper and may contain higher arthropod densities for gleaning insectivores. Variation in canopy cover and height were generally unimportant, or species preferred lower canopies, suggesting pinyon-juniper birds may be resilient to moderate, local mechanical thinning and tree mortality. However, seven species were absent or rare at Bandelier National Monument after a large-scale (> 95%) pinyon pine die-off, indicating greater sensitivity to landscape-scale and intensive (< 15% canopy cover remaining) thinning. Many species avoided stands with a greater foliage height diversity, containing high foliage cover in the canopy, midstory, and shrub-layer, and most species preferred woodlands with open canopies and simplified vertical structures.

Investigating environmental drivers of Brewer's sparrow Density in the Gunnison Basin: A spatiotemporal analysis of habitat characteristics**C Park, P Magee, K Brodhead, M van de Kerk***Presenting author:* **Caleb Park**, Western Colorado University, calebwp98@gmail.com

The Brewer's sparrow (*Spizella breweri*), a sagebrush obligate bird, faces increasing threats due to habitat degradation. Given these persistent threats, it is crucial to understand relationships between the landscape and the animals that rely on it. This study aims to combine bird point count data with remotely sensed and field collected vegetative, topographic, and climatic covariates to determine the factors that most affect the species' distribution and quantify the relationship between spatial and temporal variables and Brewer's sparrow abundance across the sagebrush ecosystem of the Gunnison Basin. To achieve this, I am conducting breeding season bird point counts, following the IMBCR protocol, from 2022 to 2024. Additionally, I am using previously collected data from 2018 to 2021 to assess the abundance and distribution of Brewer's sparrows across the Gunnison Basin over the six-year period. Remotely sensed vegetation and topographic data, including LiDAR, DEM, and high-resolution (0.5m) imagery of the Gunnison Basin collected in 2022, are being utilized to compare these spatial covariates with the distribution patterns of the Brewer's sparrow within the sagebrush steppe. Currently, remotely sensed vegetative data is still being acquired, while the 2024 bird point count data collection is scheduled to begin towards the end of May. Preliminary analysis of Brewer's Sparrow population numbers suggests similarities in fluctuations among distinct local populations (at the grid scale). Researching this complex relationship between the Brewer's sparrow and its habitat will provide valuable insights for land managers, enabling them to implement more effective and beneficial management strategies for these species.

****Does male aggression drive asymmetrical introgression of a sexually selected trait across the Flame-rumped Tanager hybrid zone?**

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Hybrid zone studies over the past decades revealed that asymmetric introgression of traits that confer a fitness advantage is common in hybridizing species. However, because establishing the advantage of a sexual trait often requires lengthy observations in the field, there is limited understanding of the actual mechanisms driving the introgression patterns observed from genomic and morphological data. In the Western Andes of Colombia, hybridization between Flame-rumped and Lemon-rumped Tanagers results in birds with a gradient in coloration and body mass (i.e., intermediate-sized, orange-rumped birds). The hybrid zone between both subspecies appears to have moved east and to higher elevations in the last century. Also, our preliminary cline analysis suggests that Lemon plumage color is introgressing into the Flame-rumped genomic background. We hypothesized that aggressive superiority of lemon-rumped males might be causing the movement of the hybrid zone and the differential introgression of genes mediating lemon color. To test for a relationship between aggressiveness and phenotype, we performed behavioral experiments to quantify male aggressive responses to taxidermic mounts that vary in rump color at different localities across the hybrid zone. We found that Lemon-rumped males are more aggressive to both conspecific and heterospecific mounts than their Flame-rumped counterparts, both in sympatry and allopatry. Moreover, hybrid males seem to respond equally to all phenotypes. Here we provide an empirical test of how sexual selection through intrasexual competition is one of the forces driving the asymmetric introgression of a sexual signal detected from genomic analyses.

Hybrid Zone Dynamics Along a Linear River System in Xiphorhynchus Woodcreepers*M Lynch, B Ramirez, M Mutchler, E Kirsch, J McCormack***Presenting author:* **Mason Lynch**, maslynch@gmail.com

Many bird species have shown a capacity to interbreed long after speciation. In lieu of genetic isolation, premating rituals have been identified as the main method of isolation. Among these rituals, song is known to change rapidly alongside genetic speciation. However, few studies have detailed the initial links between song divergence and genetic divergence within species. The woodcreeper genus, *Xiphorhynchus*, is an excellent model species for this phenomenon due to its purely genetically determined song and exclusive habitation of river systems, leading to discrete contact zones between lineages. We investigated genetic and song divergence between deeply divergent genetic lineages within the Buff-throated Woodcreeper (*Xiphorhynchus guttatus*) along the Orinoco and Ventuari rivers in Venezuela, where the two lineages with divergent song types come into contact. Genomic results support the existence of three overall genetic ancestries and two ancestries along the river system. We found the lineages across the rivers to form a hybrid zone with divergent patterns of introgression in genetics, song, and morphology.

Whole-genome data from a contact zone between Yellow-breasted Chat (*Icteria virens*) subspecies suggests possible cryptic speciation as well as hybridization**J Beam, A Calderon, A Brelsford, D Toews***Presenting author:* **Johanna Beam**, knitter5d@gmail.com

Studying the drivers of both speciation and hybridization can provide insights into what maintains reproductive isolation between populations. Rapid radiations are often studied to uncover what drives rapid diversification. However, species that are slower to diversify may show cryptic speciation or hybridization, and provide critical information on what processes facilitate genetic diversity on the other end of the speciation spectrum. The Yellow-breasted Chat (*Icteria virens*) is a passerine in the monotypic family Icteriidae, with two subspecies in the eastern and western US, respectively, that have unknown levels of divergence. Additionally, the extent to which chat subspecies may be interbreeding is unknown, suggesting the importance of understanding population structure and connectivity in chats, where plumage differences are subtle and hybridization may be more cryptic. Therefore, we used whole-genome resequencing data (6x coverage, n=30) from the intermediate region between subspecies and allopatric

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populations to estimate the extent of divergence and possibility of hybridization between them. We found that the subspecies have moderate levels of genomic differentiation with large regions of fixed differences. Additionally, we found some individuals from the intermediate zone showed hybrid ancestry. This suggests that the subspecies may be on independent evolutionary trajectories, but reproductive barriers are not complete. Further characterization of this undescribed hybrid zone will allow us to identify the levels of reproductive isolation between the subspecies.

****The impact of Blue-winged Pitta (*Pitta moluccensis*) range expansion on the conservation of the Mangrove Pitta (*Pitta megarhyncha*) in Singapore**

D Tan, F Rheindt, P Round, M Andersen

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Range expansion-mediated secondary contact between phenotypically similar sister species can often lead to the formation of hybrid zones that have unpredictable evolutionary and ecological consequences. The impact of secondary contact is especially important when one species is rare and threatened, since the formation of hybrid swarms could have detrimental effects on population viability. The recently formed contact zone between the expanding Blue-winged Pitta (*Pitta moluccensis*) and the locally critically endangered Mangrove Pitta (*Pitta megarhyncha*) in Singapore is thus of major conservation concern due to the morphological, vocal, and ecological similarities between the two species, which raises the possibility that hybridisation and introgression may occur. To better understand the causes and consequences of the Blue-winged Pitta range expansion, we collected blood samples from both species and obtained genome-wide SNPs using ddRAD sequencing. Based on these SNPs, we applied population genomic and demographic history reconstruction analyses to test the hypothesis that the Blue-winged Pitta range expansion was the result of colonisation by migratory individuals from Indochina, and that the phenotypic similarities between the Blue-winged and Mangrove Pittas would allow for hybridisation and introgression between the two species despite having diverged approximately 4 to 5 million years ago. Based on these results, we propose strategies to aid in the conservation of Mangrove Pitta populations in Singapore.

****Admixture mapping of call variation in a yellow-rumped warbler hybrid zone**

L Phung, M Baiz, D Pierce, A Brelsford, D Toews

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In birds, vocalizations are presumed to be one of the important premating reproductive barriers that could affect the evolution of new species. Songs and calls are the two types of vocalization signals: songs are melodious vocalizations that play a role in territorial defense or mate attraction, while calls are short vocalizations that are used during flight and to alarm others. Specifically in oscines, songs have been shown to be learned, whereas the role of learning versus genetics of calls is less clear-some studies have suggested call variation has a stronger correlation with genetic differences among populations. To assess this relationship further, we focus on the well-characterized Rocky Mountains hybrid zone of two yellow-rumped warbler subspecies, the myrtle warbler (*S. c. coronata*) and Audubon's warblers (*S. c. auduboni*), to perform an admixture mapping study for call variation in hybrids. This pair is known to extensively hybridize, and hybrids have highly admixed genomes-a spectrum between myrtle ancestry and Audubon's ancestry-which is highly suitable for admixture mapping. First, we quantified acoustic attributes of calls to characterize individual call phenotype objectively ($n = 145$), then assessed their acoustic variation using principal component analysis and discriminant function analysis. Second, we used genotype-by-sequencing to associate genotypes with call phenotypes using genome-wide efficient mixed model association (GEMMA). We found that call duration is highly associated with the divergence in a genomic region on chromosome 12, and we identified a few potential candidate genes in that region relating to musculature development.

***Adaptive introgression of putative carotenoid pigment genes explains geographic variation in a sexually-selected plumage trait**

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S Khalil, J Walsh, E Enbody, D Baldassarre, M Webster, J Karubian*Presenting author: Sarah Khalil, Cornell Lab of Ornithology, sarah.khalil93@gmail.com*

Ornamentation in males is one of the most conspicuous traits to differ among closely related species, and evolution of these traits, particularly coloration, is often attributed to sexual selection via female mate choice. Understanding the genetic architecture of sexual selection is a fundamental goal in evolutionary biology, as it can explain the constraints and processes that shape the expression and evolution of these traits and emergent evolutionary processes, such as introgression. To address these questions, we leverage populations of hybridizing red-backed fairywrens (*Malurus melanocephalus*) that differ by plumage color across a well-classified contact zone with a priori evidence of strong female preference of males with redder plumage. We sequenced whole genomes of 36 individuals that vary in plumage hue and found that divergence between even the most phenotypically different individuals within the hybrid zone is very low, but identified several regions with high F_{ST} estimates relative to the background divergence. To validate whether loci in these elevated regions were linked to plumage variation across the species' range, we sequenced top candidate SNPs for color differences in 285 individuals from 16 populations across the species range and conducted cline analysis on these loci. We found that 19% of these SNPs were concordant with the plumage cline (which is discordant from the neutral genetic cline), that some of these SNPs are in or around genes with putative carotenoid processing functions and evidence of selection in regions that contained those SNPs. Altogether, this suggests that the geographic variation as seen in the sexually selected plumage color in red-backed fairywrens is in part explained by adaptive introgression of putative carotenoid genes.

Mitonuclear discordance in the Bullocks and Baltimore Oriole hybrid zone**L Goch, S Billerman, I Lovette, B Butcher, J Walsh***Presenting author: Lily Goch, lpg34@cornell.edu*

The hybrid zone between Bullock's and Baltimore Orioles has been studied repeatedly over many decades, with increasing access to new statistical and methodological approaches for characterizing avian hybrid zone dynamics. For a hybrid zone to be stable, the hybridizing species must experience a balance between selection against hybrids and dispersal of hybrids and genes into the parental populations. Mitonuclear discordance, the molecular mismatch between mitochondrial and nuclear genes and their products, is increasingly suggested as a mechanism of selection against hybrids. To test for signs of discordance in these orioles, we isolated mitogenomes from fifty-six existing re-sequenced individuals (including allopatric, F1, and backcrossed birds), which as expected identified two distinct mitochondrial clades corresponding to the mitogenomes of each parental species. We then used the same whole genome data to correlate genome-wide SNPs with individual haplotypes to identify co-encoded regions. This resulted in the identification of 291 gene associations with enrichment in pathways pertaining to cell structure. We additionally identified haplotypes for 300 birds using an RFLP approach and compared mitochondrial and nuclear clines. The high number of candidate nuclear genes associated with mitochondrial haplotype along with clinal mismatch suggest a role for mitonuclear discordance in driving selection against hybrids and maintaining hybrid zone stability over time.

Assessing the mismatch between plumage and genetic clines within the palm warbler (*Setophaga palmarum*) hybrid zone**G Yoo, J Weir***Presenting author: Gihyun Yoo, University of Toronto, gihyun.yoo@mail.utoronto.ca*

Research on avian hybrid zones have revealed key insights into the genetics of speciation and the traits that maintain species boundaries. While the geographic distribution of such traits generally maps closely to hybrid ancestry, factors such as introgression of trait-controlling genes and genome homogenization through genetic swamping may lead to mismatches between the phenotypic and genetic signatures of hybridization. Here, we examine this potential mismatch in a previously uncharacterized hybrid zone between subspecies of palm warblers (*Setophaga palmarum*). Western (*S. p. palmarum*) and eastern palm warblers (*S. p. hypochrysea*) hybridize in Eastern Canada and can be readily differentiated by plumage colour. Using both reduced-representation and whole-genome sequencing, we examine

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genomic differentiation between the two subspecies, identify putative genetic regions that underlie plumage differences, and characterize both the genetic and plumage clines across the hybrid zone. While putatively hybrid individuals show intermediate plumage characteristics, preliminary evidence suggests that the observed phenotypic hybrids are potentially mismatched with their true genetic ancestry. We additionally use coalescence modelling to test two alternate scenarios that may have led to clinal mismatches, namely introgression of plumage genes and genetic swamping of hybrid ancestry in the contact zone. Our findings highlight the dynamic nature of hybridization among birds and shed light on the factors that maintain differentiation in a young subspecies pair.

First genetic evidence of hybrid Virginias x Colima warblers in West Texas, featuring patterns of admixture and SNP-phenotype associations

A Rice, J Manthey*Presenting author: Ari Rice, Texas Tech University, arrice@ttu.edu*

Despite being the focus of many investigations on phylogenetics and hybridization, Parulidae (wood-warblers) contains several genera that are poorly studied in this regard. *Leiothlypis* represents one such genus, in which none of its members were known to regularly hybridize until the 2002 discovery of suspected Virginia's (*L. virginiae*) x Colima warbler (*L. crissalis*) population in the Davis Mountains of west Texas. Since then, the composition, history, and trajectory of this seemingly isolated population has remained unknown. Here, we present the first genetic evidence of *L. virginiae* x *L. crissalis* hybridization based on blood samples from wild-caught birds. We also discuss the ecological and evolutionary implications of our findings, the possibilities of admixed birds existing elsewhere, and the extent to which admixture is reflected in birds' physical appearances. Finally, we lay the groundwork for an upcoming study addressing whether hybridization between these species is locally adaptive or simply a matter of small population size and limited mate choice in the Davis Mountains.

***Genetic assessment of breeding contact between two Fox Sparrow subspecies groups in south-central Alaska**

L DeCicco, J Withrow, K Winker, R Moyle*Presenting author: Lucas DeCicco, lhdecicco@gmail.com*

Fox Sparrows (*Passerella iliaca*) show a remarkable level of geographic variation which has been organized by taxonomists into four groups, each of which contain many described subspecies. These four subspecies groups have often been considered species, but interaction among subspecies groups on the breeding grounds is poorly understood. Here, using genome-wide genetic data, we investigate a contact zone between the red-colored boreal forest *iliaca* group and the sooty-colored Pacific coast *unalaschensis* group. This research is not based on transect-like sampling across a contact zone but rather comes from a single site where breeding contact between these groups occurs in south-central Alaska. Within lowland Boreal Forest in south-central Alaska we found a mix of nesting Fox Sparrows which phenotypically appeared to represent individuals of both the coastal and interior subspecies groups as well as some that appeared intermediate in plumage. The genomic data corroborated these phenotypic patterns and showed the presence of a highly variable genomic background within this population. These findings suggest that where these two subspecies groups come into breeding contact, some degree of assortative mating or selection against hybridization has maintained a heterogeneous population at this contact zone.

***Looks can be deceiving: the genetics of the contact zone between Calocitta Magpie-Jays**

A Pizarro, J McCormack*Presenting author: Alana Pizarro, Occidental College, pizarroa@oxy.edu*

Studying hybridization between closely related species can reveal crucial information about evolutionary processes and conservation strategies. In a previous study, we investigated the contact zone between the

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Black-throated Magpie-Jay (*Calocitta colliei*) and White-throated Magpie-Jay (*Calocitta formosa*) in western Mexico. We found evidence in throat coloration for a narrow hybrid zone. In this study, we explored the genomics of the hybrid zone using DNA from 32 historical *Calocitta* museum specimens across a north-south transect of both species. Thousands of SNPs from ultraconserved elements (UCEs) suggest limited evidence of gene flow between the two *Calocitta* species. Our results confirm the existence of the three subspecies of White-throated Magpie-Jay (*C. f. formosa*, *C. f. azurea*, and *C. f. pompata*) and suggest isolation-by-distance within Black-throated Magpie-Jays. The lack of genetic evidence for hybridization contrasts with the phenotypic results, which could relate to the much greater sampling in the phenotypic study and/or the lack of museum specimens, and therefore genetic information, from the narrow hybrid zone.

***Genomic regions associated with gut microbiome composition in the *Setophaga coronata coronata* x *S. c. auduboni* hybrid zone**

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Gut microbiome variation influences host physiology and is known to exhibit differentiation between avian species. Previous research has supported a role for the environment in shaping avian microbiome diversity, but host-specific factors remain elusive. In hybrid zones, genetic recombination shuffles divergent alleles among backcrossed individuals allowing associations between genomic regions and specific traits to be identified. In this study, we use an admixture mapping approach to investigate the contribution of host ancestry in shaping gut microbiome composition. We collected samples (N=287) from across the Yellow-rumped Warbler hybrid zone (*Setophaga coronata coronata* x *S. c. auduboni*), including from distantly allopatric sites. The narrow width of this hybrid zone (132 km wide) suggests some form of selection acts against hybrids, although the source of that selection has been unclear to date. We quantified gut microbiome variation using 16S amplicon sequencing of fecal samples, and also produced genome-wide sequence data for hosts in order to link warbler genotype to microbiome traits. This study represents a near range-wide analysis of microbiome variation across a species complex and yields important insights on the genetic factors that shape symbiotic interactions in avian systems.

***Detecting Two Secretive Marsh Species via Thermal Imaging is Comparable to Traditional Call-playback**

T Olsen, C Butler, T Barron

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Black Rails (*Laterallus jamaicensis*) and Yellow Rails (*Coturnicops noveboracensis*) are secretive species of marsh bird that winter along the Texas Gulf Coast. Both of these species are challenging to detect and traditional methods of detection utilize call-playback or rope-drags. Call-playback often requires up to 6-12 revisits in order to detect Black Rails consistently, while Yellow Rails require time intensive rope-drags in areas where they are suspected to occur. In 2023 and 2024 along the Texas Gulf Coast, we surveyed for Black Rails and Yellow Rails using two methodologies: a drone equipped with a thermal imaging camera and call-playback surveys, in order to compare detection probabilities and occupancy estimates. We used occupancy modeling to generate our detection and occupancy estimates in order to incorporate survey and site covariates that may influence detection probability. In February-June 2023, we recorded a total of 64 rails using thermal imagery: 39 Yellow Rails, 22 Black Rails, 2 Virginia Rails, and 1 Clapper Rail. Of the drone flights (4 revisits, n=49), we detected Yellow Rails on 44.11% of surveys (n=34, flights prior to migration) and Black Rails on 32.65% of surveys (n=49), compared to only detecting Yellow Rails on 12.90% and Black Rails on 46.93% of call-playback surveys conducted within the same time-period. Drones combined with thermal imaging camera may be a comparable method for detecting and monitoring Black Rails and Yellow Rails. Yellow Rails were detected particularly more frequently with the drone than with call-playback and may be an alternate method to consider during the winter when the individuals are less vocal.

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Machine-learning classification of food provisioning videos at nest sites of Flammulated Owls (*Psiloscops flammeolus*)

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In recent years, improvements in camera and data storage technologies have advanced the study of avian parental provisioning during critical nesting periods. Over four years of a long-term study in Flammulated Owls (*Psiloscops flammeolus*) from northern Utah, we deployed multiple modified trail camera systems inside of active nest boxes established by breeding pairs. Thirteen motion-triggered camera units collected about 57,000 ten second videos of potential food deliveries by parents per season. Separating actual provisioning activities from non-delivery recordings among so many videos requires tremendous community science and quality control efforts. To increase data processing efficiency, we tested an inflated 3-dimensional convolutional neural computer network using a deep learning approach to detect nest activity and delivery patterns. The system was initially trained on 400 different human activities and fine-tuned through subsets of quality-controlled owl delivery videos. We augmented videos before training by cropping sizes, adjusting brightness, and adding frame defects to teach the network to account for visual variation in videos of nests not included in the training data. Preliminary analyses based on approximately 3,000 training videos from five nests promise accuracy of proper behavior identification between 80 and 90 percent using cross validation. With such levels of precision, neural networks can aid in effectively labeling and cataloging owl behaviors from good quality videos or at least help in ranking videos to be reviewed by researchers when the visual recordings were more challenging.

Influence of sampling design on survival estimates from Motus detection data

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The Motus Wildlife Tracking network uses automated telemetry to detect tagged individuals across great distances, opening new opportunities to understand the ecology of migratory birds across the full annual cycle. However, the ability to estimate demographic parameters from Motus data is still untested and gaps in infrastructure across the network often result in sparse detection data. To improve parameter estimates, Motus collaborators need to understand how the spatial distribution of stations influence detection and estimation of key demographic parameters. Using simulation methods, I explore alternative sampling designs to determine how the spatial distribution and density of towers influences the accuracy and precision of seasonal survival estimates. Station distribution patterns explored in the analysis included fences, grids, randomly placed towers, and randomly placed towers but weighted towards areas of high focal species abundance. By simulating movement paths across each sampling array, I generated detection data and used a continuous-time, multi-state model to estimate survival rates during breeding, migration, and wintering periods. In addition to comparing fixed sampling designs, I also compare survival estimates for simulations based on the current Motus array and discuss approaches for deciding where additional towers should be placed to maximize their value for demographic rate estimation. Identifying optimal array designs that more accurately estimate demographic parameters will allow for the strategic installation of stations, which will be particularly useful for emerging regional partnerships aimed at maximizing the utility of the Motus network.

Uncrewed aerial systems provide a valuable tool for assessing duck production at local scales

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The primary goal of waterfowl conservation is to implement strategies to maintain or increase waterfowl populations. Maintenance of populations requires recruitment of new individuals into the population to offset mortality. Among upland nesting duck species, survival of potential recruits is largely dependent on habitat conditions. Hence, identifying breeding habitats that promote nest success, duckling survival, and ultimately recruitment is critical for effective waterfowl conservation. Recently, biologists in Wisconsin

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developed a decision support tool to guide waterfowl habitat restoration and retention efforts by ranking watersheds for conservation priority. The tool uses biological data to predict where breeding habitat exists for waterfowl, but the predictions of the tool have not been formally evaluated. To determine if predictions from the decision support tool accurately reflects habitats used by breeding ducks, we used uncrewed aerial systems (UAS) with thermal imaging to collect observations of breeding pairs and broods at 22 sites across a range of conservation priority rankings in Wisconsin during 2022 and 2023. We also examined potential drivers of variation in pair and brood densities at wetlands and examined the relationships between breeding pair and brood densities. The Wisconsin decision support tool provided an accurate assessment of local habitat quality for breeding waterfowl. Breeding pair density was correlated with brood density, and both are affected by local habitat conditions. UAS equipped with thermal capabilities allowed us to estimate productivity in an efficient and non-invasive manner. The use of decision support tools coupled with non-invasive UAS methods should be considered as an effective and efficient method to study waterfowl populations.

NAHPU: A modern, inclusive, and open-source digital catalog application for natural history collecting

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NAHPU (Natural History Project Utilities) is a modern, inclusive, and open-source digital catalog application, developed to streamline data entry in the field (e.g., collecting expeditions). NAHPU aids in responsible collecting by maximizing the use of each specimen (e.g., ensuring data association) and ensuring that collecting is replicable. The app simultaneously addresses the complexity of fieldwork (e.g., multi-tissue collecting, tissue quality tracking, space constraints), while eliminating secondary data entry errors for downstream data management. By leveraging the mobile revolution, NAHPU simplifies data acquisition and management, and supports inclusive collecting practices, both all of which are essential to efficient and collaborative field expeditions.

***Tracking Wildlife Movements with Networks of Fixed Radio Receivers**

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To estimate locations of individual animals, data from animal-borne radio tags can be analyzed by comparing the relative signal strength of the transmission across different receivers in the network. Automated collection of these data over time can provide wildlife movement and habitat usage information. In range-based methodology, the quality of the location estimates produced depends heavily on the calibration of the signal strength versus distance relationship and the method used to process the raw data into a location. In an attempt to produce location estimates at a finer spatial scale, a new grid search method for extracting high-quality location data from the raw signal strength data has been developed and tested on multiple networks of radio receivers. The accuracy of positions produced with this method have been shown to be 25 meters or less depending on the dimensions of the receiver network and the quality of the calibration. The ability to obtain location estimates with this level of accuracy from radio tags weighing as little as 0.35 grams enables the study of the fine-scale movements of species of bird as light as 12g (tag weight < 3% of body mass), which can not be tracked using GPS trackers. Test data demonstrating the accuracy of this new method with various receiver networks will be presented, alongside preliminary results from the deployment of radio tags on northern waterthrush (*Parkesia noveboracensis*).

Fine-scale tool for adaptive habitat management of Bicknell's Thrush using LiDAR-based metrics

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Airborne laser remote sensing (LiDAR) provides vegetation and ground height data with sub-meter accuracy, enabling fine-scale characterization of specific habitat attributes. We modeled the probability of occurrence of Bicknell's Thrush (*Catharus bicknelli*), a threatened bird species in Quebec and Canada, at a fine spatial scale (10 m resolution) in central Quebec (Canada) using LiDAR and ecoforestry map data. The model was calibrated using 139 field observations of Bicknell's Thrush positioned to an accuracy of 10 m and compared with random locations (10 random locations per observation) within a radius of 523 to 1,382 m, and validated with a completely independent dataset of 4,046 listening points. Thrush presence was higher at higher elevations, with a greater proportion of balsam fir, higher vegetation density and lower canopy height. We accounted for potential temporal changes in habitat by considering tree growth since LiDAR data acquisition and applying a temporal adjustment to canopy height, thus providing a more realistic and up-to-date annual model. The 10 m resolution used to calculate LiDAR metrics coupled with bird observations of the same accuracy enabled predictions at a consistent spatial scale. We suggest the use of different thresholds to target desired performance to achieve different habitat management or conservation objectives, and provide some examples of its application.

***Using drones equipped with thermal cameras to locate and count quail individuals and coveys: A case study using Northern Bobwhite in Mississippi, USA**

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The presence and abundance of Northern Bobwhite *Colinus virginianus* often relies on imprecise methods such as fall covey counts, which can lead to inaccurate estimates resulting in poor management practices. Drones equipped with thermal sensors have proven beneficial for monitoring wildlife but still require sufficient field validation regarding precision. We tested the application of thermal drones for locating and counting Northern Bobwhite in Mississippi, USA. We conducted flights over known locations of Northern Bobwhite representing three individual, radio-marked birds during the breeding season and seven covey locations during the wintering season shortly after dusk. Individuals and coveys were located in 67% and 86% of flights, respectively. In some scenarios, Northern Bobwhite could be seen from altitudes of 120 m because heat signatures of multiple individuals grouped together in the covey provided an easily recognizable feature, in contrast to individual birds alone. Counts were accurate for two coveys and underestimated remaining coveys, because individual birds were sometimes visually obstructed by vegetation from above. The small body size of Northern Bobwhite results in few pixels in thermal images and depends on ground sampling distance as a function of flight altitude. Our flights were tested at known vicinities of Northern Bobwhite locations, yet our method shows promise for locating unknown coveys as well. Future systematic methods may benefit from automated image recognition using computer vision and machine learning to improve count accuracy and save time, costs, and labor.

Assessing non-invasive survey methods for detecting Harlequin Ducks (*Histrionicus histrionicus*) on their breeding grounds in Montana and Idaho

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Long-term monitoring of Harlequin Ducks (HADU) in Montana, Idaho, and Alberta has documented population declines on their breeding grounds leading to broad concerns about population status in the Northern Rockies. Additionally, biologists have struggled to monitor the status and trends in the Northern Rockies breeding population due to their rarity and the ruggedness of their habitat. Previous methods have primarily relied on direct, in-person observations. However, results from these ground-based foot surveys are highly variable owed to factors outside the observer's control such as late spring flooding which can result in HADU nests being washed out and females leaving breeding streams earlier. This can affect detections of broods causing false negatives on potential breeding streams. Thus, there is a critical

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need to better understand the efficacy of existing methods and to explore other survey strategies to assess HADU population status and trends. We are comparing detection probabilities of eDNA, game camera, and ground-based foot surveys to determine their relative efficacy in detecting HADU on streams. Given that HADU breeding habitat is highly variable and complex, we are evaluating these methods as related to habitat covariates. During 2022 and 2023, we visited ten streams two times each season and tested our three methods over three days. We were able to detect HADU during the late incubation and the brood rearing season using all three methods. We will discuss field techniques and results of our efforts.

***Thinking outside the bird: Avian 3D digital models in natural history research and color analysis**

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Large-scale phenomic data from natural history collections holds the promise to combine with genomic data to understand phenotype-genotype interactions across space and time. However, unlike genomic data, phenomic data can be time-intensive to collect at scale. We report results from oBird, a hub grant of the oVert Thematic Collections Network, whose goal was to develop techniques for largely automated creation of 3D digital models of the outside of avian museum specimens for morphometric and color analysis. We developed a large catalog of digital bird specimen models in both human visible (VIS) and ultraviolet (UV) spectrums. In addition to developing and refining a rapid modeling technique, we use these models to visualize instances of UV and VIS avian color evolution. Birds have the capability to see into the UV and VIS light spectrum, many species also produce UV reflectance from their plumage indicating that UV may be used in visual communication. We imaged and modeled specimens in both spectrums to visualize color diversity and plumage patches across the entirety of each bird's exterior. We measured the proportion, placement, and intensity of UV reflective patches to investigate the evolution of UV coloration. We then compared the UV data to VIS color data to examine similar trends in the evolution of other colors. We find that UV coloration is widespread throughout birds and that UV and VIS coloration evolves at different rates in birds. Overall, we show that 3D digital models of bird museum specimens provide useful tools to collect and analyze large-scale color data in birds.

***Phylogenetic signal in immune system managed microbiota of Connecticut avifauna**

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Studies of host-associated microbiota in birds have thus far found weak evidence for the impact of host species on the composition and diversity of gut bacteria; instead, environment, diet, and period of the annual cycle appear to be the primary factors driving structure of gut microbiota. However, specific subsets of an individual's microbiota may be managed by host associated factors such as the immune system. One function of the adaptive immune system of birds is to act as a barrier between bacteria in the gut and the circulatory system. Here, we adapt Ig-Seq, a method of targeting and separating immunomodulated populations of gut bacteria, to an avian model and test this method on a broad taxonomic sampling of Connecticut avifauna using two immunoglobulins, IgA and IgY. We test the hypothesis that microbiota in feces that have interacted with the bird's immune system will contain stronger phylogenetic signal than non-interacting microbiota, as recognition by the immune system may imply historical interactions important to a host species' fitness. We characterize the taxonomic and functional composition of gut microbiota from 20 bird species and use a comparative phylogenetic approach to determine if and how the avian gut microbiota is influenced by host species. This study provides a novel approach to increased understanding of the relationship between birds, the immune system, and their associated microbial symbionts.

Where does the microbiome come from? Investigating in ovo microbial

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colonization in house sparrows**S Wolfe, B Trevelline, M Rowe**Presenting author: **Sophia Wolfe**, sww64@cornell.edu

The gut microbiome is critical for the development and physiology of host organisms. Recent evidence suggests that in oviparous taxa, gut microbiota may be acquired in ovo, possibly via maternal transmission or via trans-shell penetration of bacteria from the nest environment. However, the relative contributions of these potential pathways to gut microbiome composition are not well resolved. Furthermore, whether gut microbiota contribute to embryo growth and survival is currently unknown. In this study, we used eggs from captive house sparrows (*Passer domesticus*) to explore the likely mechanisms of microbiome acquisition, investigate the potential correlation between egg microbiota and embryo phenotype, and test whether eggs harbor a microbiome that can colonize a developing embryo. We examined the microbiota of (1) eggs dissected immediately after lay to assess microbiome composition early in development (and to limit any trans-shell penetration by environmental bacteria); (2) eggs collected immediately after lay that were surface sterilized and incubated under sterile conditions (and thus free of environmental influence throughout development); and (3) eggs that were incubated under natural conditions (to assess microbiota of embryos exposed to maternal and environmental influences throughout development). We compared the microbiota of eggs and embryos across these groups using both culture-based methods and culture-independent sequencing techniques (16S rRNA amplicons), then linked this data to embryo mass and survival. This study provides new insights into the sources of microbiome acquisition and the role of the microbiome in development.

The gut microbiome influences digestive phenotypes in a wild passerine*B Trevelline, J Houtz, J Sanders, C Andreadis, N Morris, M Rowe, A Moeller**Presenting author: **Brian Trevelline**, Kent State University, brian.trevelline@gmail.com

The digestive system is a major interface between an animal and its environment, and harbors complex microbial communities that can profoundly influence host phenotypes. However, the vast majority of this research has been conducted in model organisms, leaving a large knowledge gap regarding how the gut microbiome shapes the phenotypes of wild vertebrates. Advancement has been further slowed by a lack of diverse animal models reared under germ-free conditions in which microbiome composition can be precisely controlled, precluding experimental investigation of the impacts of the microbiome on vertebrate ecology and evolution. We used a novel experimental system to generate germ-free House sparrows (*Passer domesticus*) to experimentally test whether the gut microbiome affects avian digestive phenotypes. We hand-raised a total of 27 germ-free sparrow hatchlings, the gut microbiome of which were compositionally indistinguishable from negative controls, demonstrating the feasibility of generating germ-free birds using simple aseptic techniques and open-source gnotobiotic isolators. After hatching, chicks were hand-raised on sterile formula and were inoculated with either sterile water (germ-free) or 7.5 mg of adult sparrow feces (conventionalized) 7-times per day for 7 days. Conventionalized sparrows exhibited enhanced development of digestive organs compared to germ-free individuals, providing the first experimental evidence that the gut microbiome shapes host digestive phenotypes in a non-model vertebrate. These results demonstrate that the gut microbiome is essential to the digestive function of wild passerines, which may have far-reaching consequences on animal physiology, performance, and its role in the environment.

Disentangling relationships between diet and gut microbial diversity in American Kestrel nestlings*J Houtz, M Melo, J Therrien, A Cornell**Presenting author: **Jennifer Houtz**, Allegheny College, jhoutz@allegheny.edu

Gut microbiota are increasingly recognized as important drivers of host health and fitness across vertebrate taxa. Given that gut microbial composition is directly influenced by the environment, gut microbiota may also serve as an eco-physiological mechanism connecting host ecology, such as diet, and physiology. Although gut microbiota have been well-studied in mammalian systems, little is known about

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how gut microbial diversity and composition impact morphological and physiological development in wild birds. Here, we characterized both diet and gut microbial diversity of free-living American kestrel (*Falco sparverius*) nestlings throughout development to test whether gut microbial diversity predicts host morphological and physiological traits in either contemporary or time-lagged manners. Gut microbial alpha diversity on day 21 of nestling development was positively correlated with diet alpha diversity representative of the majority of nestling development (days 5–20). Gut microbial alpha diversity early in development was negatively correlated with body mass in both contemporary and time-lagged manners. Gut microbial alpha diversity early in development was positively correlated with blood glucose later in development. As nestlings experience rapid growth demands in preparation to fledge, these time-lagged associations may indicate that gut microbial diversity at early critical developmental windows may determine the future trajectory of morphological and physiological traits underlying metabolism that ultimately impact fitness.

****The spatiotemporal distribution of nocturnal bird migration across a tropical landscape**

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The study of migratory birds has yielded innumerable insights into ecology, evolution, and environmental change-but past research and their resulting insights have been strongly biased towards the temperate northern hemisphere. The lack of information about migratory flyways in the tropics hinders efforts address rapid population declines. To address this knowledge gap, we quantified the dynamics of nocturnal migration across Colombia, a strategically located country for birds entering and leaving South America. We leveraged a network of weather surveillance radars and autonomous recorders to estimate and compare the volume, height, and flight directions of birds at three sites across four years. We observed migration dynamics that differed markedly from the weather-driven paradigm that characterizes temperate latitudes. Instead of observing episodic pulses of birds, we documented gradual passage of migration within a season, where calendar day was the dominant variable explaining migration passage, rather than wind assistance. Wind support did not explain the volume of birds aloft, but did help explain the altitudes at which birds chose to fly, likely due to the consistency in how wind direction changes with altitude in the tropics. We also found spatial and seasonal variation in the magnitude of migration, with the highest estimated numbers of birds within the Magdalena River Valley. Birds in our study region oriented north towards the Caribbean in spring, with minimal evidence of north-westerly directions towards Central America. Without reliance on wind support, departures from South America must be heavily dependent on fuel, highlighting the urgency in managing critical stopover habitat. Our results are the first to document the relationship between atmospheric conditions and regional bird migration in South America.

Seasonal weather and autumn migration timing of North American raptors

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Climate change is advancing the timing of spring arrival across migratory bird species, but shifts in autumn migration timing are more variable. These diverse responses may be the result of differences in weather correlates of autumn departure timing across species. We used eBird and Daymet data to assess the relationship between the departure timing of four migratory raptor species (Broad-winged Hawk, Osprey, Swainson's Hawk, and Turkey Vulture) and four weather variables (maximum temperature, minimum temperature, precipitation, and snow) from 2002 to 2021. We used a sliding window analysis to find the periods within the year when each weather variable best predicted a species' departure timing. We then created full weather models for each species and used climate data from NA-CORDEX to forecast departure timing from 2022-2075. The period of sensitivity to each weather variable differed between species, and included evidence of some carry-over effects from the breeding season. Maximum temperature was correlated with departure timing for all species, minimum temperature and precipitation were correlated with the departure timing of several species, and snow was only correlated with timing for Broad-winged Hawks. The forecast analysis showed that Swainson's Hawks and Osprey will advance

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their autumn departure and Turkey Vultures will delay their autumn departure. We used an exploratory approach to assess the unique environmental factors related to the autumn departure timing of four common migratory raptor species and predicted possible shifts in departure timing given these relationships. This approach provides potential for assessing species-specific factors related to shifts in phenological events.

Migration and stopover ecology of Western Willet in the U.S. Great Plains region

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Many shorebird species travel long distances through a range of environmental conditions while relying on a network of stopover locations to rest and refuel. Migrant shorebirds in the U.S. Great Plains may be more vulnerable to these conditions than other birds due to the extreme nature of weather events in this region and variable availability of stopover habitat. We used Willets (*Tringa semipalmata*) as a model species to assess the influence of environmental conditions on migrant shorebirds. Specifically, we sought 1) to describe and quantify Willet migration ecology (dispersal and habitat use) in the Great Plains and 2) to evaluate how migration characteristics like stopover duration, distance of flights between stopovers, and habitat use at stopover sites are influenced by environmental variables like weather, surface water availability, and land cover types. We GPS-tagged 18 Western Willets on their nonbreeding grounds along the Texas Gulf Coast in 2022 and 2023. Preliminary results show that northward migration lasted 5.3 ± 2.9 days with 4.0 ± 2.6 stopovers/migration, and southward migration lasted 6.2 ± 4.6 days with 1.5 ± 2.6 stopovers/migration. We used geospatial analysis to examine land cover characteristics of stopover locations. Willets used locations with land cover compositions different than those available at random locations within a 1 km radius ($\chi^2 = 77.0$, $p\text{-value} = 1.04 \times 10^{-10}$); Willets exhibited a preference for stopover sites containing emergent herbaceous wetlands and not containing cultivated crops. This study gives insight into Willet migration ecology and will refine projections of shorebird responses to environmental condition variability, which will become more extreme with climate change.

The spatiotemporal effects of seasonal migration on avian community assembly

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The annual movements of seasonally migratory birds, which travel between separate breeding and non-breeding distributions, bring about profound spatial redistributions of biodiversity multiple times per year. Migrants are exposed to different combinations of environmental conditions and species interactions over space and time, while also bringing about continuous disassembly and reassembly of bird communities as they move through their annual cycles. However, the relationship between seasonal migration and community assembly remains poorly explored. To bridge this gap, we assess spatiotemporal variation in phylogenetic community structure in North American songbird communities as a consequence of migration-driven turnover in community composition. Using eBird species distributional models, we generated weekly estimates of the phylogenetic dispersion of passerine communities across North America and throughout the annual cycle. We find that as seasonal migrants drive shifts in spatial patterns of passerine biodiversity, their movements bring about analogous spatial redistributions in continental-scale patterns of phylogenetic community structure. This finding suggests that the movements of migrants drive seasonal variation in the predominant phylogenetic community dynamics of passerine communities, revealing the influence of seasonal migrants in driving diversity patterns at multiple scales of spatial organization.

****Stopover ecology and conservation of migratory landbirds in the eastern United States**

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Migratory landbirds are experiencing dramatic population declines in North America, but little is known about the important habitats they use as stopover sites during migration. We used data from weather surveillance radar to map seasonal stopover densities of landbirds across the eastern U.S. during spring and autumn migrations. We identified stopover hotspots covering 2.47 million hectares that consistently support high densities of migrants across years. However, only 16.7% of these sites are hotspots in both seasons. Deciduous forest is the most important habitat type, with high concentrations of birds in forest fragments embedded in broadly deforested regions, especially in spring. While protected areas have higher stopover densities of birds, only 1/3 of hotspots are covered, and many of these protected areas are still subject to extractive uses. We also found evidence that the agricultural Midwest is an anthropogenic migration barrier for many landbirds, affecting their flight and stopover behaviors. In summary, a well-distributed network of well-protected stopover areas, complementing conservation efforts on the breeding and wintering grounds, is essential to sustaining healthy populations of migratory landbirds in North America.

****Crossing the Strait: Wind and uplift facilitate route selection for a soaring migrant in spring**

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Ecological barriers influence migratory routes resulting in the formation of detours. Among facultative and obligate soaring raptors, various flight strategies are used during migration. Both use favorable winds and thermals to successfully migrate. However, obligate soarers are reliant on atmospheric conditions as prolonged flapping flight is expensive energetically. Therefore, obligate soarers circumvent large expanses of water and cross at geographical bottlenecks, minimizing the amount of open water they cross to save energy. Few studies have directly investigated how atmospheric conditions influence route choice and water crossing behavior during northbound spring migration at a high concentration bottleneck. Here we use the Red-tailed Hawk, *Buteo jamaicensis*, to investigate this question at the Straits of Mackinac in North America. 36 GPS transmitters were deployed during spring migrations spanning 2021-2023. We recorded 54 water crossings; each was categorized as either optimal or non-optimal based on the amount of water crossed. Crossing events were annotated with atmospheric predictors including wind speed, wind direction and uplift potential to elucidate what conditions predict the use of either route by Red-tailed Hawks. We found uplift potential has a significant effect on both route choices. When uplift is available it aids in sustaining lift, leading to a crossing event. Wind speed and wind direction also affected route choice among individual hawks. Overall, light supportive winds promoted an optimal route choice, while light crosswinds promoted the use of a non-optimal route to complete the cross. We provide evidence showcasing the behavioral plasticity of Red-tailed Hawks when they cross open water in a unique freshwater system. Our findings corroborate that crossing strategies are dynamic and change depending on the local weather. However, conditions selected, ultimately influence route choice, timing, and strategy during spring migration.

****The ecological importance of Delaware Bay near-shore habitat to transient songbirds during migration**

T Mohyuddin, C Heckscher

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Nearctic-Neotropical migratory songbirds are experiencing dramatic population declines, partly due to habitat loss. Boreal-breeding songbirds are of particular concern. Sea level rise (SLR) is a significant cause of coastal habitat loss, especially along the Delaware Bayshore, where rates of SLR are approximately twice the global average. The Delaware Bay is centrally situated along the Atlantic flyway. The role of the Bayshore as a globally significant stopover region for migratory songbirds is unknown. In the present study, we investigated migrant use of a forested coastal saltmarsh hummock via mist-netting at Milford Neck Conservation Area, Kent County, Delaware. We collected data during spring and fall migration, from April to May of 2020 and 2021, and from September to November in 2020 and 2023. Each individual captured received an individually numbered USGS leg-band, and we took morphometric

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measurements. Adjusted for effort, the total number of migrants each season was over 100 birds per 100 net hours, significantly higher than capture rates at important stopover sites elsewhere along the Atlantic Coast. Weather was a significant predictor of both total migrant and boreal migrant abundance, while capture time was a significant predictor of age in boreal migrants. Our results are the first to thoroughly quantify the use of the Delaware Bay coast to migratory songbirds using capture-recapture techniques. The results of this study, combined with existing data from research on SLR in Delaware Bay, can be used to identify and prioritize focal areas and coastal habitats for conservation, management, and restoration.

****Migratory airspace corridors and stopover habitat landscapes identified for four declining Nearctic-Neotropical migrant birds**

R Brodie, A Roth, A Buckardt Thomas

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Nearctic-Neotropical migrants undertake harrowing journeys during autumn and spring migration that are consequential for survival and fitness. Migrating forest birds navigate landscapes characterized by forest-to-agriculture conversion, urban development (buildings and light pollution), and forest fragmentation. Despite our knowledge of the risks associated with migration, airspace and stopovers used during migration are poorly understood. Species vary in migratory connectivity strength and patterns; thus, we developed spring and autumn migratory corridors for four Nearctic-Neotropical migratory forest birds experiencing population declines: Canada Warbler (*Cardellina canadensis*), Cerulean Warbler (*Setophaga cerulea*), Golden-winged Warbler (*Vermivora chrysoptera*), and Wood Thrush (*Hylocichla mustelina*). We combined several telemetry tracking data types with eBird Status and Trends products to estimate migratory connectivity, produced least-cost paths, and developed integrated migratory airspace corridors. Additionally, we focused on identifying important stopover habitat landscapes as a starting point for future localized stopover habitat modeling. A hierarchical modeling framework was used to characterize stopovers (landscape scale) within spring and autumn migration corridors. In addition to quantifying the amount of stopover habitat within each corridor, finer-resolution (~2 km²) environmental covariates were analyzed to assess habitat selection in landscapes shared by the four focal species during migration. This research is an important preliminary step to assessing survival and fitness during migratory periods and will inform full-annual cycle conservation planning.

***Do Magnolia Warblers and American Redstarts utilize flight calls for intraspecific or interspecific communication?**

A Sidare, S Morris

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Prior studies have shown that migrating warblers respond to flight calls from conspecifics, indicating the use of such calls for intraspecific communication. Given the overlapping migration timing of many warbler species, flight calls may also serve as a means of interspecific communication. This study aimed to compare the flight calling behavior of two warbler species, American Redstarts (*Setophaga ruticilla*) and Magnolia Warblers (*S. magnolia*), in response to conspecific calls versus a variety of mixed species calls. We hypothesized that birds would respond more frequently to conspecific recordings compared to mixed species recordings, particularly those devoid of conspecific calls. Collaborating with the Appledore Island Migration Station in Maine, we conducted experiments using captive warblers in a soundproof chamber. Birds were exposed to conspecific recordings, mixed species recordings with conspecific calls, or mixed species recordings lacking conspecific calls. We assessed each individual's vocal responses. American Redstarts responded most to conspecific recordings and least to mixed recordings lacking conspecific calls (Likelihood Ratio=28.6, df=2, $p<0.001$). Similarly, Magnolia Warblers showed the strongest response to conspecific calls and the weakest to mixed recordings without conspecific calls. (Likelihood ratio=54.98, df=2, $p<0.001$), with no significant difference observed between the mixed species cues ($p=0.23$). Both species were more likely to respond to both mixed cues as opposed to spontaneously ($p<0.001$). These responses demonstrate that while intraspecific communication appears predominant, the response to mixed species cues suggests a potential role of flight calls in interspecific communication.

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GulfCast: a forecasting system for spring trans-Gulf bird migration arrival events**A Abbott, K Horton***Presenting author: Annika Abbott, Colorado State University, annika.abbott@colostate.edu*

Each spring, more than two billion birds migrate through the Gulf of Mexico region en route to breeding grounds in North America. As part of these migrations, many birds make energetically taxing, nonstop overwater flights across the Gulf of Mexico. This makes the northern Gulf coast region critical for migratory birds as it provides the first possible stopover habitat for resting and refueling following trans-Gulf crossings. The importance of this stopover habitat, coupled with increasing anthropogenic threats in the Gulf region, makes migrants vulnerable and highlights a need for conservation action. Ecological forecasting presents a valuable tool for advancing conservation in this critical region by predicting key periods of high migratory activity. Here, we built and evaluated a migration forecasting model using twenty years of weather radar and atmospheric data from the Gulf region to predict spring trans-Gulf migration arrival events on a day-by-day basis. By providing details on when high numbers of migratory birds will make landfall, this forecasting system has conservation utility for mitigating threats such as light pollution and wind energy infrastructure, while also engaging birdwatchers and the public more broadly.

A slippery slope: Precipitation niche breadth determines monsoonal down-slope elevational shifts of passerine birds in the Western Ghats of India*V Akshay, C Campbell, M Belitz, B Loiselle, R Guralnick***Presenting author: V. A. Akshay, akshayvinodanand@ufl.edu*

Avian elevational migration is the seasonal movement of birds along elevational gradients. Past research has focused on shifts between breeding and non-breeding grounds, with little attention to movement during complete annual cycles. Here, we quantified elevational migration of resident passerine birds across three seasons in the Western Ghats of India, and tested body size, dispersal ability, environmental tolerance and diet as potential drivers of elevational migration distance. We used eBird data between 2013 - 2023 to quantify elevational migration. We calculated seasonal bias-adjusted median elevational quantiles for 174 resident species, and quantified distance as the difference between seasonal median elevations per species. We built Phylogenetic Generalized Least Square (PGLS) models to test the effect of body size, dispersal ability, environmental tolerance and diet on elevational migration distance. We found 75 species (43%) to be elevational migrants in at least one season. Species predominantly shifted down-slope (86%) during the monsoons (June - October), and up-slope (81%) in the summer (March - May), with no clear pattern in the winter season. PGLS models determined that species' precipitation niche breadth was negatively associated with elevational migration distance in the monsoon, however winter and summer shifts yielded no significant results. These findings suggest that monsoonal conditions drive species to shift their elevational distribution down-slope, adding support to the reduced foraging opportunity and physiological tolerance hypotheses. Further, our bias correction method is generalizable to large scale citizen science data, opening new possibilities for macroecological research.

Rest, refuel, recover: Investigating the physiological importance of a Lake Ontario stopover site for Swainson's Thrushes (*Catharus ustulatus*) during autumn migration**G Orfanides, A Soule, J Salto, L Travers, S Pagano***Presenting author: Susan Pagano*

Stopover events serve many roles for migratory birds, and understanding the ways by which birds use stopover habitat can inform conservation and habitat management plans. However, few studies have thoroughly investigated the roles of stopover for birds outside of refueling events, much less provided direct evidence as to how physiological metrics in birds change over the course of stopover. In this study, we sampled Swainson's Thrushes (*Catharus ustulatus*) at Braddock Bay Bird Observatory (BBBO) on the

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south shore of Lake Ontario to investigate stopover patterns of this species at the site. A blood sample was taken from nearly all individuals captured during a singular fall banding season at BBBO-including any subsequent day recaptures-to derive the most complete possible picture of stopover habitat use and migration patterns. We measured plasma metabolites to assess refueling state and nutritional condition, and we used leukocyte counts and the bacterial killing assay to evaluate immune condition. Additionally, we molecularly sexed all individuals to explore sex-related patterns in physiological condition and migration strategy. Physiological metrics were primarily analyzed in the context of sex, migration timing, and-for recaptured individuals-time spent at a stopover site. Results provide insight into the importance of stopover for physiological recovery in songbirds and biological factors that may influence stopover habitat use and migration patterns.

***The evolution of migration is associated with distinct climates in temperate-versus tropical-breeding birds**

E Johns, O Johnson, M Harvey*Presenting author: Emily Johns*, University of Texas at El Paso, ejohns@miners.utep.edu

Avian migration, particularly long-distance seasonal migratory movements, have captured researchers's attention for many years. However, the evolution of migration remains obscure, in part due to limited understanding of the full range of migratory strategies such as short-distance and intratropical movements. We examine the climatic drivers of migration in suboscine birds, a group of roughly 1,300 primarily Neotropical species with a complex array of migration strategies. Our reconstructions of the evolutionary history of migration reveal that migration is lost approximately twice as often as it is gained, highlighting the lability of migratory behavior in the group. We find that, as predicted, migratory behavior in temperate-breeding, long-distance migrant suboscines is driven by temperature seasonality, presumably associated with the vacation of high latitudes to avoid resource drought in winter. Short-distance migration in tropical-breeding species, however, has evolved in association with seasonality in precipitation. Tropical regions with high precipitation seasonality contain a mix of migrant and non-migrant species, but a higher proportion of species vacate these areas than tropical regions with more stable precipitation. The contrasting impacts of climate on the evolution of avian migration across species and regions highlight the complexity of climate-movement associations and the challenges associated with identifying how future climate change might impact organisms depending on the drivers underlying their migratory behavior.

***Migratory behavior influences annual seasonal resource dynamics in an inland shorebird**

A Pierce, P Marra, A Harrison, M Wikelski, C Duchardt, S Dinsmore, M Wunder*Presenting author: Allison Pierce*, allison.pierce@ucdenver.edu

Seasonal migration is well researched behavioral phenomenon pervasive across the animal kingdom. Yet, the eco-evolutionary drivers of migrations are still poorly understood in most migratory species. Migratory behavior is an adaptive strategy for coping with seasonal dynamism of the environment and is an integral component of complex life history dynamics mediated by metabolism. In this study, we used this framework to evaluate the extent that seasonality is a migratory driver in Mountain Plovers (*Anarhynchus montanus*), a partially migratory inland shorebird. We used direct tracking of migrating plovers to characterize the extent migration modulated seasonal dynamics in food resources approximated by sub-surface soil temperature and vegetative greenness (NDVI) experienced during the annual cycle. We found that migratory behavior in plovers results in dampening of seasonal variation in resources except during the early breeding season. Furthermore, we found reduced seasonal variation in food resource proxies where non-migratory plovers are known to occur compared to breeding locations used by migrants. Our results suggest that seasonal resource dynamics may be a driver of migration but that other factors such as reproductive timing and/or differential survival may influence life history trade-offs and contribute to the nature and maintenance of migratory behavior in the species.

***Population declines and phenological shifts are changing migrating bird**

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communities**J DeSimone, E Dalton, L DeGroote, M Furst, S Morris, A Patterson, E Cohen***Presenting author: Joely DeSimone*, University of Maryland Center for Environmental Science, joely.desimone@umces.edu

Seasonal bird migrations are characterized by numerous species sharing the airspace and stopover sites often in high densities, providing opportunities for a variety of species interactions that could influence migratory success, including competition and the transfer of diseases or social information. The rapid declines of many migratory species and species-specific shifts in migration timing are both likely contributing to changes in the co-occurrence of migrating species, with consequences for the degree and type of species associations and interactions among migrating birds. For instance, steep population declines of a species that historically signaled high quality stopover habitat reduces the availability of that social information for other species or, conversely, those same declines could reduce competitive effects. At the same time, differential phenological shifts could form or dissolve interspecific relationships as temporal co-occurrence increases or decreases. We analyze data collected from five bird observatories across eastern North America over the past 3-5 decades, characterize overall phenological shifts and changes in species abundance, and demonstrate that temporal co-occurrence is significantly changing for numerous species pairs. Bray-Curtis dissimilarity analyses reveal that the stopover communities early, late, or at the peak of a migration season are significantly changing over time, influenced by a combination of phenological shifts and species abundance changes. Our results encourage a view of migration that considers the effects of population processes on entire stopover communities of co-migrating species.

Unexpected behavioral alteration in migrating birds around artificial light at night**D Osterhaus, K Boland, A Lawson, K Horton, B Van Doren, P Cutler, T Wright, M Desmond***Presenting author: Dylan Osterhaus*, dylano@nmsu.edu

Artificial light at night (ALAN) interferes with in-flight behaviors of avian migrants and may lead to mortality at lighted structures. While studies have examined how ALAN at large-scales impacts migration, finding increased call rates in association with ALAN, few have documented the behaviors of migrants around individual or small sources of ALAN. To address this question, we collected full-night acoustic recordings during fall migration at 50 sites in 2021 and 55 sites in 2022 in southern New Mexico within an ~550 km² area. Half of the sites were illuminated by small sources of ALAN. We used the Nighthawk algorithm to generate counts of flight calls and compared between sites with and without ALAN. We used generalized linear mixed models to examine the relationship between call counts and the presence of ALAN and examined covariates corresponding to temporal variables that may affect migration. We tallied 2.34 million calls in 65,568 recording hours with most calls given by Parulids (38%) and Passerellids (54%). We found that small sources of ALAN altered in-flight migration behavior, with call counts being lower at illuminated compared to dark sites. However, this difference was only seen early in the migration season. Additionally, we found the strongest difference in call rates between lighted and dark sites during the middle of the night. Regardless of lighting, call rate increased throughout the night and decreased over the migration season. Our findings contrast directly with other studies of call rates as they relate to ALAN. Further research is needed to determine whether differences in call rates are caused by avoidance of ALAN or altered calling behavior, both of which are irregular and unexpected behaviors.

Navigating transitions in the US Central Flyway: the annual timing of songbird migration tracks seasonal waves and changing land surface conditions in the fall more than spring*C Adams, M Tomaszewska, G Henebry, K Horton***Presenting author: Carrie Ann Adams*, Colorado State University, caadams1@ualberta.ca

Understanding the relationship between songbird migration and environmental cues is crucial for assessing the impacts of climate change on avian life histories. We investigated the synchronization of

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spring and fall migration phenologies with environmental conditions across latitudes and years in the US Central Flyway. We examined the influence of temperature, Enhanced Vegetation Index, relative humidity, and land surface green-up/dormancy on migration phenology, using 10%, 50%, and 90% cumulative passage dates from radar observations. Contrary to expectations, spring migrants did not track any conditions across latitudes, suggesting they prioritized optimizing arrival phenology over resource tracking en route. Conversely, peak fall passage occurring approximately 30 days before the dormancy date across all latitudes, indicating that migrants may have tracked a specific vegetation phenophase, such as fruiting, as it progressed southward to fuel their migration. While annual changes to spring migration phenology were primarily driven by temperature, fall migration phenology displayed flexibility in adjusting to interannual changes in various environmental conditions. Our findings underscore the close relationship between vegetation-related indices and fall migration phenologies, raising concerns about potential phenological mismatches during this less-explored migration season. Despite the observed phenological plasticity, long-term trends indicate substantial changes in temperature and land surface phenophases experienced by migrants. For migratory birds, phenological adaptation has not been sufficient to mitigate climate changes within the flyway that may impact resource availability.

Impacts of climate change on songbird condition during migration

C Ramos*Presenting author: Claire Ramos, Colorado State University - Pueblo, claire.ramos@csupueblo.edu*

Conservation of migratory songbirds can be particularly challenging as these animals require three distinct habitats for successful completion of their life cycle: breeding habitat, wintering habitat, and migratory habitat. The migratory phase of the life cycle of these animals may be the most critical as migratory behavior is physiologically stressful and dangerous. This was clearly demonstrated by a mass migratory songbird die-off that occurred in early Sept. 2020 in the southwestern United States. Thousands of dead migratory birds were found over the span of just a few days. It is thought that this die-off was a result of a lethal combination of drought conditions reducing food availability, poor air quality caused by wildfires, and a freak snowstorm. In the southwest, the frequency of drought, wildfire, and severe weather is predicted to become more common as the climate continues to change, increasing the challenges faced by migratory birds. Migratory songbirds were captured and their condition assessed during migration in Southeastern Colorado. Measurements of condition were found to be correlated with drought and air quality indices, however there is variation in how different groups of birds respond to these challenges. These data represent a starting point to help understand how birds respond to environmental challenges. Future research will focus on additional measures of physiological stress and individual survival.

The influence of weather, geography and species' natural history on reoriented diurnal songbird migration in the Keweenaw Peninsula, Michigan

Z Gayk, B Van Doren*Presenting author: Zach Gayk, Copper Country Audubon, zachgayk@gmail.com*

Examining how songbirds (Passeriformes) migrate over dangerous water bodies has value for understanding their behavior and migratory ecology. Millions of songbirds fly over the Great Lakes region of North America each spring and fall. As songbirds encounter strong westerly winds while crossing the Great Lakes, migrants may experience nocturnal wind drift, and subsequent diurnal reorientation, which has been poorly studied. We surveyed diurnal songbird migration along the south shore of Lake Superior in the Keweenaw Peninsula, Michigan by recording songbird flight calls at 12 sites in spring and fall from 2022-2023. We wanted to understand the influence of nightly wind patterns on the occurrence and size of diurnal migratory movements along the Keweenaw Peninsula, as well as the influence of local geography on diurnal migration. We used a machine learning model (Nighthawk) to detect and classify flight calls in 9720 hours of acoustic recordings. We found 1.7 million preliminary flight call detections of 110 taxonomic groups of migrants at our 12 sites in 2022-2023. We found that wind direction predicted the occurrence and size of diurnal migration in the Keweenaw Peninsula, with the largest movements occurring the morning after westerly winds over Lake Superior. We observed seasonal differences in the route of

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songbirds, with more spring detections on the north shore of the peninsula, and more fall detections on the south shore. We also found species-specific differences in the abundance of diurnal migrants, which may indicate that species' flight speed, mass, and migratory strategy may predict their susceptibility to wind drift and subsequent diurnal migration.

Shifting gears in a shifting climate: birds adjust migration speed in response to spring vegetation green-up

B Amaral, C Youngflesh, M Tingley, D Miller

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Globally, forty percent of all birds migrate seasonally, a strategy that allows them to track their climatic niches and maximize time spent in favorable habitats. The benefits of migration depend on birds' ability to overlap the peak of resources in space and time using a combination of endogenous and exogenous cues. While birds shift their migration phenology in response to changing climate, the mechanisms by which this happens are poorly understood. Here, we investigate the spring migration speed of 55 species of eastern North American Passerines. We focus on whether birds use vegetation green-up, a measure of spring arrival, as a cue to shift their migration speed; and if so, how changing migration speed affects arrival time at breeding sites. We calculated speed at the migration front using arrival dates derived from 16 years of eBird data. Similarly, we calculated the advancement speed of forest vegetation green-up using satellite data. On average, songbirds migrate northward during spring at a mean speed of 63 km/day. We observed strong non-linear effects of latitude, with bird migration speed accelerated, and green-up speed slowed as the distance from the equator increased. Annual and spatial variation in bird migration speed depended on the local green-up date and how quickly green-up was advancing northward: years with earlier and faster green-up were associated with higher migration speeds. Bird arrival relative to green-up was strongly influenced by two variables: how early green-up was, and how fast birds were migrating. This suggests birds can shift migration speed to 'catch up' with earlier springs. However, the stronger effect of green-up date compared to migration speed suggests that birds do not fully compensate for arrival time by simply migrating more quickly. Climate change will likely outpace birds' ability to speed up their migration and adapt to new phenological regimes.

Linking energetic constraints to thermal variation during spring migration for northern pintail under current and projected climatic conditions

J McGovern, E Tanner, G Eccles, K Kraai, D Collins, P Link, C Overton, M Casazza, M Cline, J James, C Hilton, B Ballard

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Climatic variation during spring migration compounds energetic costs to birds already under selective pressure to maximize fitness by balancing time and energy requirements en route. For example, thermal stress associated with thermal variation adds physiological costs. Energy expended to respond to these physiological stressors can further compound energetic requirements at multiple scales, and can carry implications for subsequent fitness. Under projected climate change scenarios, increased incidence of extreme weather events and warming trends may further constrain activity patterns and energetics during migration. The northern pintail (*Anas acuta*; hereafter, 'pintail') arrives earlier than most dabbling duck species to breeding areas of the Prairie Pothole Region of North America. This likely exposes individuals to the species' lower thermal limits. Pintail also demonstrate earlier migration related to spring warming trends. We will use spring migration data from female pintail fitted with GPS/GSM transmitters, equipped with accelerometers, in their Southwestern U.S. wintering range (n= 203; 2019-2023). We will examine the constraints thermoregulation may place on migratory activity under present and projected climatic conditions. To accomplish this, we will model the relationship between standard metabolic rate (based on microclimate model-predicted air temperatures) and overall dynamic body acceleration (energy expenditure) using generalized additive models. This will allow us to predict the effects of climate change on migration activity patterns. We expect our approach will provide a more mechanistic understanding of avian migration energetics in relation to present and projected climatic conditions, and inform adaptive

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conservation planning.

Characterizing candidate migration genes across the parulid warbler radiation**S Szarmach, K Bennett, A Wood, D Toews***Presenting author: Stephanie Szarmach, The Pennsylvania State University, sjs7465@psu.edu*

Many migratory traits have a genetic basis, and candidate genes associated with migratory variation have been identified through within-species comparisons of populations differing in migration strategy. While certain genes seem to influence migratory traits in multiple species, it remains unclear to what extent parallel genetic mechanisms are responsible for the repeated evolution of similar migratory phenotypes. Previous work comparing candidate genes across avian orders found that genetic variants did not consistently differ between migratory and sedentary species at a broad taxonomic scale. However, instances of parallel evolution may be more likely in closely related passerines with a strong innate migratory program. The parulid warblers are one such group exhibiting a diversity of migration strategies where migration has been lost and gained multiple times. We used a phylogenomic approach to explore whether variation in candidate genes is associated with variation in migratory traits across 103 species in the parulid warbler radiation. We first compared divergence across the genomes of sister species pairs differing in either migratory propensity or distance and determined whether regions of high divergence overlapped with candidate genes. We then compared phylogenetic trees constructed from candidate gene sequences to the parulid species tree to identify instances of parallel divergence or introgression. Finally, we assessed rates of sequence evolution in candidate migration genes in migratory compared to sedentary species and long-distance compared to short-distance migrants. This study provides insights into the molecular evolution of a complex behavioral trait across an avian radiation.

Migration distance and genetic diversity are strongly correlated in the boreal avian assemblage*T Pegan, A Kimmitt, B Winger***Presenting author: Teresa Pegan, tmpegan@umich.edu*

Bird species that breed at high latitudes vary considerably in the location of their nonbreeding ranges, which has implications for rates of overwinter survival and potentially for demographic stability. In the North American boreal avian assemblage, species migrating long distances to low latitudes experience higher annual survival than short-distance migrants and nonmigratory species, which overwinter at higher latitudes. Here, we test whether effects of migration distance on survival accrue over evolutionary timescales to influence standing genetic diversity. Populations experiencing demographic stability are expected to have greater genetic diversity (reflecting greater effective population size) than populations subject to survival bottlenecks, including large bottlenecks imposed by glacial cycles and localized bottlenecks imposed by harsh winter conditions. We therefore hypothesize that migration distance promotes genetic diversity due to an influence of nonbreeding latitude on demographic stability. We generated data using whole-genome, population-level datasets from 35 species of boreal birds (~1800 samples total), which we sampled across the contiguous eastern boreal belt. We use phylogenetic comparative methods to reveal a strong positive correlation between migration distance and standing genetic diversity. Our results suggest that migration distance promotes effective population size, perhaps by mediating the extent to which populations experience unstable conditions at high latitudes, with implications for how migration influences species' evolutionary trajectories. The relationship between nonbreeding latitude and genetic diversity parallels a global relationship between latitude, genetic diversity, and population demographic stability that is present in many taxa, highlighting the importance of nonbreeding ranges for migratory bird population demographics.

Does migration promote speciation? A comparative test in two large passerine clades*G Calabrese, R Safran, D Rabosky***Presenting author: Gina Calabrese, University of Colorado Boulder, gina.maria.calabrese@gmail.com*

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Seasonal migration is performed by birds across the planet, and shapes their ecological and evolutionary contexts. Migration has been hypothesized to promote speciation through mechanisms including: temporal or geographic isolation, or divergent ecological selection resulting from different migratory routes ('migratory divides'); geographic isolation resulting from the loss of migration in a population of an otherwise-migratory species; or the colonization of new, geographically-disjunct breeding areas by migrants. Further, migration has been implicated in genetic divergence and incipient speciation in a few bird species, including Barn Swallows, European Blackcaps, and Swainson's Thrushes. However, migration may also reduce population structure by increasing dispersal, thereby impeding speciation. To test whether migration generally promotes speciation, we used a comparative phylogenetic approach at a broad taxonomic scale. Specifically, we tested the association between speciation rates and migration in two large clades of new world birds, the Suboscines and the Emberizoidea, comprising 10-15% of all birds. We used multiple methods of inferring trait-based diversification, including lineage-specific speciation rates and state-based speciation extinction models. Our results differed across methods and taxonomic scales, raising questions about the robustness of current trait-based diversification approaches. Overall, we conclude that there is no evidence of faster speciation in migratory lineages in these groups. We discuss the biological implications of this finding, as well as the problems of inference posed by available trait-based diversification methods.

***Parallel and convergent evolution in genes underlying seasonal migration in the Common Yellowthroat (*Geothlypis trichas*).**

L Zamudio, A Bueno, C Bossu, P Dunn, N Sly, E Anderson, C Rayne, B Hernandez-Banos, K Ruegg

Presenting author: Luz Estela Zamudio, UNAM, zbluzetuky@gmail.com

The genetic basis of migration has been widely studied across different taxa. However, it remains unclear which genomic regions influence migratory abilities and whether they are similar across species. Here, we employed a comparative phylogenomic approach to gain valuable insights into the predictability and repeatability of the genes underlying migratory behavior. By analyzing genome wide genetic data from 196 individuals collected from 22 locations across the breeding range of the Common Yellowthroat (*Geothlypis trichas*), we identify suites of genes with parallel signals of genetic change as well as some examples of genetic convergence. We found strong signals of genetic parallelism in genes linked to the core clock network, the flight energetics and morphology potentially related to flight aerodynamics. Otherwise, genes upstream or downstream of the core clock network were less similar across population and species level comparisons. Our study provides compelling evidence that the evolution of complex traits, such as migratory behavior, is not constrained to a single pathway. Instead, our findings demonstrate the existence of multiple possible evolutionary trajectories leading to the development of this trait.

***Modeling survival and connectivity of a migratory waterbird using a continuous-time, multi-state approach**

A Van Tatenhove, E Stuber, C Rushing

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American white pelicans (*Pelecanus erythrorhynchos*) are migratory, nearctic waterbirds that have experienced notable spatial variation in population trends across their range. These trends may be driven by markedly different anthropogenic impacts and environmental conditions experienced across the annual cycle, including human development, pesticide use, persistent drought, and disease. Given the spatial variability in these threats, seasonal migratory connectivity has important implications for future population dynamics and survival. Even so, migratory connectivity and regional variation in annual survival remain poorly understood in this species. Here, we describe a novel continuous-time, multi-state capture-recapture model applied to 63 years of band recovery and re-sight data from the North American Bird Banding Laboratory to quantify migratory connectivity and survival between pelican summer and winter ranges. Capture-recapture data are typically modeled in discrete time, but band recoveries may occur at any point throughout the year, making continuous-time models more appropriate and

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computationally efficient for these data types. Furthermore, our approach efficiently handles large numbers of undetected individuals, which vastly reduces computational time for large band-recovery data sets. We found that despite low migratory connectivity across summer and winter regions, annual survival varied regionally, likely due to spatial variation in environmental conditions and anthropogenic impacts. Our results offer important context for understanding historical pelican population dynamics, and may be used to inform current and future management strategies for American white pelicans across North America.

****Range-wide fluctuations in migratory connectivity for the American Redstart over the last century****H Stevens, C France, P Marra***Presenting author: Henry Stevens*, Georgetown University, henrycstevens@gmail.com

One consequence of climate change are shifting species' ranges. Recent evidence suggests that the breeding origin of American Redstarts (*Setophaga ruticilla*) spending the nonbreeding season in Jamaica is shifting southward in response to prolonged winter drought. Here, we present evidence that these fluctuations in breeding origin have occurred range-wide over the past century, and are linked to nonbreeding season rainfall. Specifically, we predicted that the mean breeding origins of redstart populations from key nonbreeding areas (MEX, COL, VEN, JAM, PAN, CRI) would shift southward or northward following multiple drought or wet years on the nonbreeding grounds, respectively. To test this, we sampled tail feathers from 200 redstart museum specimens and 170 live birds, and used stable-isotope analysis of hydrogen to estimate the breeding origin for each redstart. We then grouped estimates of individual redstart breeding origins into distinct regional populations and time periods. Finally, we used ANOVAS to estimate the strength of the shift in mean breeding origin for each population of redstarts over time. Nonbreeding locations that experienced predominantly wet conditions since 1900 (e.g., COL) resulted in redstart populations exhibiting a significant northward shift in their mean breeding origin, and vice versa (southward shift for locations with prolonged drought conditions; e.g., VEN). Our study is one of the first to show how rainfall controls range dynamics for migratory birds. Future studies should pair this mechanistic understanding of how rainfall affects range dynamics with future climate scenarios to understand how climate change acting throughout the annual cycle will alter range shifts for migratory birds.

Stable isotopes identify migratory connectivity for heavily harvested sea duck populations*S Endyke, D Nelson, E Cohen, K Martin, H Vander Zanden, T Katzner***Presenting author: Sarah Endyke*, sarah.endyke@umces.edu

Species-specific information about movement of waterfowl within and among migratory flyways is critical for understanding the appropriate scale and extent for management and conservation. Long-tailed Ducks (*Clangula hyemalis*) and Surf Scoters (*Melanitta perspicillata*) are of high management priority due to their unprotected status, their increasing vulnerability to overharvest, and the lack of baseline data about their populations, including migratory connectivity. We used feathers from >600 first-year Long-tailed Ducks and Surf Scoters harvested across all four North American flyways to identify the strength of migratory connectivity within their populations. We inferred fledgling grounds using a dual stable isotope approach with hydrogen and sulfur ($\delta^2\text{H}$, $\delta^{34}\text{S}$) values. We then compared the inferred fledgling grounds with harvest locations to investigate the degree to which these species move within and among flyways. Preliminary analyses indicate that first-year Surf Scoters generally exhibit stronger migratory connectivity within and among flyways than do first-year Long-tailed Ducks. For example, an estimated 91% of Surf Scoters, but only ~56% of Long-tailed Ducks, wintering in the Atlantic flyway had inferred fledgling grounds in the Atlantic flyway. The results of this study can help to inform flyway-specific harvest regulations for Surf Scoters and Long-tailed Ducks.

First GPS-tracking of migration routes and overwintering locations of the

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imperiled Oregon Vesper Sparrow**S Rockwell, J Stephens, B Altman***Presenting author: Sarah Rockwell, Klamath Bird Observatory, smr@klamathbird.org*

Oregon Vesper Sparrow (*Pooecetes gramineus affinis*), the unique subspecies found west of the Cascades, is under review for ESA listing because of its small population size (<3,000 birds) and declining trend. A better understanding of overwintering locations and migratory stopover sites used by Oregon Vesper Sparrow, and potential threats originating there, are key information gaps needed to target conservation actions. Our objectives were to: 1) describe locations used during fall migration, winter, and spring migration, including habitat types, and 2) compare migration phenology and non-breeding locations used by different breeding populations. In 2020-2022 we captured, banded, and fit archival GPS tags on 26 adult Oregon Vesper Sparrows in the Klamath Mountains ecoregion, and 14 in the Willamette Valley, Oregon. Data retrieved from 8 returning birds revealed a striking variety of migration strategies, with substantial overlap between the two breeding regions. Oregon Vesper Sparrows departed nesting areas between 19 Sept and 7 Oct; most used routes along the Sierra Nevada foothills just east of California's Central Valley. Length of fall migration ranged from 4 to 69 days, as some individuals employed lengthy (~2-month) fall stopovers before continuing south. Stationary wintering areas ranged from the latitude of Yuba City/Sacramento to outside of Bakersfield, CA (~500 km apart). Spring departure dates for 4 individuals ranged from 31 Mar to 10 Apr, and spring migration duration lasted 6-21 days. Because of the wide variety observed in fall stopover length, wintering latitude, and migration duration, more research is needed to understand the full variation of Oregon Vesper Sparrow migration strategies to ultimately apply this information for conservation benefit.

Genetic variation and migratory connectivity of the Loggerhead Shrike (*Lanius ludovicianus*)**H Fox, C Bossu, A Carpenter, A Chabot, K Ruegg***Presenting author: Holden Fox, Colorado State University, holdencfox@outlook.com*

The loggerhead shrike is a partially migratory grassland bird experiencing persistent, range-wide declines. The impact of movement-related mortality on shrikes remains poorly understood, while little is known about their migratory routes or individual dispersal. Here we use whole genome resequencing of loggerhead shrikes across their full annual cycle to delineate genetically distinct breeding populations of shrike and quantify the extent of population connectivity. We identify 5 distinct genetic clusters of shrikes across the eastern portion of the range, with the greatest variation occurring in the Great Plains region. Our next step in this analysis will be to identify population specific migratory connections and link our data with population specific demographic trends. These results can be used to inform targeted, region-specific conservation strategies for this species in the face of rapid environmental change.

Network analysis reveals range-wide migratory connectivity and key stopover sites for a declining Neotropical-Nearctic migratory bird, the Blackpoll Warbler**J Duali, B DeLuca, S Mackenzie, J Tremblay, B Drolet, S Haché, A Roberto-Charron, M Holguin-Ruiz, R Boardman, H Cooke, C Rimmer, K McFarland, P Marra, P Taylor, R Norris***Presenting author: Jelany Duali, University of Guelph, jduali@uoguelph.ca*

Understanding the spatio-temporal linkages between populations across the annual cycle of migratory birds is essential for their effective conservation and management. Unfortunately, knowledge of range-wide migratory connectivity is still limited to a small number of species. Using data from 45 light-level geolocators deployed at 10 sites across its breeding range in North America and at one site in Colombia, we assess patterns of range-wide migratory connectivity in a declining songbird, the Blackpoll Warbler (*Setophaga striata*). We built and analyzed networks representing spring and fall migrations. Each network included breeding, stopover, and nonbreeding areas (nodes) and the flow of individuals moving between them (edges), which we estimated by combining our tracking data with relative abundance estimates from eBird's Status and Trend database. Overall, inter-population mixing was high between the breeding and nonbreeding grounds, and during migration. Despite this, eastern and western

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breeding populations differed in their use of certain stopovers and were concentrated on opposite sides of the nonbreeding range. We identified several nodes that were key to maintaining network connectivity or acted as mixing points for individuals from different breeding regions. Highly ranked nodes were located on the east coast of the U.S., Venezuela, and northern Brazil in the fall, and the southeast U.S. in the spring. Our results not only identify regions that should be prioritized in conservation efforts but also provide vital information for the development of population models linking trends in Blackpoll Warbler populations to processes occurring throughout this species' range.

***Imperfect detection biases $\hat{I}^2$ diversity estimates based on whether species are shared between sites**

Y Wang, D Zeng, Y Zhao, M Tingley, M Cadotte, P Ding, X Si*Presenting author: Yue Wang, wymoon666@126.com*

$\hat{I}^2$ diversity measures the variation of species composition among sites that is a key component of biodiversity measurement. However, it remains unclear how imperfect detection, a common form of sampling error, affects the estimates of $\hat{I}^2$ diversity. Here we simulated the processes of imperfect detection based on species' compositional statuses (i.e., shared species between two assemblages, or unique species only belonging to one assemblage), and used a 10-year avian monitoring dataset collected on 36 subtropical reservoir islands to examine how imperfect detection affects $\hat{I}^2$ diversity estimates as a function of island area and isolation. Both simulation and empirical analyses found that imperfect detection overestimated taxonomic, functional, and phylogenetic $\hat{I}^2$ diversity due to biased observations of shared species. The extent of overestimation in avian $\hat{I}^2$ diversity increased with the difference in island area. Our study reveals a general mechanism of understanding $\hat{I}^2$ diversity estimates under imperfect detection through species compositional status.

Avian Carcass Persistence and Scavenging in the Chihuahuan Desert: Implications for Carcass Surveys

T Huycke, D Osterhaus, K Boland, F Abadi, M Desmond*Presenting author: Thomas Huycke, huycketom@gmail.com*

Carcass surveys are often used to assess avian mortality; however, estimates from these surveys may be biased by multiple factors, including the removal of carcasses by scavengers prior to surveys. To inform surveys and improve avian mortality estimates, we quantified carcass persistence times, removal rates by scavenger species on White Sands Missile Range in 2023, as part of a larger study examining avian mortalities due to artificial light at night. We also analyzed potential drivers of variability in persistence time, including weather variables such as thermal amplitude and exposure to precipitation, and distance to road, using parametric survival models. We placed 101 House Sparrow (*Passer domesticus*) carcasses in the spring and 113 in the fall and monitored each with camera traps. We found a mean persistence time of 50.9 hours, with 65% (95% CI [59%, 72%]) of carcasses persisting after 24 hours and only 3% [1.6%, 6.9%] remaining after one week. The primary scavenger was the Spotted Ground Squirrel (*Xerospermophilus spilosoma*) which scavenged 17.8% of carcasses. Our analysis revealed that none of the covariates had a significant effect on persistence time. Overall, our findings indicate that scavenging of avian carcasses occurs at high rates by a wide variety of scavengers, similar to those reported in other ecoregions. To counteract the scavenging bias in mortality estimates from carcasses, our data suggests that carcass surveys should be conducted frequently, potentially daily, or a correction factor should be used to account for scavenging loss. Our study provides the data necessary to correct for scavenging loss in the northern Chihuahuan Desert and helps to inform the planning of future survey efforts.

A point-level trend model for the North American Breeding Bird Survey that explicitly incorporates detection probability

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The North American Breeding Bird Survey (BBS) is the current gold standard for status and trend estimation for breeding birds in North America. Trends are estimated at the route level from the change in relative abundance for each BBS route, which are collections of 50 three-minute point counts conducted along a 40-kilometre stretch of road each year. However, this means that the BBS analyses have always lacked a way to explicitly incorporate information on detectability (or detection probability), because we do not calculate trend at the individual point-count level. We are therefore missing opportunities to connect changes in breeding bird population trends to potential changes in detectability, which can be caused by changes in the landscape. Here, we demonstrate for the first time a model that allows for trend estimation at the point level, rather than at the route level. We tested this point-level model for several species of birds sampled by the BBS, and show that modelling at the point level does not significantly change the estimated trends compared to modelling at the route level. We then extracted percent forest coverage for all BBS points in Ontario from 2011 – 2022, and used the freely available NA-POPS detectability estimates to explicitly incorporate detectability into the BBS analysis. This explicit incorporation of detectability caused both increases and decreases in trend, depending on the species, but also created more uncertainty around the estimates because of propagating forward the variation from the detectability estimates. We conclude by providing guidance to continue this point-level analysis on a larger scale, and discuss implications pertaining to population forecasting and data integration.

Accounting for location uncertainty in stop-level Breeding Bird Survey (BBS) analyses

R Burner, A Kirschbaum, J Hostetler, N Anich, E Striegel, N Niemuth

Presenting author: **Ryan Burner**, U.S. Geological Survey, rburner@usgs.gov

Many ecological inferences are based on environmental conditions where taxa occur or are absent. However, location uncertainty in species records is pervasive, particularly for historical data. The North American Breeding Bird Survey (BBS) was designed decades ago for trend analyses that do not require precise spatial information. However, there is increasing interest in leveraging stop-level BBS data for finer-scale ecological questions. Yet naive attempts to do this, e.g., by assuming consistent stop spacing, can introduce substantial error. To address these challenges, we developed a Bayesian model to incorporate location uncertainty into BBS analyses. We (a) quantified stop location uncertainty using digitized locations available for a subset of stops, then (b) derived corresponding NLCD-based habitat cover uncertainty distributions for each stop. Next, we (c) specified these habitat distributions as informative priors in our model, estimating stop-level habitat covariates while simultaneously (d) modeling the responses of 37 bird species to forest, grass/hay, and development (400 m radius) across the upper Midwest. To test our method, we compared posterior habitat distributions to known habitat cover for a subset of GPS-digitized stop locations and found that posterior distributions consistently converged on true habitat values. Our method unlocks the potential of the extensive BBS dataset for fine-scale spatial analyses and highlights the importance of precise spatial metadata. More broadly, it provides a framework for how location uncertainty can be estimated and incorporated into analyses of other data types via informative priors, reducing bias and permitting ecological inferences at finer spatial scales.

When birding hotspots get too hot: understanding the emergent properties of fire-related disturbance on spatiotemporal biases in citizen science data

E Jacobo, J Manning

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Citizen science projects provide valuable data on species presence, counts, phenology, and behavior. Despite its drawbacks compared to probabilistic sampling methods, these projects benefit from data contributed by multiple observers across extensive geographic regions. Thus, citizen science data can provide longitudinal and cross-sectional datasets poised for ecological research and monitoring. However, environmental disturbances may affect when and where observers choose to search for target species, which can have unintentional consequences in the resulting species data and its utility in ecological research and monitoring. Using the eBird data repository, we investigated the direct and indirect effects of wildfires on spatiotemporal patterns of observer bias in citizen science data. We built models to explain

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locality selection and the probability of returning to a locality in response to fire and other non-fire-related environmental variables. Our analysis showed that fire size, severity, distance from fire, and time since fire affected locality selection and the probability of returning to a locality. Closer, more recent, larger, and more severe fires had the greatest impact on spatiotemporal patterns of observer bias. Researchers using citizen science data can follow our modeling approach to estimate probabilities and calculate disturbance-related observer bias-corrected ecological parameter estimates. Without this, observer biases underlying citizen science data will likely lead to spurious results. We propose recommendations to maximize the value of citizen science data in ecological research and monitoring.

Inter- and intraspecific variation in visible and thermally relevant wavelengths of light

A Shultz, T Lee, M Barrett, L Pilon, T McGlynn

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Plumage coloration can vary across species and populations, and can be correlated with latitude, environmental conditions, habitat, or light environment. Gloger's rule describes patterns of plumage brightness, and states that birds in wetter, hotter areas tend to have darker plumage. The relationship between temperature and plumage coloration is consequently less-well defined, although some previous studies have shown a relationship between near-infrared (NIR; wavelengths 701-2500 nm) and climate variables in animals. Furthermore, no studies have examined variation in the mid-infrared (MIR; wavelengths 7.5-14 μ m), which is important for exchanging heat with the environment and therefore thermoregulation. In this talk, we examine three climatically variable populations each of five bird species that live in open habitats (Northern Bobwhite; Common Raven), closed habitats (Steller's Jay; Song Sparrow), or are active at night (Great-horned Owl) and quantify MIR and NIR absorption and emissivity. Across species, UV-NIR absorption was highest in Common Ravens, followed by Song Sparrows, and then the remaining species. Northern Bobwhites had the highest levels of MIR emissivity, meaning that they exchange the most MIR with the environment. Other species were not significantly different from each other. Across populations, only Northern Bobwhites and Song Sparrows showed variation in UV-NIR absorption, and only Northern Bobwhites showed variation across populations in MIR emissivity. Together, these results show that variation across species and populations in thermally relevant wavelengths is present and should be further explored both among species and populations.

****Using 3D models to further understand structure's role on feather wettability**

F Muzio, M Rubega

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Birds rely on their feathers to provide many vital functions. Water repellency is crucial because many other feather functions rely on dryness for success. Despite the importance of feather water repellency, there are major gaps in our understanding of how it is achieved. We know that water repellency is the result of feather structure, primarily the microstructures. We also know feather microstructure morphology shows considerable variation across birds, but we don't fully understand how this variation affects feather wettability. The ever-growing technology of 3D modeling has opened research opportunities across various STEM fields. Researchers now can construct complicated 3D models to further understand the mechanics of biological structures. Here we use micro-computerized tomography scanning (μ CT) to obtain detailed 3D feather scans. We scanned feathers at a high-definition, 3-micron scale resolution to effectively capture barbule and hooklet structure. We used these scans to create various 3D models where we altered microstructure morphology. We use these models for both computerized wettability simulations and to 3D print physical models for various wettability tests. Using these models, we aim to gain a better understanding of the direct effect of microstructure morphology on feather wettability.

****Birds in the Southwestern United States Delay Their Timing of Molt During the Spring While Advancing it During the Fall**

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K Kittelberger, M Neate-Clegg, C Sekercioglu*Presenting author: Kyle Kittelberger, University of Utah, kyle.kittelberger@utah.edu*

Molt, the replacement of old, worn feathers with new ones, is one of the most important events in the annual cycle of birds. Although we know an increasing amount about the effects of climate change on the timing of other avian events (such as migration and breeding), there has been relatively limited work conducted on alterations in molt phenology over time. In this study, we utilized a twelve-year bird banding dataset from southeastern Utah to examine long-term trends in the molt timing of body and flight feathers in both the spring and fall migratory seasons. Specifically, we assessed whether birds at the community and species level were molting earlier or later over during spring and fall and, if so, whether these trends in molt phenology were influenced by life-history traits or climate variables. We found that there were significant temporal trends in molt timing in both seasons, such that birds were delaying the timing of their body feather molt in the spring and advancing the timing of their body and flight feather molt over time in the fall. We, therefore, reveal that North American birds in the Southwestern United States are undergoing long-term phenological changes by shifting the timing of a physiologically demanding component of their annual cycle. We also found that several birds at the species level advanced the timing of their molt in the fall, while one species delayed their molt timing in the spring during our study period. Finally, we highlight the influence of climate on molt phenology, with El Niño/Southern Oscillation, precipitation, and maximum temperature all being associated with significant advances or delays in molt timing. This study provides the first examination of long-term trends in molt phenology of birds from North America, and one of the few long-term examinations in general of changes in avian molt.

Species limits, systematics, and island biogeography in East Asian white-eyes (*Zosterops japonicus*, *Z. meyeri*, *Z. montanus*, *Z. simplex*) based on multilocus Sanger and RAD sequencing datasets.

H Mays, B McKay, D DeRaad, I Nishiumi, C Yao, M Boyd, N Hofmeister, L DeCicco, M Venkatraman, F Zou, C Kim, K Kawakami, R Lin, K Garrett, S Aguillon, J McCormack, R Moyle, A Shultz, L Kubatko

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Zosterops white-eyes are renowned as exemplars of island diversification and are widely studied in speciation research. However, lingering questions remain among groups within *Zosterops* regarding their systematics. Among these persistent questions is the taxonomy of the East Asian white-eyes (*Zosterops japonicus*, *Z. meyeri*, *Z. montanus*, and *Z. simplex*). While *Z. simplex* has been delimited from the remaining taxa, *Z. montanus* was recently subsumed into *Z. japonicus*, and while *Z. meyeri* is still considered a distinct species few analyses have included this taxon. We investigated the systematics of the East Asian white-eyes for up to 143 individual samples across a broad range including all but one of the six recognized subspecies of *Z. japonicus* and seven of the nine subspecies of *Z. montanus*. In addition, our analysis included *Z. meyeri*, a geographically diverse sampling of *Z. simplex*, the other Philippine *Zosterops* (*Z. everetti* and *Z. nigrorum*), and the migratory *Z. erythropleurus* from mainland Asia. Relationships and species limits were tested using a molecular dataset of 15,704 SNPs from a RADseq library and a Sanger sequencing dataset including two mtDNA loci (COI and ND2) and seven nuclear protein-coding genes. The *Z. japonicus*/*meyeri*/*montanus* clade represents a late radiation of white-eyes across Wallacea and the Philippine archipelago with a final colonization of the Ryukyus, the main islands of Japan, and the oceanic archipelagos of the Izu and Ogasawara Islands. *Z. montanus* forms a paraphyletic group with the populations of the northern Philippine islands of Luzon and Mindoro more closely allied with *Z. meyeri* and *Z. japonicus*. Additionally, we found evidence of genetic structure splitting *Z. japonicus* into continental and oceanic island populations. These analyses suggest there may be justification for reinstating species rank for the Japanese populations of *Z. japonicus* and perhaps elevating populations of *Z. montanus* on Luzon and Mindoro to species.

Phylogeography of the Indian Scimitar Babbler (*Pomatorhinus horsfieldi*)

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The Indian subcontinent, with its dramatic tectonic history and high biodiversity, is a biogeographic medley of diversification patterns. Recent studies show that many endemic taxa are more distinct than implied by current taxonomy, yet there is little congruence in diversification patterns within the subcontinent across the few lineages that have been studied. The Indian Scimitar-Babbler (*Pomatorhinus horsfieldi*) is an endemic bird distributed across the montane and wet-zones of the peninsula. We conducted a phylogeographic analysis using genomic information from historical museum specimens and recent surveys. We tested (1) if described subspecies are distinct lineages; (2) whether the divergence patterns fit predictions of dispersal based on past climate change; and (3) whether plumage and morphological variation is congruent with genetic differentiation. Our analyses indicated a closer relationship of the Sri Lankan population to the northern Western Ghats than to the geographically more proximate southern Western Ghats. Our results also show the presence of cryptic diversity within this widespread species with more complex patterns of diversification than previously hypothesized by stepping-stone models. This study highlights the benefits of combining historical and recent samples to produce one of the first comprehensive phylogeographic analyses of Indian species.

Correspondence between phylogenomic data and species and subspecies taxonomy in suboscine birds

M Harvey, G Bravo, A Aleixo, J Bates, T Chesser, J Cracraft, B Smith, A Cuervo, M Lentino, J Perez-Eman, A Navarro-Siguenza, C Ribas, L Silveira, R Moyle, S Claramunt, M Rego, O Johnson, M Sotelo, D Lane, D Tan, M Andersen, E Derryberry, R Brumfield

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Suboscine passerines currently represent over 10% of all birds, and roughly one out of three of species in the bird-rich Neotropics. Although many suboscine species are cryptic, vocalizations and more recently genetic data have been leveraged to delineate species boundaries in certain taxa and to elevate populations to species status. The number of cryptic taxa deserving species status in the group, however, remains unknown. We use data from an ongoing project on suboscine systematics to explore this issue. We examine the distribution of divergence times between lineages considered species, subspecies, and populations. We identify outliers that might merit taxonomic re-evaluation. We present data on gene flow between lineages at different taxonomic levels. And we open a discussion about the utility of universal thresholds and prospects for consistency in avian species taxonomy.

Unraveling the mystery of the Mesoamerican Steller's Jays (*Cyanocitta stelleri*) with phenotypic and genomic data

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The combination of genomic and phenotypic data is a powerful tool that can aid in better understanding complex geographic patterns of phenotypic variation. The Steller's Jay, a corvid species found across a wide latitudinal gradient, inhabits mountain ranges from southern Alaska to northern Nicaragua. Across this range, phenotypic differences most notably in color and crest length occur in both clinal and discrete patterns, but suspected hybridization in central Mexico has led to complex patterns of variation. Previous work examining phenotypic and genetic structure in the Steller's Jay has been done on only subsets of the entire species' range but has found significant population structure with strong ecomorphological ties. Here, we use traditional morphometric variables from 124 specimens paired with a SNP dataset to assess the range-wide phenotypic and genetic variation of the Steller's Jay (*Cyanocitta stelleri*). Most notably, a population found across the Isthmus of Tehuantepec in Honduras is genomically and phenotypically divergent. Additionally, a canonical variates analysis using the morphologic measurements gives moderate support for assignment to the identified genetic clusters. By examining differences in morphology in conjunction with genomic data, we find that the Steller's Jay is likely composed of multiple distinct genetic lineages which, once delineated, help to unravel complex patterns of phenotypic variation.

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Genomic data place “the [Western Hemisphere’s] most enigmatic bird species”, the Blue-headed Quail-Dove (*Starnoenas cyanocephala*), in a phylogenetic context and indicate that it is a biogeographic relic.**J Oswald, B Boyd, A Grant, M LeFebvre, B Stucky, R Guralnick, K Johnson, J Allen, D Steadman***Presenting author: Jessica Oswald, U.S. Fish and Wildlife Service, oswaldj3@gmail.com*

Islands are well-known for their unique biodiversity and significance in evolutionary and ecological studies. Nevertheless, extinction of island species accounts for most human-caused extinctions, which have accelerated in recent millennia. Pigeons and doves (Columbidae) are noteworthy for the high number of island endemics, as well as for the risks those species have faced since human arrival. In the Caribbean, no other living dove species has a more nebulous taxonomic affinity than the Blue-headed Quail-dove, *Starnoenas cyanocephala*. This endangered Cuban endemic has been considered more similar, both behaviorally and phenotypically, to Australasian species than to the geographically much closer 'quail-dove' species of the Western Hemisphere. Here we use whole genome sequencing and phylogenomic approaches to investigate the phylogenetic relationship of *Starnoenas* to other pigeons and doves. We find that the Blue-headed Quail Dove is the sole representative of a lineage diverging early in the Cenozoic radiation of doves and pigeons. This species is sister to all of the Columbinae subfamily, which are found world-wide. Therefore, *Starnoenas* is a highly distinctive evolutionary lineage, which should elevate its priority for conservation.

Species delimitation of the western fire-eye antbird (*Pyriglena maura*)**M Sotelo, M Harvey***Presenting author: Manuelita Sotelo, msotelo7@miners.utep.edu*

The delimitation of species is crucial for understanding the evolutionary history of biodiversity and indispensable for supporting conservation efforts. Whole genome analyses have greatly contributed to this task by facilitating the taxonomic reevaluation of numerous lineages, revealing that many populations or subspecies that were initially described based on morphology, geography, or a few molecular markers, warrant indeed full species status. *Pyriglena maura* (western Fire-eye antbird) is a species complex composed of six recognized subspecies widely distributed from south Colombia to northwest Brazil. The subspecies inhabit humid Andean Forests or dry forests adjacent to the Andes, and their range boundaries roughly correspond to geographic barriers associated to genetic breaks in other bird taxa. Despite dramatic variation in female plumage among most subspecies pairs, full species status has not been granted to any subspecies due to a lack of substantial variation in vocalizations compared to other species pairs within the same genus. Covering most of the distribution range of *P. maura*, we analyze the whole genome of at least ten individuals per subspecies to determine, through a series of clustering and phylogenetic methods, whether a new phylogenetic hypothesis is needed for this species complex. Despite some evidence of gene flow between lineages, our results suggest that current *P. maura* consists of at least three different species that rapidly diverged within approximately the last 1 million years.

A diamond in the rough — Carnegie Museum of Natural History Section of Birds*S Brady***Presenting author: Serina Brady, Carnegie Museum of Natural History, ssbrady94@gmail.com*

As one of the largest ornithological collections in the United States, the Carnegie Museum of Natural History (CM) Section of Birds is a global treasure. With over 190,000 specimens from across the world, including study skins, taxidermy mounts, skeletons, spread wings and tails, eggs and nests, and fluid-preserved birds, our collection is a hub of research and conservation efforts. CM's unique and diverse holdings of species from the Neotropics and Canada and specimens from over 85% of the world's countries provide a comprehensive view of avian biodiversity. Most of our specimens were collected in the early 20th century, and changes in staff and museum mission have led to new protocols and practices being implemented, strengthening the preservation of this invaluable resource. I will share these new practices and advertise for our Livezey Study Grants, hoping to increase the use of the Carnegie Museum

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of Natural History even further.

****Delimiting the Loggerhead Kingbird (*Tyrannus caudifasciatus*) Species Complex using a Holistic Approach****A Worm, E Donahue, P Brewer, B Dossman, T Boves, A Sweet**Presenting author: **Alexander Worm**, Arkansas State University, alexanderj.worm@gmail.com

As threats to global biodiversity increase, there is a need to resolve disputed species lineages and uncover any additional diversity through identifying cryptic species, potentially before they are lost. The Loggerhead Kingbird (*Tyrannus caudifasciatus*) represents one such disputed species lineage. Currently, the species is comprised of seven subspecies located across multiple Caribbean islands, however the taxonomic status of these populations remain disputed since being described. Most recently, Garrido et al. (2009) recommended elevating the Hispaniolan and Puerto Rican subspecies to species status based on evidence from their distribution, plumage, morphology, and vocalization. This recommendation has gone unheeded, potentially due to the absence of genetic analyses. Here, we combine genomic and morphological data to delimit the Loggerhead Kingbird species complex with a specific goal of testing the hypothesis that subspecies on Hispaniola and Puerto Rico are each separate species. We extracted genomic DNA from tissue samples from each of the seven currently recognized subspecies. Using mtDNA and genome-wide SNP data we then investigated the genetic clustering of samples to determine each island populations' (sub)species status. We also measured and analyzed morphometric data from specimens housed in the Smithsonian to further inform our delimitation of the complex. Using multiple lines of evidence, we partially agree with Garrido's assessment and recommend elevating the Puerto Rican subspecies to a separate species and suggest, less definitively, that the Hispaniola population remain a subspecies. These island populations' unique genetic diversity and evolutionary potential warrant safeguarding.

****A comprehensive whole-genome phylogeny for the Red-tailed Hawk (*Buteo jamaicensis*)****B Robinson, B Butcher, L DeCicco, I Lovette, B Sullivan, J Walsh**Presenting author: **Bryce Robinson**, Cornell University, bryce@ornithologi.com

The Red-tailed Hawk (*Buteo jamaicensis*) is a common, widespread, and highly diverse species with the potential to serve as a model for broad patterns and processes in the ecology and evolution of Raptors. The species includes 16 described subspecies that inhabit most of North and Central America, the Caribbean, and a few isolated islands off the coast of Mexico. Despite much debate regarding the taxonomic designations of the insular taxa, and populations highly divergent in appearance, there has been little work to understand the relationships between distinct populations. To resolve these relationships and provide a foundation for understanding the evolutionary history and development of diversity in this species, we sequenced whole genomes of multiple individuals of each of the described taxa from a combination of blood samples collected in the field and historical museum specimens. We also include individuals from the allopatric Rufous-tailed Hawk (*Buteo ventralis*) of southern South America to assess its relationship to *B. jamaicensis*, and to provide context for assessing relationships of allopatric populations in the Pacific and Caribbean, as well as those highly diverged in appearance. We discuss the implications of our results and how a comprehensive phylogeny can serve as a foundation for further investigations into the ecology and evolution of this emblematic Raptor.

****Discordance among genetic, morphological, and acoustic divergence in the most polytypic antbird, the Plain Antvireo (*Dysithamnus mentalis*)****R Lima, S Bolívar-Leguizamón, F Bocalini, L Silveira**Presenting author: **Rafael Lima**, rafael-dlima@hotmail.com

The Plain Antvireo is the most polytypic species in the Neotropical family Thamnophilidae, with as many as twenty named and eighteen currently recognized subspecies. Current classifications remain based on

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early analyses of morphological variation, despite the widely known importance of vocalizations and the recently implicated importance of postmating isolation in antbird speciation. We combine plumage and acoustic trait data and genome-wide genetic markers to characterize the nature and pattern of geographic variation and population structure of the Plain Antvireo, and to assess the validity of its component taxa. Additionally, we conducted field playback experiments on allopatric populations that differ vocally to assess the significance of their vocal differences as a potential premating reproductive barrier. Our results establish that only 12–14 populations are phenotypically diagnosable, and those form six nuclear genomic clusters. In contrast with its geographically structured nuclear genome, the species is characterized by negligible mitochondrial DNA differentiation among populations. Our data suggest that premating reproductive isolation is weak or nonexistent between most lineages. Acoustic trait divergence was generally shallow, and playback experiments revealed no behavioral song discrimination between populations. In addition, we identified several hitherto unknown contact zones and documented hybridization wherever the ranges of differentiated populations met. By contrast, some lineages exhibiting sizable genome-wide divergence may have evolved some postzygotic isolation. While our results significantly refine our understanding of the geographic variation and population structure of the Plain Antvireo, we highlight that further study of the contact zones we identified is needed to establish levels of overall reproductive isolation between populations in the 'gray zone' of speciation.

The role of structural variation in shaping coloration phenotypes in the rapid capuchino Seedeater radiation

M Recuerda, C Kopuchian, A Di Giacomo, L Campagna*Presenting author: Leonardo Campagna, Cornell University, lc736@cornell.edu*

Understanding how genetic changes lead to phenotypic differences is a central goal in evolutionary genetics, where the increased affordability of second generation (short-read) sequencing has fueled the field's growth. In wild birds, single nucleotide polymorphisms (SNPs) remain the main genetic marker associated to trait changes, generally overlooking structural variants (SVs: e.g., insertions, deletions). This is likely because third-generation sequencing technologies (long-reads) are required for robust SV detection and characterization. Here we aim to uncover the role that SVs may have in shaping plumage coloration in the twelve species that comprise the capuchino Seedeater radiation (*Sporophila*). Previous work found that genetic changes (SNPs) near a handful of coloration genes associate strongly to plumage differences. To explore if SVs may also shape coloration patterns, we generated a pangenome from 32 haploid genomes derived from seven species, sequenced using Pacific Biosciences HiFi long-reads. We next characterized the genomic landscape of SV variation, including genetic changes derived from transposable elements. We further leveraged the capuchino pangenome to genotype an additional 142 individuals for SVs, for which we previously had generated short-read sequencing data. We conducted a genome outlier scan based on the collective genotypes of both SVs and SNPs, and illustrate how SVs and not only SNPs associate to changes in coloration across species. Our study shows how genetic variants which may be causal are overlooked when SVs are not taken into consideration, highlighting that although many phenotypes have been initially associated to specific SNPs, the underlying reality might be more complex.

Circulating corticosterone predicts near-term, while H/L ratio predicts long-term, survival in a long-lived seabird

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Assessing stress in wild populations is important in many ecological and conservation contexts because the physiological responses of individuals to stressors can be used to identify at-risk populations and the ability to respond appropriately to stressors is related to individual quality and fitness. Yet, one of the great challenges in ecophysiology is linking physiological measures in wild animal populations with changes in individual fitness. Here, we examined two indices of stress, namely, circulating baseline corticosterone concentration ([Cort]) and the heterophil:lymphocyte (H/L) ratio, in a long-lived seabird, the Nazca booby (*Sula granti*) and their relationship with current individual state and subsequent survival and residual and

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lifetime reproductive success. [Cort] was related to sex, age, and current reproductive effort in that males, older birds, and birds currently engaged in a breeding attempt birds had higher [Cort]. [Cort] was negatively associated with survival to the next breeding season. The H/L ratio was not associated with the current state of birds but predicted cohort-specific long-term survival. Lifespan and reproductive performance are correlated in Nazca boobies; therefore, our results suggest that the H/L ratio may be useful as an indicator of overall fitness, while [Cort] can be used to predict current or near-term fitness in this species.

****Fueling thermogenesis in a wet, cold winter: The interactive effects of rain and cold temperature on metabolism, fat, feeding and behavior in captive finches.**

J Karr, J Devereaux, D Swanson, J Cornelius

Presenting author: **Jessica Karr**, Oregon State University, karrj@oregonstate.edu

Short-duration, high-intensity precipitation events are projected to increase with climate change, which could negatively impact the fitness of avian species if thermogenic capacity cannot counter sudden changes in heat loss. Long-term cold exposure induces an increase in metabolism in many species, but how avian thermogenic capacity and physiology are impacted by long-term exposure to precipitation in different thermal conditions is largely undescribed. We measured metabolic and physiological responses of 48 red crossbills (*Loxia curvirostra*) held in warm (21°C) or cold (6°C) temperatures and dry or rain precipitation treatments over the winter season. Birds experienced rain daily for 30 minutes, and we measured summit (Msum) and basal (BMR) metabolic rates after 1, 8 and 14 weeks of exposure. Food intake, activity, and fat reserves were measured, and tissues were collected three days post final metabolic measurements. We found that Msum increased with both decreasing temperatures and rain exposure. Msum correlated positively with heart and pectoralis muscle masses. Neither temperature nor precipitation were predictive of BMR. Temperature and precipitation impacted activity and food intake over time, but there was no correlation between food intake and activity among treatment groups. Birds in cold, rain treatments maintained larger fat reserves across the duration of the study compared to the other treatments and increased enzymatic function of lipid metabolism by the end of the study. These findings suggest that cold rain induces expansion of thermogenic capacity in songbirds and may require individuals to invest more energy into self-maintenance under similar conditions in the wild.

***Effects of protein metabolism on immune function dynamics during experimental fasting and refueling in migratory White-throated Sparrows (*Zonotrichia albicollis*)**

E Rogers, A Gerson

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While protein is a critical source of energy and/or endogenous water for migrating birds, amino acids also play a critical role in regulating the vertebrate immune system. The immune system is resource intensive and often trades-off against competing demands such as migration. Immune function may be condition dependent; immune function is lower in migrating birds in poor condition and recovers rapidly at stopover. But despite the importance of protein as a fuel source during migration, it is unknown how fat and lean mass independently affect immune function in birds. Our aim was to investigate the effects of body composition change on multiple classes of immune defenses during a fast-and-refueling experiment in migratory White-throated Sparrows (*Zonotrichia albicollis*). We brought autumn migrating birds (n=36) into captivity and fasted birds for 22 hr to simulate an overnight flight; we fasted birds with or without water using established restriction protocols and used quantitative magnetic resonance to measure differences in body composition. As predicted, birds fasted without water had higher rates of lean mass loss, but similar rates of fat loss, compared to birds fasted with water. To estimate constitutive immune function, we collected blood samples before and after the fast and measured bacterial killing ability and IgY concentration. In a separate procedure, we fasted birds and then injected them with LPS from *E. coli* to stimulate an acute phase response (APR) and measured the resulting expression of two pro-inflammatory cytokines (TNF α and IL-6). Unlike constitutive defenses, which are energetically inexpensive to maintain, the APR incurs substantial energetic costs when triggered and is thus more likely to be impacted by other

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demands. Our results shed light on the consequences of protein loss for critical physiological systems in migratory birds and immune function dynamics during migration.

Impact of gut microbiome modulation on nestling House Sparrow physiology

K Rosamond, M Rowe, G Czirják, P Parker, L Chubiz, K Matson*Presenting author: Kristen Rosamond, kristenrosamond@gmail.com*

During early life, a diversity of microbes colonize animals, including their gastrointestinal tract. Host-associated bacterial assemblages comprise a portion of the gut microbiome which undergoes fluctuations and successions until becoming more stable in adulthood. Various factors such as dietary changes, environmental stressors, and pathogen exposure can alter the dynamics of gut microbiome colonization. Existing research has shown that such alterations can affect health outcomes including immune system function, growth rate, and disease susceptibility. However, these interactions are poorly understood in wildlife. We altered gut microbiome colonization in nestling House Sparrows (*Passer domesticus*) by administering either a probiotic or antibiotic to birds three times throughout their first week of life. Then, we administered a noninfectious immune challenge (lipopolysaccharide, LPS) in the second week to examine if a probiotic- or antibiotic-triggered gut microbiome disruption influenced the response to LPS. We collected fecal samples from nestlings to measure gut microbiome composition and structure, as well as plasma samples to measure physiological indices. We expected that nestlings fed probiotics, which increase microbial stimulation of the immune system, would respond more strongly to LPS; we expected those fed antibiotics would have less microbial stimulation and thus respond more weakly to LPS. Understanding how gut microbes influence the physiology of wild birds can provide insight into the ecological interactions impacting their health and survival.

Sitting ducks: Examining the physiology and behaviour of incubating eiders in the Canadian Arctic as a potential response to climate change driven heat stress.

E MacDonald, O Love, G Gilchrist, S Bellefontaine, R Smith, E Geldart, H Ter Hofstede, C Semeniuk*Presenting author: Emily MacDonald, emily.macdonald2@mail.mcgill.ca*

Warming ambient temperatures driven by climate change can increase a bird's risk of heat stress, negatively impacting their physiology and behaviour. Cold-adapted species may be particularly vulnerable to over-heating, due to their robust ability to retain body heat in cold environments. This risk is expectedly amplified during reproduction when body temperatures and energetic workloads approach their annual maxima. In this study, we examine changes in heart rate and incubation behaviour of nesting common eiders (*Somateria mollissima*) - an arctic-breeding sea duck that fasts during their ~25-day incubation on sun-exposed nests - as a response to thermal stress and overheating. In the summers of 2019, 2022, and 2023, we substituted one egg with a previously validated 3D-printed replica containing a heart rate recording microphone in focal eider nests ($N = 62$; $n = 12, 14$ and 36 , respectively) during laying at a long-term breeding colony in the Qaqsauqtuuq, East Bay Migratory Bird Sanctuary, Nunavut. We then recorded incubation behaviour using in-nest thermal probes and collected ambient/radiative temperatures using weather monitoring equipment at each nest site and across the island. Maximum seasonal ambient temperatures ranged from $19.8\text{ }^{\circ}\text{C}$ – $26.7\text{ }^{\circ}\text{C}$. We are now assessing the relationship between variation in environmental parameters, heart rate (a proxy for metabolic energy use) and incubation behaviour (nest-attendance and agitation) within and among study years to determine whether incubating eider hens are heat stressed. Our results will help determine a declining arctic sea ducks vulnerability to the direct effects of climate change, informing timely management strategies and encouraging protective policy action.

Ontogeny of thermoregulation in tree swallows (*Tachycineta bicolor*): complex effects of age and body mass

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Understanding the development of thermoregulation in nestling birds can give insight into potential responses to rapid environmental change, as well as the impact of early life conditions on ontogeny. In this study, I investigated the ontogeny of thermoregulation in tree swallows (*Tachycineta bicolor*) by examining cooling rate and change in body temperature in nestlings aged between 2 days and 12 days. Nestling cooling rate and ability to maintain body temperature was assessed via a cooling challenge of 20 degrees C. Changes in body temperature were recorded using cloacal measurements and the first and second order cooling constants were calculated, as well as the predicted equilibrium temperature based on cooling rate. Overall, cooling rate decreased with nestling age and increased with nestling body mass. Tree swallow nestlings showed limited thermoregulatory ability early in development as predicted equilibrium temperatures were close the cooling challenge temperature of 20 degrees C at days 2-4, but showed a steady increase as nestlings became older and larger. However, contrary to predictions, there was no clear age at which the ability to maintain body temperature appeared. Rather, the interaction between nestling age and body mass was complex in nestlings five days and older. In addition, the effect of early life experience on tree swallow thermoregulation will be discussed. These results provide valuable insights into the ontogeny of thermoregulation in tree swallows and highlight the complex interplay between body mass, nestling age, and thermoregulatory capacity during early development.

***European Starling and House Sparrow populations respond to their environment differently in their native and non-native ranges**

K Davis, H Sofaer, H Smith, H Heldbjerg, L Pejchar

Presenting author: **Kristin Davis**, New Mexico State University, kristin.p.davis@gmail.com

European Starling (*Sturnus vulgaris*) and House Sparrow (*Passer domesticus*) are two common, widespread, and invasive species that have experienced notable population declines over the past 50 years in both their native ranges in Europe and non-native ranges in North America. European declines largely have been attributed to habitat loss and changes in food availability resulting from agricultural intensification; reasons for decline in North America are unknown. Moreover, it is unknown whether population drivers differ between the species' native and non-native ranges. We fit generalized linear mixed effects models to 25 years (1992 – 2018) of site-level count data from 26 countries participating in the Pan-European Common Bird Monitoring Scheme and count data from the North American Breeding Bird Survey to investigate whether abundance of European Starling and House Sparrow responded differently to land cover, climate, and elevation in their native European versus non-native North American ranges. For both species, abundance responses as well as environmental range limits differed between the native and non-native range. Changes in abundance along gradients of land cover often were stronger in the non-native than native range. In addition, House Sparrow and European Starling were observed in areas with warmer average temperatures and drier breeding seasons in North America compared to Europe. Our findings demonstrate how species' environmental associations can vary within niche boundaries and could inform regional conservation or management and land use policy to support European Starling and House Sparrow populations in their native ranges and reduce them in their non-native ranges.

****Comparison of swallow and martin trends from three large-scale data sources**

M Belotti, B Gerber, Y Deng, W Zhao, V Simons, G Perez, S Maji, D Sheldon, J Kelly, K Horton

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Estimating abundance trends of bird populations across scales is important in evaluating conservation targets and creating effective conservation strategies. Particularly in the case of aerial insectivores, current efforts to estimate trends through time generally point towards wide-spread species declines, though regional patterns vary. For nearly six decades, the Breeding Bird Survey (BBS) has served as the only large-scale and systematic approach to quantify bird population trends in North America. Recently, however, eBird has added new trend estimates to its Status and Trends products. Moreover, radar data of aerial insectivore roosting populations yield a third complementary source of trend information - however, a systematic comparison of these approaches is lacking. To achieve this extracted estimates of the

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number of birds gathering in swallow and martin roosts from data captured by 12 radar stations from 2001 to 2021 in the Great Lakes region. Using these radar-derived population estimates, we built a metric of total seasonal population impact and used it to fit a hierarchical generalized additive model to produce estimates of average yearly percent change from 2012 to 2021. We developed a method to compare estimates of percent change per year derived from all three data sources to investigate the likelihood of agreement of trends by direction across our study region. We found a high probability of agreement across all three sources of observed declines in the region surrounding Lake Ontario and Lake Erie. While differences in trends were apparent across methods, areas of agreement in declines should be viewed as priority conservation regions to investigate mechanisms of declines and possible mitigation efforts.

Influence of a changing ocean on Marbled Murrelet (*Brachyramphus marmoratus*) chick provisioning behavior

C Frisinger, J Dachenhaus, K Osborne, D Roby, K Nelson, M Betts, J Rivers*Presenting author: James Rivers, jim.rivers@oregonstate.edu*

Flexible parental care strategies may be critical for offspring survival under variable environmental conditions. From 2017 to 2022, we conducted a large-scale study in western Oregon aimed at identifying the factors affecting population recruitment in the threatened Marbled Murrelet (*Brachyramphus marmoratus*), a cryptic, forest-nesting seabird. During our study, a shift from warmer, less productive ocean conditions to cooler, nutrient-rich ocean conditions provided an opportunity to investigate how marine environmental variability influenced murrelet parental care. To quantify parental care, we used chick provisioning behaviors obtained from continuous video recordings at 18 nests representing >1300 feeding events, with each event consisting of a single forage fish being provisioned. We found a difference in the mean daily chick feeding rate between years with warmer (2.0 ± 1.2 feedings/day) and cooler ocean temperatures (2.9 ± 1.4 feedings/day). Additionally, we found that 66% of nests provisioned under warmer ocean conditions experienced days with no feeding events, compared to only 8% of nests provisioned under cooler ocean conditions. Time to fledging varied from 30 to 45 days, and mean fledging age was 8 days older in years characterized by warmer ocean temperatures, leading to greater predation risk in warm ocean periods than during cool ocean periods. Our study demonstrates that warmer, less productive ocean conditions can have a pronounced impact on chick provisioning rates in piscivorous seabirds and suggests that murrelet chick provisioning behavior cannot fully compensate for poor ocean conditions.

Understanding Territorial Absences: Insights into Bald Eagle Hiatuses in the Northern Colorado Front Range

D Bove, R Conrey, M Middleton*Presenting author: Dana Bove, Front Range Eagle Studies, danajbove@gmail.com*

Limited unpublished studies and analysis of field data indicate territorial bald eagles in the northern Colorado Front Range are non-migratory. Building upon this foundational understanding, our research investigates short-term territorial absences, which we term 'hiatuses'. We have identified three temporally distinct hiatus periods, and each is associated with specific nesting events: Non-success related, which follows nest failure (~early to mid-June), post-juvenile dispersal, which occurs coincident with or after fledgling dispersal (~late July through September), and post-fledging dependence desertions, which is primarily observed in females. Field studies from 16 eagles across eight territories reveal that 8 individuals take hiatuses while 8 do not. Type 1 and 2 hiatuses were taken by territorial pairs, while Type 3 desertions are limited to females. Telemetry data from 22 territorial adults, each representing one eagle per territory, suggest that 8 of these individuals took hiatuses, likely encompassing most of Type 1 and 2 hiatuses. Preliminary telemetry analysis indicates that hiatus destinations trend towards the mountains approximately 50 to 80 km southwest, and the mountains and foothills around 120 to 200 km north-northwest of Denver, respectively. The question arises whether these hiatus destinations reflect pre-migratory stops inherent prior to territory holdings. Extrapolations based on limited telemetry data from 8 migratory individuals-comprising 4 former territorial males and 3 eagles tagged as

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juveniles-suggest that hiatus destinations were integral migratory stops prior to territorial establishment.

****Climate and resource variability entrain ecological dipoles in boreal bird irruption****I Widick, B Zuckerberg, J LaMontagne, C Strong, M Young***Presenting author: Ivy Widick, University of Wisconsin - Madison, widick@wisc.edu*

Avian irruption is the facultative winter migration of many individual birds outside of their resident range in response to climate and resource variability. Within a species, the synchronized movement of individuals creates regional anomalies in abundance. Due to associations with environmental variability, those regional patterns oscillate over time, forming ecological dipoles at continental scale. We used community science data on bird abundance and empirical orthogonal function analysis to identify irruption modes in a suite of nine boreal birds. Using winter temperature and tree seed production, we defined modes of variability in environmental drivers. We then compared spatiotemporal patterns of irruption in nine bird species to two potential environmental drivers, climate and resource variability, using maximum covariance analysis. Across species, we detected latitudinal and longitudinal modes of irruption, demonstrating north-south migration as well as a pendulum migration dynamic across the northern United States and southern Canada. All species demonstrated the expected associations with either climate or resource variability or both. In total, seven out of nine species displayed associations consistent with the climate variability hypothesis whereas six species showed support for the resource variability hypothesis. Even though these drivers were broadly important in explaining annual variability in bird abundance, unique patterns emerged among species' relationships with environmental variability. While irruption dynamics are likely formed by the influence of multiple environmental drivers, future climate change could disrupt cycles of variability, potentially altering spatial and temporal patterns of irruption.

Consequences of ignoring detection in estimating productivity from repeated brood counts*A Young, M Desmond, B Millsap, F Abadi***Presenting author: Aaron Young, New Mexico State University, aarony@nmsu.edu*

The development of N-mixture models that account for imperfect detection has improved our ability to model count data such as seasonal productivity. However, for raptor species including burrowing owl (*Athene cunicularia*), common survey and modeling approaches often do not account for variable detection probability. Further, even when detection is modeled, non-independent detection of individuals in family groups can bias productivity estimates. We conducted a simulation study to assess the performance of 3 different modeling approaches for productivity estimates. We compared models that 1) do not account for detection, 2) account for detection using a Poisson-binomial distribution, and 3) account for correlation on detection using a Poisson-beta-binomial distribution. We generated repeated-visit data sets with varying levels of detection probabilities and correlation and examined whether these models provide accurate estimates of productivity. We also applied these modeling approaches to 2 real-world data sets: repeated-visit counts of burrowing owl and Cooper's hawk (*Accipiter cooperii*) productivity. Our preliminary results suggest that models that do not account for detection (regressions of mean or max counts) tend to severely underestimate productivity, while N-mixture with a binomial detection model can substantially overestimate productivity when detection is highly correlated, as in our owl data set. Correlation values associated with our hawk data set did not substantially bias estimates from Poisson-binomial models. N-Mixture with a Poisson-beta-binomial detection model accurately captured true productivity at all detection probabilities and correlation values. Our results suggest that use of the Poisson-beta-binomial model when estimating productivity should be considered in a wider range of situations.

Physiological mechanisms of dispersal limitation in Neotropical rainforest birds and implications for tropical biodiversity*H Pollock**

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Presenting author: **Henry Pollock**, henry.s.pollock@gmail.com

Neotropical rainforests are the global epicenter of bird diversity, but why are there so many species in the Neotropics? Because the majority of speciation occurs in allopatry, one explanation for the incredibly high diversity of Neotropical birds is dispersal limitation. Specifically, the inability to move or disperse effectively should promote (1) allopatric separation of populations, (2) population differentiation, and (3) eventual speciation over evolutionary time. Although dispersal limitation has long been invoked to explain patterns of species diversity in Neotropical birds, the physiological mechanisms limiting dispersal ability are only beginning to be understood. Here, I conducted a literature review and compared three popular hypotheses about the physiological underpinnings of dispersal limitation in Neotropical birds: (1) narrow thermal tolerances, (2) visual sensitivity to light, and (3) limited metabolic capacity. My literature synthesis demonstrated that there is little evidence supporting hypothesis (1), suggesting that temperature sensitivity is unlikely to contribute to dispersal limitation. However, recent studies have provided robust evidence for hypotheses (2) and (3). Namely, forest understory birds have a) larger eyes and greater sensitivity to light than open habitat species, and (b) smaller wings and pectoralis muscles as well as lower myoglobin activity in flight muscles. Our findings suggest that sensitivity to light and limited metabolic capacity are the proximate mechanisms underlying limited dispersal ability in tropical rainforest birds. More broadly, our results indicate that evolution in stable environments can select for physiological specialization, with important implications for evolutionary patterns of species diversification and ecological resilience to environmental change such as forest fragmentation.

****Effects of Territory Density and Helper Sex on Red-cockaded Woodpecker Productivity****L Pharr, C Cooper, C Moorman, N Hostetter, C Sorenson, J Walters***Presenting author:* **Lauren Pharr**, North Carolina State University, lpharr@ncsu.edu

Over the past several decades, densities of the endangered Red-cockaded Woodpecker (*Dryobates borealis*; hereafter RCW) have increased due to intensive restoration and management of long-leaf pine forests and the strategic placement of artificial cavities. We used data from long-term nest monitoring of the RCW to understand current trends in reproduction over the years at 3 three locations: the Sandhills region in south-central North Carolina, Marine Corps Base Camp Lejeune on the central coast of North Carolina, and Eglin Air Force Base on the Gulf Coast in the western panhandle of Florida, and how it may relate to various factors including territory size, and helper sex ratios. We have found that RCWs are initiating laying earlier, with much larger clutches early in the season. In North Carolina, the larger clutches are not resulting in higher productivity due to elevated partial brood loss. However, in the southwestern portion of the range, increases in clutch sizes do not compensate for elevated brood loss, and the resulting declining productivity might be a preview of the future in North Carolina.

****Dynamic occupancy models reveal the impacts of habitat fragmentation on an old-growth forest specialist in Alberta****T Hart, A Crosby, L Leston, F Schmiegelow, E Bayne***Presenting author:* **Taylor Hart**, University of Alberta, tah@ualberta.ca

The Black-throated Green Warbler (*Setophaga virens*) is an old-growth interior forest specialist listed as a species of special concern in Alberta, due to concerns of habitat loss and fragmentation on their breeding grounds in the boreal forest. To understand their long-term spatiotemporal patterns in response to changing forest landscapes, we revisited past monitoring sites across Alberta, selected for their habitat suitability using the 'cure4insects' package in R. We used dynamic occupancy models to investigate the impact of distance to anthropogenic edges, such as seismic lines, roads, and harvested areas, on this warbler's colonization and persistence probabilities, as well as site turnover rates. We found that Black-throated Green Warblers were more likely to colonize and persist at sites further away from these disturbances, especially from the more abundant disturbance types, harvests and seismic lines. Notably, even in suitable habitats, we found high rates of site turnover, indicating low site stability. The results of our dynamic occupancy models highlight 'source' sites that merit greater conservation efforts compared to

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locations with higher turnover. Ultimately, ensuring the long-term persistence of Black-throated Green Warblers on their breeding grounds in northern Alberta will require the preservation of large tracts of undisturbed old-growth forests.

Invasion Genomics of the Scaly-breasted Munia (*Lonchura punctulata*) Reveals Multiple Introductions and Human-mediated Genetic Swamping in the Native Range

J Alderson, A Shultz, C Hung, C Yao, K BurnsPresenting author: **Jonah Alderson**, jonah042957@gmail.com

The Scaly-breasted Munia (*Lonchura punctulata*) is a songbird native to southern Asia. Due to its popularity in the pet trade, the Scaly-breasted Munia has become established in several parts of the world. We sequenced whole genomes of 37 individuals representing three introduced North American populations (southern California, northern Florida, and Puerto Rico) as well as several native populations (Taiwan, Philippines, Singapore, and China). Our results indicate that the Scaly-breasted Munia has at least two genetically independent introductions in North America. Puerto Rico and southern California cluster together and show signs of possible admixture with a different population, as compared to Florida. We also show evidence of non-native populations being introduced to the native range of the Scaly-breasted Munia. The pet trade seems to be gradually swamping pre-existing population genetic structure in the Scaly-breasted Munia, eroding current subspecies boundaries. Some introduced populations exhibit not only admixed genes but other signs of selection throughout the genome. The Scaly-breasted Munia represents an ideal opportunity to examine the effects of admixture and human-mediated secondary contact on the genome, as well as the effects of novel habitats on an introduced species.

Bald Eagle population growth despite high mortality

R Conrey, M Middleton, B Snyder, J Snyder, J Gammonley, M SmithPresenting author: **Reesa Conrey**, Colorado Parks and Wildlife, reesa.conrey@state.co.us

Bald Eagles (*Haliaeetus leucocephalus*) have made a dramatic recovery from DDT-era lows. In Colorado, the number of Bald Eagle nests has increased exponentially in recent decades, with eagles occupying patches of native vegetation within the urbanizing landscape of the Front Range. As the human population continues to expand, development and land use change create concerns about impacts on Bald Eagles, a species which generates high levels of public interest. To better understand demographics and space use of Bald Eagles and impacts of human disturbance, Colorado Parks and Wildlife has partnered with Bird Conservancy of the Rockies Bald Eagle Watch and many local partners to find and monitor eagle nests, and in 2020, we began tagging eagles with GPS/GSM transmitters. Here we report on productivity and survival rates. Apparent nest success has averaged 75 – 80%, with a higher rate of nests fledging three eaglets than has generally been reported in the literature. However, nest success dropped by ~20% in 2022, possibly attributable to an outbreak of Highly Pathogenic Avian Influenza (HPAI). Over half our sample of tagged adult male eagles have either died or lost or abandoned territories. Causes of mortality have included electrocution, vehicle strikes, HPAI, West Nile Virus, lead, and unknown sources. Given the continued increase in nest numbers, this relatively high rate of adult mortality and territory turnover were unexpected, suggesting that population growth is sustained by reproduction and immigration.

***Population dynamics, density dependence, and morphological change in the Island Scrub-Jay (*Aphelocoma insularis*)**

J Mouton, M Pesendorfer, S Morrison, S SillettPresenting author: **James Mouton**, The Ohio State University, mouton.13@osu.edu

Understanding contemporary population trends and their ecological drivers over time is a key goal in population ecology and critical for effective management and conservation. For species that live in

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variable environments, this includes estimating the effect of abiotic and biotic variation on key demographic processes to determine if the population could buffer against extreme conditions. We constructed an integrated population model to (1) assess population trends and (2) examine ecological drivers of population growth in Island Scrub-Jays (*Aphelocoma insularis*) from 2009-2019. Island Scrub-Jays are medium-sized corvids endemic to 250-km² Santa Cruz Island, California, USA, and are vulnerable to impacts of climate change and novel infectious disease due to their small population size and restricted range. Our results show that population size increased slightly over the last decade despite a period of severe drought. We also found evidence that density dependence, precipitation, and acorn abundance affected fecundity and the survival of non-breeding individuals, while minimum winter temperatures reduced breeder survival. Interestingly, mean bill size increased and tarsus length decreased among jays. Overall, our results provide an optimistic snapshot for this species, but also emphasize the species' continued vulnerability in the long-term due to its small population size and several emerging anthropogenic threats.

Demographic history of the Calcariidae family (longspurs and snow buntings)

L Cueto Aparicio, J Ross, K Marske, K Winker, G Wiley

Presenting author: **Luis Cueto Aparicio**, University of Oklahoma, l.cueto@ou.edu

The Calcariidae family, which includes longspurs and snow buntings, employs three habitat-use strategies: grassland specialists, arctic tundra specialists, and mixed users (arctic tundra and grasslands). During Pleistocene glacial cycles, these species underwent severe habitat changes due to climate shifts, which affected their demographics and genomic landscape. We aim to understand how these climatic fluctuations impacted the demographic and genetic variability of Calcariidae species according to their habitat-use strategy. To address this question, we use genomic data, demographic models (PSMC), and several indexes of genetic diversity. Our results suggest that during the last glacial period, grassland specialists were the most successful group. This advantage may have arisen because the grassland habitat remained relatively stable and continuous despite the strong climatic variations during glacial cycles. In contrast, arctic tundra specialists exhibit low population sizes, likely due to the cyclical advance and retreat of glacial layers, extreme latitudinal displacements, and habitat fragmentation. Currently, it is crucial to analyze the demographic and genetic profiles of species that are severely affected by economic activities and climate change, such as grasslands and tundra specialist

Spatially structured population or metapopulation? A case study with a threatened shorebird

R Swift, M Anteau, K Ellis, G MacDonald, M Ring, M Sherfy, D Toy, D Koons

Presenting author: **Rose Swift**, U.S. Geological Survey, rosejs swift@gmail.com

Species that are spatially distributed among patches of suitable habitat are often assumed to meet the criteria of a metapopulation. Metapopulation dynamics are determined not only by within-patch birth and death processes but also by between-patch dispersal movements of individuals that are infrequent, but critical to maintaining population viability across space and time. The degree to which the northern Great Plains piping plover (*Charadrius melodus*) breeding population functions as a metapopulation depends, in part, on the rate of movement amongst patchily distributed breeding areas. Here, we examined annual adult survival and breeding dispersal probabilities for 2,582 individuals at two spatial scales between 2014 and 2019. Consistent with a metapopulation structure, annual survival varied among breeding regions and across years (range: 0.741 – 0.898). We nevertheless found that breeding dispersal probabilities were high and unbalanced at both spatial scales examined, suggesting high connectivity within this region in contrast to metapopulation dynamics. Further, we detected context-dependent effects of reproductive success on dispersal decisions that differed based on the direction of dispersal. Our results here, as well as previous findings, contradict the paradigm that northern Great Plains piping plovers are structured as a metapopulation, and instead suggest a patchily distributed, likely panmictic, population, which has

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important implications for the conservation and management of this listed species. Our findings are also a general reminder that in the absence of robust knowledge of movement, spatial variation in birth and death processes across patches should not be conflated with metapopulation structure.

A three-decade study of recruitment in a migratory songbird: early life effects depend on population density and timing of breeding

S Mueller, N Wheelwright, D Mennill, A Newman, S Doucet, J Burant, S Dobney, G Mitchell, H Spina, B Woodworth, R Norris

Presenting author: Sarah Mueller, University of Guelph, sdmueller02@gmail.com

Recruitment of juveniles drives population dynamics. However, the ecological factors influencing recruitment are often poorly understood because juveniles disperse away from their natal areas, making them difficult to track from birth to breeding, especially in migratory species. Many extrinsic (e.g., population density, weather) and intrinsic (e.g., body mass, brood size, parent age, fledging date, hatching order) predictors can influence juvenile survival rates, but the potential for interactive effects between these variables on recruitment remains less clear. To evaluate ecological drivers of variation in local recruitment rates, we used 27 years of detailed reproductive data from a highly philopatric population of migratory Savannah sparrows (*Passerculus sandwichensis*) breeding on Kent Island, NB, Canada. The probability of local recruitment was lower for offspring of younger males vs. older males, higher for offspring from first broods vs. second broods, and differed based on the mating status (monogamy or polygyny) of the nest. Recruitment probability also declined at higher population densities and later fledging dates but, most interestingly, these declines were more severe for lighter nestlings. These findings suggest that the effects of early life conditions in the nest on recruitment depend on both ecological context and timing of breeding. Our results demonstrate the importance of considering multiple predictors of recruitment simultaneously and how these predictors can interact to shape population demography.

****Are the abiotic drivers of morphological variation in a tropical bird the same across space as they are across time?**

K Jordan, G Barrile, J Brawn, C Tarwater

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Understanding how species respond to abiotic factors is crucial for predicting species' responses to climate change. Studies often use a space-for-time substitution, whereby they evaluate how species respond across space to predict how they will respond to climate change over time. One of the major underlying assumptions of this approach is that species will respond similarly to abiotic factors across time as they do across space, and that local adaptation to abiotic factors is minimal. This study investigates this assumption by examining whether the abiotic drivers of morphological variation in the Black-crowned Antshrike (*Thamnophilus atrinucha*) are consistent across temporal and spatial scales. Using long-term temporal data (1977 - present) and spatial data (2016-2017) along a precipitation gradient in Panama, we analyze how body mass changes in relation to various precipitation metrics. Our research aims to determine if the same abiotic variables drive changes in body mass across time and space for both short-term and long-term rainfall metrics, or if we observe evidence of local adaptation to rainfall. This study both contributes to our understanding of how tropical birds respond to changing abiotic factors and whether one of the underlying assumptions of space-for-time substitutions is valid in this region of the world.

Phylogeography of Common ground doves and their lice: host-parasite evolution in island and mainland populations

P Brewer, A Worm, A Sweet

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Oceanic islands are ideal systems for understanding genetic diversity related to ecological context.

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Although free-living species from islands receive attention, little is known about island parasites and their host. Common ground doves (*Columbina passerina*) and their parasites are an attractive system to compare genetic variation with habitat connectivity. Despite their lack of long-distance migrations, *C. passerina* have dispersed throughout North and South American and Caribbean islands. *Columbina passerina* are hosts to several lice, including *Physconelloides eurysema*. Because lice are obligate parasites, we can compare the genetics of birds and their lice between islands and mainland populations to understand phylogeographic histories. We aim to address: 1. Are there differences in genetic diversity among *C. passerina* island and mainland populations? 2. Is the phylogeography of *Physconelloides* lice congruent with their hosts? To compare patterns of genetic diversity between *C. passerina* and *Physconelloides* lice, we obtained whole-genome sequences from island and mainland populations. We generated single nucleotide polymorphisms (SNPs) to estimate population structure of *C. passerina* and their lice. We calculated genetic diversity within each population. Overall, we found evidence for five populations of *C. passerina* from the Caribbean islands. Surprisingly, island populations of *C. passerina* had higher genetic diversity compared to the mainland populations. We also found both *C. passerina* and their *Physconelloides* from the Bahamas are genetically distinct. We also found lower genetic diversity in birds and lice from the small, isolated Cayman Islands. Our results show that host-parasite interactions and phylogeographic processes can be variable in an ocean island system.

***Unveiling Intentions: Exploring Attitudes and Behavior in Citizen Science Participation through the Lens of the Theory of Planned Behavior**

S Moreno, P Warren, S Lerman, P Marra, B Evans, R Reitsma, B Butler

Presenting author: Sebastian Moreno, sebastianmor@umass.edu

Citizen science engages non-professional volunteers in scientific research that advances scientific understanding. Programs like Christmas Bird Count and eBird amass extensive datasets and contribute to global avian monitoring efforts. One notable initiative, Neighborhood Nestwatch (NN), launched in 2000, aims to enhance avian ecological understanding and promote community involvement in bird monitoring across an urban-to-rural gradient. Despite its success, there remains a limited understanding of the factors driving participation in citizen science projects, particularly those marked by limited training and reduced social interactions between participants and scientists. Using the Theory of Planned Behavior (TPB), we explored motivations of 390 NN participants conducting resight forays and reporting data on color-banded birds. Our preliminary results indicate that attitude toward participation is positively influenced by participants' sense of importance in contributing to scientific research, connecting with nature, and contributing to bird conservation efforts. Furthermore, the subjective norm, reflecting societal approval, is strongly correlated with the perception that friends, family, and neighbors view bird monitoring as important, while perceived behavioral control, indicating ease of behavior performance, is positively associated with participants' confidence in understanding the provided reading materials. Notably, the perceived importance of scientists' endorsement did not significantly affect subjective norms. Findings from this study can inform the design of more effective communication and intervention strategies, ensuring that participant requirements are met while advancing the scientific goals of citizen science programs like Neighborhood Nestwatch.

Expanding the scope of ornithology by engaging diverse communities

S Lerman, S Moreno, P Warren

Presenting author: Susannah B Lerman, USDA Forest Service Northern Research Station, susannah.b.lerman@usda.gov

A question scientists, managers, and birders often ask is how they, their team, or their project can engage with diverse communities in ornithological research, management, or outreach events. This is a critical question to grapple with as the conservation of birds is intricately linked with human experiences with nature. Our fascination with birds spans throughout human history. No doubt, a bird's ability to fly, both short and epic distances, can conjure one's feelings of freedom. Further, they sing intricate songs, exhibiting dazzling colors and feather patterns, are frequently visible, and are found in our bustling city centers, neighborhood parks, backyards, and wild places. Birds surround us and can strengthen our

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sense of place, and their familiarity can increase the accessibility of the science we share and inspire conservation action. However, inequities in people's access to bird diversity exist in many cities around the world. Thus, while birds represent an ideal platform for engaging with the public, broadening engagement is an essential component of supporting more equitable access to birds and other nature experiences. To effectively answer the question posed above requires additional information about who we mean to engage and why it matters, the motivation and objectives for engagement, and how to expand the scope of ornithology – essentially the who, what, why, and how. In this presentation, we aim to provide an entry point for exploring these issues, and we provide examples of action that can be taken, drawn from the literature and our professional experiences.

****Leveraging local ecological knowledge to search for undocumented birds in Papua New Guinea**

J Gregg, J Boersma

Presenting author: Jason Gregg, Montana State University, jason.j.a.gregg@gmail.com

Tropical forests are inhabited by the majority of Earth's bird species yet remain undersurveyed. This limits our understanding of geographic distributions, patterns of diversity, and the conservation status of many taxa. Indigenous and local communities who call these landscapes home are critical partners for achieving intragovernmental global conservation goals and highly knowledgeable about regional biodiversity. Leveraging expertise of these communities can be a powerful approach to filling information gaps, and external investigators should view their role as one of connecting knowledge networks in an inclusive, equitable, and locally beneficial manner. Structured interview questionnaires are an important tool for incorporating local ecological knowledge into biodiversity surveys. My team combined interview questionnaires with bird surveys and camera trapping in Papua New Guinea to produce the first photos and video footage of the Black-naped Pheasant-pigeon (*Otidiphaps insularis*), a critically endangered terrestrial bird in the family Columbidae that had been undocumented for over a century. I am now adapting our methods for use in surveys of other poorly-known bird communities in the southwest Pacific. I will discuss incorporating ethnobiological interviews for searching for 'lost' species, how discovery narratives may be problematic, and how international biodiversity surveys can be designed for local benefit.

****The Global Urban Bird Survey: A novel approach to quantifying urban bird diversity through community science.**

P Preston, I Raji, A Syingi, D Mennill, L Martin, M Thiam, P Martin, G Serpa, F Bonier

Presenting author: Paul Preston, Queen's University, paul.preston@queensu.ca

Birds make up a vital and dynamic part of urban biodiversity across the globe; however, accurate measures of the abundance and diversity of birds in cities have been difficult to obtain as current methods for surveying birds are not designed to be conducted in dense, urban environments. Surveys of birds in cities typically occur in parks and green spaces, and generally in wealthy neighborhoods and cities in developed nations. These biases prevent us from effectively evaluating how birds use all the habitats found in cities, worldwide. It is imperative that we develop surveys that include a range of urban habitats and implement these surveys across both developing and developed nations to better understand biodiversity in cities. We developed the Global Urban Bird Survey, a community-based method for inventorying the birds in a city via acoustic recorders, to address the biases and limitations of previous methods. Community members were trained and coordinated by local expert collaborators, and then conducted repeated surveys in five cities around the world (Dakar, Senegal; Nairobi, Kenya; Rio de Janeiro, Brazil; Paris, France; and Toronto, Canada) between 2022 and 2024. Survey locations follow a stratified block-randomized design within the core of each city, and therefore are unbiased and distributed across habitats within the city. Here, we compare the ability of the Global Urban Bird Survey to accurately measure diversity and occurrence of species with that of more commonly used methods such as eBird and Breeding Bird Atlases to assess the potential value of this novel method. Global urbanization presents a profound challenge to species that live in cities, and understanding variation in bird occurrence and diversity in cities across the globe is important for mitigating negative impacts that cities have on

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biodiversity.

duckDNA: Engaging waterfowl hunters in the science of conservation genetics*R Moore, K Tucker, A Tunstall, K Victor, V Musni, M Brasher, P Lavretsky***Presenting author: Rae Moore, Ducks Unlimited, rmoore@ducks.org*

Contemporary genetic research is a critical component of wildlife management, providing researchers with information on a wide variety of behavioral, physiological, and ecological variables. Researchers at the University of Texas at El Paso (UTEP) recently began investigating the development of a hybrid swarm in the Atlantic Flyway as a result of historical release of domesticated game-farm mallards and subsequent hybridization with wild mallards. Hybridized mallards show differences in behavioral and morphological traits, which may impact migration patterns and annual productivity. Additionally, this pattern of hybridization is spreading westward across North America. Thus, it is crucial to build a spatially broad genetic database to monitor this trend across flyways. However, data collection at this scale suffers from geographic, temporal, and financial restraints. To address this need, Ducks Unlimited, Inc. and UTEP initiated a pilot project to engage waterfowl hunters in providing tissue samples from harvested ducks across the U.S. This project, termed duckDNA, aims to create the world's largest database of waterfowl genomes and enable expanded studies of genetic processes in waterfowl and their implications for population management. Over the course of the 2023–24 waterfowl hunting season, we received over 4,200 applications from interested hunters. We selected 313 hunters across 47 states for participation, with submissions from another 26 hunters that harvested hybrid specimens. This presentation will provide an overview of the duckDNA project and summarize findings from the 2023–24 season, including community engagement and planned improvements for the 2024–25 season.

Can we have citizens resight color banded passerines visiting feeders? Insights from a Brazilian low budget project*E Alexandrino, M Alcantara, G Costa, L Campos, T Bessi, B Matinata, K Ferraz***Presenting author: Eduardo Alexandrino, Cornell University, eduardoalexandrino@hotmail.com*

There is an expectation that citizens' enthusiasm for nature will support ecological projects based on citizen science anywhere. In 2019, aiming to investigate impacts caused by bird feeders in Brazil, the project 'Did I see a banded bird!?' started to monitor banded passerines visiting a feeder in the private reserve Legado das Índias (Atlantic Forest, Southeastern Brazil) with tourist's assistance. This reserve is a famous hotspot for nature enthusiasts in Brazil, receiving annually thousands of visitors from different nationalities. Visitors are invited to report time, day, and band combination of each banded bird observed through social media, email or phone messages to the project team. We banded 78 birds of 25 species (each individual with exclusive color and sequence) between Nov/2019 and Nov/2023. Within this period, 75 citizens reported 226 records of 32 banded birds in 97 days, while project's team achieved only 180 records of 27 birds in 25 days. Although 91% of citizen's records were valid (i.e., bird photography or text reporting a correct color of bands; date and time correctly reported), 13% took months to be reported to the project team and 26% were found in tourist's social media without any mention of our project (i.e., they were lost records). We also observed behaviors of other 46 visitors that were not aware of the project. Twenty-eight looked at the bird feeder when a banded bird was present. However, only seven visitors reported their records, indicating that 75% of useful records for the project are being lost. Although citizens are amplifying temporal extension of our low budget monitoring, we still need to devote substantial effort to engage them. Otherwise, the robustness of our investigation of impacts of supplementary feeding on wildlife will be compromised, as well as our intention to share knowledge among citizens.

Familiarity with social partners influences affiliative interactions but not spatial associations in feral parakeets*C O'Connell, A van der Marel, E Hobson***Presenting author: Elizabeth Hobson, University of Cincinnati, elizabeth.hobson@uc.edu*

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To successfully navigate complex social environments, animals must decide who to interact with, when, and how often. These social decisions are necessary to balance the risks and benefits of associating and can have important consequences for individual fitness and group stability. We investigated how familiarity among group members of monk parakeets (*Myiopsitta monachus*) affected the presence, context, and frequency of several spatial and affiliative association types. We created a captive group of 22 feral-caught parakeets from four geographically distinct capture sites. Using social network analysis and permutation tests, we identified patterns of assortativity across several spatial associations and affiliative interactions. We then compared the presence, strength, and timing of associations among birds from the same site (familiar) and across sites (strangers). We found that proximity between birds was unaffected by capture site, but that affiliative interactions, like allopreening and beak touching, occurred significantly more often among familiar birds. All affiliative interaction networks, but not spatial networks were more densely connected, and most relationships were stronger among familiar birds compared to strangers. Lastly, we found that most affiliative interactions, but not spatial associations, among strangers occurred significantly later in the experiment compared to familiar birds. Our results provide evidence that monk parakeets discriminate between familiar and unfamiliar birds and suggest that birds use their previous experiences to make affiliative social decisions. Insight into how and when individuals decide to allocate their affiliative investments has important implications for conservation outcomes, like successful reintroductions to the wild, by maximizing survivability and reproduction post-release.

***Social associations of the endangered koloa maoli and the role of plumage and genetic relatedness**

P Keerthipriya, C Malachowski, B Dugger, K Uyehara, A Engilis, J Eadie, P Lavretsky, S Turnbull, C Zagnoli-Robb, C Wells

Presenting author: **P Keerthipriya**, Colorado State University, keerthipriya.palanivel@colostate.edu

The koloa maoli (*Anas wyvilliana*) is the last remaining endemic duck species found in the main islands of Hawai'i. The biggest threats facing this species are hybridization with feral mallards, and avian botulism outbreaks. Currently, the island of Kaua'i contains the largest population of genetically pure koloa, which are largely restricted to the island. Little is known about social relationships in sedentary bird populations, but information on social associations in koloa might shed light on preferences for or against feral mallards and hybrids, and inform planned translocation efforts of koloa to other islands. Additionally, other non-migratory species of island birds, including some in Hawaii, show microgeographic spatial genetic structuring, in which individuals found close together are more related than those found farther apart. Spatial genetic structure is a potential liability for maintaining koloa genetic diversity, if highly localized outbreaks of botulism remove entire lineages of genetic diversity. From 2010-2015, koloa were captured, banded, and recaptured on Kaua'i. We used the adult capture data to infer social associations from trap co-occurrence. We constructed social networks, and examined whether koloa have preferential associations based on plumage traits (monochromatic 'koloa-like' vs dichromatic 'mallard-like') or genetic relatedness (for a subset of genotyped ducks). We also used genetic and location data to look for evidence of female and/or male microgeographic structure in koloa. While we did find persistent social associations in adult koloa, they were not apparently influenced by plumage traits. Thus, koloa do not seem to prefer individuals with mallard-like plumage. Importantly, we found no spatial patterns of relatedness within the largest refuge. This suggests that localized botulism outbreaks will not remove correlated genetic diversity in this endangered endemic.

****Dining with Wolves: Are the Rewards Worth the Risks?**

S Richman, D Tomback, N Grevstad

Presenting author: **Summer Richman**, summer.merrell@ucdenver.edu

In the wild, Common Ravens (*Corvus corax*) and, where sympatric, Black-billed Magpies (*Pica hudsonia*) (Family Corvidae) show up quickly at gray wolf (*Canis lupus*) kills and scavenge carcasses, often feeding near wolves. Ravens and magpies also visit wolf enclosures at wildlife sanctuaries in Colorado. Individual birds attempt to take meat from wolves, but no information is available on the relative frequency of food rewards vs. bird injury or death. Working at the Colorado Wolf and Wildlife Center, Divide,

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Colorado, we asked whether ravens and magpies associate with wolves at feeding time; what proportions of ravens and magpies are rewarded with food per enclosure; whether individual wolves differ in their reaction to the birds; and if the birds are harmed by interacting with wolves. We also examined the effects of food type, food amount, and daily temperature on trends in bird numbers. We observed wolf and bird behavior during daily feeding tours across 20 visits and within seven to eight wolf enclosures per visit. Overall, 33% of ravens and 43% of magpies received food rewards within each enclosure. Individual wolves differed in their responses to ravens and magpies but most often ignored bird presence. We found no effect of food type on bird numbers but a trend in higher raven numbers with food amount. There was a statistically significant negative relationship between daily maximum temperature and number of ravens, and a significant positive relationship between daily minimum temperature and magpie numbers. Dining with wolves represented a moderately high probability of food reward and overall low risk to ravens and magpies.

****Corticosterone manipulation alters patterns of social interaction in breeding tree swallows**

T Ryan, C Taff, D Chang van Oordt, M Pipkin, M Vitousek

Presenting author: Thomas Ryan, Cornell University, tar87@cornell.edu

Social interactions can serve as a source of information that helps calibrate reproductive decision making and could be especially important to organisms experiencing a challenging environment or event. Here, we assess how a common social tactic-visiting neighbors' nests by breeding female tree swallows (*Tachycineta bicolor*)- is impacted by an experimental increase in corticosterone levels. We hypothesized that birds facing challenges invest more heavily in gathering social information, and that this is mediated by corticosterone. We also hypothesized that the value of the information provided by challenged birds is lower, and thus they are visited less by conspecifics. Corticosterone levels were manipulated by a minimally invasive technique using corticosterone dissolved in a DMSO gel placed atop a fake egg adhered inside the nest. Female swallows treated with exogenous corticosterone engaged in more trips to neighbors' nests and were visited less frequently than controls. This effect was most apparent in the period when nestlings were young-immediately following the end of the treatment period-and dissipated as nestlings aged. Females that visited other nests more fed their own nestlings at a lower rate, suggesting that these social interactions may be costly. These results are consistent with a function of social information in contextualizing challenges-potentially to inform fitness-critical decisions-and suggest that corticosterone mediates social information gathering.

***Tracking social bird behaviour highlights the changing value of human resources for desert species across seasons.**

K Oswald, U Roll, O Berger-Tal, T Rozenberg, K Oswald, O Keynan, G Oliveira de Caetano, S Toledo, R Nathan

Presenting author: Krista Oswald, Ben-Gurion University of the Negev, knoswald@gmail.com

The Anthropocene is characterized by rapid and intense environmental changes, necessitating species to produce accelerated and diverse coping mechanisms. Animal behaviour can potentially be quickly modified to help animals adjust to these rapid changes. For desert species, human development may help buffer against resource scarcity and provide reliable resources in an otherwise stark environment. We used high-throughput tracking technology to explore group behaviour of a social living bird (the Arabian babbler - *Argya squamiceps*) in a mosaic of human-modified and semi-natural habitats in the Negev desert, Israel. We tracked 21 birds that belonged to 10 groups over 134 days, collecting 727,605 localizations from late summer to early winter, a period in which natural resources increases. We highlighted that groups made use of different habitats as seasons changed. Toward winter, we found groups spent more time outside settlements, had smaller home-ranges, and were less territorial. Moreover, birds' resource dependence inside settlements altered inter-group interactions. We further

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found that even a small section of uncultivated agriculture land (~1 km²) prevented daily movement. All together, we see how the interaction between resource availability and modified or natural habitat, alongside seasonal environmental changes, are key to understanding animal behaviour in the Anthropocene.

****The scale of social information use in an endangered metapopulation****M Beatty, R Fletcher***Presenting author: Meghan Beatty, meghan.beatty@ufl.edu*

Habitat characteristics are expected to influence avian dispersal, but empirical investigations on the role of other information use in real-world metapopulations remains limited. Social (e.g., conspecific density or reproduction) and private (e.g., personal reproduction) information can drive dispersal by modifying individual behavior. Birds may gain information from exploring multiple patches before dispersal and the scale of information use may differ between emigration and immigration. The Everglade snail kite (*Rostrhamus sociabilis plumbeus*) is an endangered wetland raptor endemic to Florida in the U.S.. Snail kites are semi-colonial nesters with access to social information. Yet, it is unknown whether kites use social information. We determine if, what form (i.e., conspecific density or reproduction), and at what scale social information was used for both emigration and immigration, and if these relationships were stronger or weaker than private information use over 24 years. Using mark-recapture data on banded adults re-sighted at nests, we estimated the relationship between information available in the previous year and dispersal in the following year. We considered social information available at three scales: within 2 km of the nest, individual wetland, and region. In addition, we experimentally tested social information use with playback and decoy equipment. We found emigration had the strongest relationship with personal reproduction, where kites with successful nests were less likely to emigrate (a win-stay, lose-switch strategy). Immigration had the strongest relationship with conspecific reproduction (i.e., number of nests) in a wetland in the previous year. Kites were attracted to playback and decoy treatments, corroborating long-term observational data. Great effort is put into maintaining breeding habitat for endangered birds. These results highlight how birds may also rely on social information and use it differently in emigration and immigration.

Designing effective stewardship and post-restoration management plans through co-production to protect vulnerable Gulf of Mexico coastal birds**N Michel, J Fuller***Presenting author: Nicole Michel, National Audubon Society, nicole.l.michel1@gmail.com*

Coastal breeding birds are vulnerable to human disturbance, and as a result conservation plans recommend increasing stewardship efforts (e.g., fencing, signage, and outreach) designed to reduce and mitigate these impacts. While coastal bird stewardship efforts have a long history and demonstrated impact across the Gulf, uncertainties remain about best practices. We implemented a NOAA-funded co-production process, bringing together scientists, resource managers, and other impacted and influential parties from across the western Gulf of Mexico. Together we designed a study to address uncertainties that hinder decision-making and implementation of effective stewardship activities. Here, we present our process as a case study of a co-production effort to conserve coastal birds in the Gulf. We used Structured Decision Making to build a broad and diverse co-production team, develop and refine a problem statement, derive influence diagrams and research questions, and select hypotheses for further study through a series of virtual workshops and planning calls. This led to submission of a proposal to investigate the relative efficacy of various stewardship activities implemented across a range of ecological and social site conditions, and the additive impact of community-wide education and outreach campaigns (i.e., Community-Based Social Marketing) to alter human behaviors (thereby reducing human disturbance to coastal-breeding birds at study sites)? Over the next five years we will conduct collaborative research to address these questions and develop, share, and implement scientifically based, management-ready, effective stewardship plans to conserve coastal breeding birds across the Gulf of Mexico.

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Bird song matters for psychological well-being along an urban community trail*K Sanchez, L Ferguson***Presenting author: Karina Sanchez*, University of New Hampshire, urbanbirdnerd@gmail.com

Humans in developed countries spend much of their time indoors. This disconnect can deprive individuals of the health benefits that nature provides. There is emerging evidence that both biodiversity and natural sounds can play a role in human well-being. In addition to spending more time indoors, many individuals are choosing to live in more urban settings, where access to nature can be even more difficult to achieve. One of the more ubiquitous soundscapes across the globe is that of birdsongs. Birdsong diversity in natural areas has been demonstrated to positively impact people's well-being and experiences in nature. However, there are few studies with mixed results on whether this natural soundscape achieves a similar positive effect on humans living in urban areas. In this study, we experimentally tested the effect of birdsong and perception of birdsong diversity on people's psychological wellbeing along an urban community walking trail. We hypothesized that the presence of birdsong alone will have a positive effect on perceived restoration. Further, we hypothesized that if individuals are aware of the diversity on the trail, their perceived restoration would be higher. We artificially exposed trail users to ten bird species songs on speakers between August and October 2023. We collected 120 survey responses from users during our control periods and 133 survey responses during our treatment periods. Preliminary results suggest that the presence of birdsong positively impacts perceived restoration and well-being in trail users. As cities prioritize accessible outdoor spaces for residents to recreate, studies such as ours can provide key insight into why spending time outdoors can positively impact community wellbeing.

People and Birds: Balancing Conservation Priorities through Coproduction of Scientific Knowledge and Human Dimensions**A Dayer, K Holland, D Yeany, M Young, A Roth, C Stanley, Q Carvey***Presenting author: Ashley Dayer*, Virginia Tech, dayer@vt.edu

The Road to Recovery (R2R) initiative formed in response to the loss of 3 billion birds. R2R's vision is to use targeted and actionable science to recover North American bird populations before they become endangered or extinct. While many in the conservation community acknowledge that both biological and social sciences are important, the reality is – for conservation and action- they are inseparable. Bird conservation is inextricably linked to human dimensions via shared resources, shared landscapes, and shared conservation threats and needs. R2R is taking an approach to incorporating social science, co-production and communications through a more holistic group of partners in conservation. In doing so, support is guaranteed across diverse partners, those implementing and those impacted by conservation actions, and strives to eliminate the implementation gap. In this presentation, we will provide considerations for using a coproduction approach to bird conservation in both research and conservation delivery as well as incorporating human dimensions work through examples from R2R recovery efforts for tipping point species including species Evening Grosbeak, Yellow-Billed Cuckoo, Golden Winger Warbler and more.

Ethnoornithological Study in Two Communities of Tlahuiltepa, Hidalgo, Mexico.**K Uribe Valero, G Alcántara Salinas, R Ortiz Pulido***Presenting author: Karla Paola Uribe Valero*, karlauv28@gmail.com

Ethnoornithology explores the knowledge that have human communities about birds, shedding light on perception, classification, uses and symbolism. In this study, we document and analyze it in two communities of Hidalgo State, Mexico. Using ethnographic methods, we gathered information from 31 individuals (ages 14 to 90), yielding 61 local names for 82 bird species. Morphosyntactically, 40 names use monomial nouns (e.g., 'Cachitas' for *Bombycilla cedrorum*); 7 use binomials (e.g., 'Collita' for *Myioborus pictus* y *M. miniatus*); 25 comprise a noun and modifier (as in 'Zopilote redondo' for *Coragyps atratus*); and 1 contains three lexical units (e.g., 'Ticolote picametate' for *Glaucidium brasilianum*). These names often reference bird attributes. Prominent avian species in the region include calandria (*Icterus* spp. and *Pheucticus melanocephalus*), jilguero (*Myadestes occidentalis*), paloma (*Columbidae*), and

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gallina de monte (*Dendrotyx barbatus*). Although the indigenous language is no longer spoken, certain indigenous names persist, e.g., 'Titisha' (for *Herpetotheres cachinnans*) and 'Mexcodo' (for the gizzard). Studies like this have the potential to contribute to avian local conservation efforts by allowing us rescue, conserve, value and use the ornithological knowledge developed during centuries within the human communities.

Narco-trafficking and counterdrug efforts as emerging threats to forest birds in Central America

A Rodewald, A Lello-Smith, N Magliocca, M Strimas-Mackey, K McSweeney, S Sesnie, E Nielsen

Presenting author: **Amanda Rodewald**, Cornell Lab of Ornithology, Dept Natural Resources & Environment, arodewald@cornell.edu

Complex socioecological dynamics can have unexpected consequences for biodiversity conservation. Narco-trafficking is one such example that accelerates forest loss through the construction of illegal roads and landing strips to move bulk shipments of narcotics, expansion of cattle pastures to launder money and control territory, and subsidization of land-grabbing and resource extraction in previously remote regions. We examined the interplay between narco-trafficking and biodiversity conservation by quantifying the spatial congruence of important areas for resident and migratory forest birds and lands that are likely to attract cocaine traffickers in the future given their constant displacement by counternarcotic activities. Our work leverages eBird data and research by Magliocca et al. 2022, who estimated changes in landscape suitability for cocaine trafficking in Central America. Following peak interdiction activities, suitability for narco-trafficking increased within 69% of the most important areas for tropical residents and 62% for migratory birds. Over half of migratory species had >25% of their global population – and 20% of species had >50% – within areas expected to become more suitable for narco-trafficking. Moreover, areas of increased suitability coincided with the largest remaining forests in Central America and lands that are disproportionately settled by Indigenous people. Our research reinforces the idea that seemingly unrelated social issues can have serious consequences for cultural and biodiversity conservation. We encourage the U.S. and Central American nations to reform drug policies in ways that improve collaborative governance, enhance transparency and the rule of law, and especially, strengthen Indigenous and community rights, land tenure, and capacity.

***Human dimensions of cat and collision caused bird mortality**

S Carlson, T Phillips

Presenting author: **Shelby Carlson**, Cornell Lab of Ornithology, scc268@cornell.edu

North American bird populations have decreased by nearly 30 percent since 1970 (Rosenberg et al. 2019). After habitat loss, predation by free-roaming domestic cats (*Felis catus*) and collisions with windows are among the leading causes of bird mortality throughout the continent. Predation by cats and collisions with windows collectively result in the loss of over 3 billion birds every year in the United States alone (Loss et al. 2015). While extensive research has been dedicated to understanding the ecological consequences of cat and collision caused bird mortality, relatively little has been conducted to understand human thought and behavior as it relates to these inherently anthropogenic sources of bird mortality. In fact, although the earliest scientific record of a bird-window collision in North America dates back to the early 1800s (Nuttall, 1832), only four studies published to-date have applied theories and methods from the social sciences, and only two have undergone peer-review. Here, we present quantitative survey data collected from approximately 4,000 residents of the United States and Canada to better understand public perceptions of and preferences for the myriad evidence-based mitigation strategies available to-date. Using experimental survey design, we also examine the effect of different message framing regarding these mitigation strategies to better inform future public communication efforts by conservation scholars, practitioners, and policy-makers alike. Advancing current understanding of the human dimensions related to avian mortality caused by window collisions and cat predation, this study provides a critical contribution toward bending the curve to bring birds back.

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Novel broadcast transmitter reveals differences in acoustic structure between broadcast and whisper songs of 'Oma'o (Myadestes obscurus)*A Navine, K Paxton, E Netoskie, E Tysall, E Paxton, P Hart***Presenting author: Amanda Navine, University of Hawai'i at Hilo, navine@hawaii.edu*

Acoustic signaling is a common mode of communication for many animal species and is well studied in birds. However, the overwhelming majority of studies on avian vocal behavior have focused on high-amplitude broadcasted songs and calls that are easily discerned by the human ear. Low-amplitude 'whisper songs' are a taxonomically broad phenomenon that could play an important role in the suite of behaviors birds use to communicate. Due to its cryptic nature, there are inherent difficulties in capturing high quality whisper song recordings without interrupting natural behaviors. Thus whisper song acoustic structure is poorly understood and its potential function remains the subject of debate. Here, we present one of the first quantitative assessments of the acoustic structure of whisper song in birds. Using a novel broadcast transmitter we collected high quality recordings of broadcast and whisper songs from the ʻŌmaʻo (Myadestes obscurus), a thrush species endemic to the Island of Hawai'i. The transmitter was attached to the birds and broadcasted radio-signals of all vocalizations produced by the individual to distances over 100 m away which minimized disruption of the birds' normal behavior while recording. We demonstrate that ʻŌmaʻo whisper songs are a distinct class of vocalization that differ from broadcast songs in acoustic characteristics beyond amplitude, such as song length, frequency, and length of silent intervals between notes. These findings, in conjunction with habitat-associated variation in the rate at which ʻŌmaʻo emit these vocalization types, indicate broadcast and whisper songs likely serve separate functions.

****Battle of the Banded: Variation in Avian Singing Behavior Reflects Fighting Ability****E Stewart, J Kelley***Presenting author: Erin Stewart, University of Wyoming, estewa12@uwyo.edu*

Animals communicate through various mechanisms, one of which is sound production. Among birds singing serves many different functions, but one of the primary functions is territory defense. Though the act of singing alone serves as a deterrent to competitors, the particular way in which individuals sing conveys additional information regarding their fighting ability, also known as resource-holding potential (RHP). RHP is the likelihood that an animal will win a competition for a resource, and is linked to the traits of the individual. I examined the relationship between RHP and singing behavior using the chestnut-backed antbirds (*Poliocrania exsul*) as a model system. Males and females of this tropical species form long-term pair bonds and sing and duet year-round to defend permanent territories. I investigated whether individual song traits (including song type, skill, and consistency) and pair song traits (including duet number and coordination) communicate RHP in this species. I used body size and territory quality as intrinsic and extrinsic proxies for fighting ability respectively, following the assumption that bigger birds on higher-quality territories are better fighters. My results indicate that multiple components of individual and pair song are correlated with body size and territory quality. Overall, this shows that vocal traits do indeed convey information about fighting ability such that animals are likely able to assess opponents through song alone before deciding whether to escalate to physical conflict or flee.

****Investigating the function of extreme variation in the Corvid female-specific 'rattle call' display and the mechanisms responsible****C Tarango, J Fitzpatrick, N Sly***Presenting author: Christopher Tarango, cat253@cornell.edu*

The 'rattle' is a female-specific display given by some members of the avian Family Corvidae. Predominantly directed toward conspecifics during active or potential territorial disputes, the rattle call is typically a rapid series of staccato clicks given with the bill pointed skyward while flaring the tail feathers and bobbing the entire body up and down. Unlike many studies of avian song, the rattle display's multi-modal nature provides powerful support for homology in phylogenetic analysis, even when

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comparing extremely diverged vocal elements. Though the display remains relatively stable across genera, the rattle vocalization of the genus *Aphelocoma* shows incredible patterns of variation, both across and within species. The Florida Scrub-Jay (*Aphelocoma coerulescens*) had been previously known to give three distinct rattle call types, more than any other species. To study this variation and address each of Tinbergen's four questions, I recorded over 1000 rattle calls from 150 individual females spanning all genetic populations across Florida. I also examined recordings from three collaborators for a total dataset that spans four decades. The calls and their individual notes were measured using Raven Pro software. I found evidence of at least six previously undescribed rattle types and seven distinct note types. One population that maintained elements of three call types in 2010, had just one by 2023 despite the relative density of birds remaining stable. In this talk I will provide evidence for the function of this variation, potential mechanisms by which novel call types arise, the development of the call over a female's lifetime, as well as the evolutionary history of the rattle call display.

Patterns of geographic song variation in both morphology and performance in Atlantic seaside sparrows (*Ammodramus maritimus*)

G Hough, M Shah, O Vilceanu*Presenting author: Gerald Hough, Rowan University, hough@rowan.edu*

Seaside sparrows (*Ammodramus maritimus*) have a complex song that can include whistle, sweep, trill and buzz elements. These birds sing 3-5 different songs per bird, and there is a notable lack of song sharing between males in each locale. One common feature of these songs is that they tend to end with either a trill or a trill/buzz combination. To date, there has been no rigorous morphological analysis of song content, order of syllables, and performance metrics of their songs, and whether song morphology and performance varies geographically across the species range. As a first step, we examined 179 different songs that we personally recorded from 12 different locations in New Jersey (NJ) and Delaware (DE) from 2012 to 2023. We then calculated the relative frequency of syllable types per song and measured the trill performance by multiplying the bandwidth with the number of trill elements for each trill in the song. We found statistically significant increases in the number of trill elements in more southwestern songs (DE, western NJ), as well as increased terminal trill performance. Since these birds do not match song types with neighbors like in other species, trill performance may be a better indicator of male quality than matching songs of mentor or perceived superior males in communities with higher sparrow density (DE), and less important in less dense areas (Eastern NJ). Trill rates also significantly increased in songs where birds sang more than one trill. In addition, eastern NJ birds had simpler songs with less elements (4 vs 6) and more non-trill elements than DE birds. While admittedly derived from a limited dataset, these results suggest several patterns of geographic variation that may be missed if simply looking for groups of birds sharing unique songs in one region.

****How loud do birds sing?**

S Lapp, T Rhinehart, E Bayne, D Yip, B Edwards, E Knight, J Kitzes*Presenting author: Samuel Lapp, sam.lapp@pitt.edu*

Quantifying birds' singing volume is necessary for many behavioral and physiological studies on energy budgets, mate preferences, and other social interactions. Song volume can be estimated from digital recordings given distance to the bird, the recording hardware calibration, and habitat attenuation. Experiments have measured a handful of species' singing volumes, which are typically between 75-95 dB SPL re. 20 μ Pa at 1 m. Acoustic monitoring with automated recording units (ARUs) provides an opportunity to greatly increase the quantity and diversity of song volume estimates in natural conditions. However, the distance to a singing bird in ARU data is unknown. Therefore, we devise and apply a workflow for estimating bird song volume from ARU data, using acoustic localization grids to record and triangulate birds and a novel statistical model to estimate source volume and habitat attenuation. We apply the method to two avian forest communities. We collected thousands of calibrated recordings of bird songs with known positions and estimated the source volume of songs from 14 species in wild bird

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communities in Pennsylvania and Alberta. Species' mean song volumes were 86-100 dB SPL re 20 μ PA at 1 m, and within-species variability in song volume was high (stdev. 7.4 dB). The model's estimate of habitat attenuation of sound (after accounting for spherical atmospheric loss) was non-significant ($p=0.52$). We caution that song volume estimation in forested environments may be error-prone due to angle-dependent attenuation when ARUs are deployed directly on trees. We provide open-source Python implementations of our workflow to facilitate further study of bird singing volume with passive acoustic monitoring.

***Geographic variation in a call vocalization of the Carolina Wren (*Thryothorus ludovicianus*) in the southeast United States**

S Palmer, D Zapata, R Kimball*Presenting author: Shelby Palmer, University of Florida, shelbypalmer@ufl.edu*

Vocal signals are integral to avian communication, and most bird species possess a suite of distinct vocalizations of various levels of stereotypy. Much research has focused on intraspecific variation in songs, complex vocalizations specific to Passerines (songbirds) given mostly by males to defend territories and attract mates. Intraspecific variation in calls, the remaining suite of vocalizations, has received less attention in Passerines but is well-suited for investigating evolutionary processes, as calls are usually less acoustically complex than songs, vary less within individuals, and are less subject to vocal learning in the Passeri suborder. This project investigates geographic variation in a call of the Carolina Wren (*Thryothorus ludovicianus*), a songbird occupying the eastern United States and northern Mexico. The call of interest, known by the onomatopoeia 'cheer,' appears to have an acoustically distinct variant in the southeast United States. Although population- and individual-level variation in Carolina wren songs is well-studied, geographic variation in the 'cheer' has not been quantified, nor have hypotheses for its variation been proposed. This project aims to (1) derive quantitative measurements of the 'cheer' across its putative transition zone, (2) investigate whether the transition is related to geographic or physical environmental variables, and (3) provide a high-resolution map of 'cheer' variation to facilitate future population genetic work in Carolina Wrens. Acoustic data will be collected in latitudinal transects across the putative transition zone in summer 2024 and 'cheer' variation will be quantified using R scripts written by the author to automate multivariate acoustic data extraction.

***Conservation Status of Globally threatened Lesser Adjutant Stork (*Leptoptilos javanicus*) in the Terai Wetlands of Nepal**

P Pandey*Presenting author: Prava Pandey, National Lake Conservation Development Committee, prabhapandey2012@gmail.com*

Lesser Adjutant Stork *Leptoptilos javanicus* is wading bird often found in large rivers and lakes of Nepal, India, Sri Lanka, Bangladesh, Myanmar, Thailand, Vietnam, Malaysia, Laos, Singapore, Indonesia and Cambodia. It is the local resident species in the lowland of Nepal generally distributed in wetlands of 250m altitude. It feeds mainly on fish, frogs, reptiles and large invertebrates, carrion, small birds and rodents. The species is listed as Vulnerable in IUCN Red List of Threatened Species. Hunting, over fishing, wetland degradation, loss of nesting trees agricultural changes and wetland pollution resulted in declining of Lesser Adjutant Stork. This study aimed to provide the population status, habitat preferences, potential threats and the conservation activities for the Lesser Adjutant through the nest search, individual count and monitoring conservation activities done by the different stakeholders in the Terai wetlands of Nepal. Vulnerable Lesser Adjutant storks are successfully breeding at higher numbers than expected in Nepal. The study of the species across the country's southern plains indicates their population are increasing. Monitoring the number of Lesser Adjutant and activities indicates about the status of wetlands ecosystem. However, more conservation related work needed to be done to return back for the species population. For this, different stake holders including local governments are helping in awareness raising programs for this important bird whereas conservation action plan related to wetlands and its inhabits species are to be upgraded by the Provincial and Federal Government of Nepal.

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***Assessing the success of the release of captive White-rumped Vultures in Nepal**
A Joshi, J Mallord, K Bhusal, D Rana, I Chaudhary, D Thakuri, B Karki*Presenting author: Ankit Bilash Joshi, Bird Conservation Nepal, ankit@birdlifeneपाल.org*

The population of Gyps vultures, particularly the White-rumped Vulture, has drastically declined 97% in South Asia, with Nepal, experiencing a decline of 91%, mainly due to unintentional poisoning from diclofenac. To combat this, Nepal banned diclofenac in 2006 and initiated a breeding program to reintroduce vultures into the wild. Around 60 adult White-rumped Vultures have been part of the breeding program at the Vulture Conservation Breeding Centre in Chitwan National Park, successfully producing 18 fledglings. Releases of captive-reared and bred vultures began in November 2017. These birds undergo health checks before transfer to the release aviary, where their behavior is monitored for up to six months. Subsequently, they receive another health check and satellite tagging before soft release into the wild. 139 White-rumped Vultures, both wild and captive birds, have been tracked to monitor their survival. Annual survival estimates for adult and subadult vultures are similar to those in other parts of the world, but released birds experience higher mortality rates, especially among adults. No evidence suggests that deaths were caused by diclofenac poisoning. Predation, infection, and electrocution are identified as main causes of death. The breeding program has made amendments to improve success, including hygiene maintenance, rotational feeding, and expanded flight training. However, some challenges persist, such as vultures being picked up as weak because they have been in the breeding center for more than a decade. Improved pre-release fitness checks and health examinations are now conducted. Efforts to prevent electrocution and dog aversion training are under discussion for potential implementation before release. Improvements to the post-mortem protocol aim to reduce uncertainty regarding the causes of death.

Population genomics and disease susceptibility in the endangered white-winged duck *Asarcornis scutulata***C Balakrishnan, D Foote, P Bolton***Presenting author: Christopher Balakrishnan, National Science Foundation, christopher.balakrishnan@gmail.com*

The white-winged duck (WWD) *Asarcornis scutulata* is one of the rarest species of waterfowl in the world. Whereas the WWD range once spanned South and Southeast Asia, now only small, fragmented populations persist. As a part of a broad conservation strategy, Sylvan Heights Bird Park in Scotland Neck, NC has maintained a captive breeding population of WWD since the import of birds to the United States in the 1970s. Management of the captive population, however, has been challenged by the birds' high susceptibility to avian tuberculosis (*Mycobacterium avium*). We used whole genome sequencing to compare patterns of genetic diversity in captive and wild WWD. Overall levels of genetic diversity in WWD were extremely low, similar to other endangered or threatened bird species. We found that current WWD held at Sylvan Heights have reduced genetic diversity, longer- and more runs of homozygosity (ROH) relative to birds sampled 25 years ago at the same facility. Most importantly, we found that more highly inbred individuals had shorter lifespans, succumbing to tuberculosis infections earlier in life. Taken together our findings suggest that long-term captive breeding of WWD is not sustainable without improved measures to prevent or treat *Mycobacterium* infections and/or the incorporation of additional genetic diversity into the captive population

****Can nesting in boxes mitigate nest site loss due to sea level rise for endangered Northern Atlantic roseate terns (*Sterna dougallii*)?****J Espinosa, M Rubega***Presenting author: Jessica Espinosa, jessica.espinosa@uconn.edu*

The roseate tern is a federally endangered, migratory seabird that breeds in the North Atlantic and winters in the southern hemisphere. Great Gull Island, located at the mouth of Long Island Sound, is one of only three highly populated island colonies in the western hemisphere, making it a critical source population for other colonies. However, rising sea levels threaten nest site loss, especially for nests located in the rocky

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revetment surrounding the island. Previously we examined nest vulnerability to sea level rise and found many rock nests on the island are vulnerable by 2100. Thus, if roseate tern populations on the island are to persist, management actions will need to be taken. Nest boxes are one tool we can use to create more nesting habitat higher on the island and potentially mitigate nest site loss. We aimed to determine drivers of occupancy and productivity to assess if roseates could maintain similar breeding success in box and rock nests. As only about 1/4 of the 2500 nest boxes currently on the island are occupied, we determined which characteristics led to highest box occupancy and designed an experiment to examine nest box characteristics in a controlled setting, finding certain box types were more likely to be occupied than others. Finally, we monitored chicks in both rock and box nests to understand how productivity compares between habitat types and among box types. Here, we present results that suggest box nests have similar productivity to rock nests and are a viable management strategy to combat nest site loss for this population.

***Convergent niche shifts of endangered parrots (genus *Amazona*) during successful establishment in urban southern California**

B Ramirez, R Freeland, A Muhlheim, A Zellmer, D DeRaad, E Kirsch, M Mutchler, M Secor, K Reckling, M Schedl, B Durham, W Tsai, R Terrill, S Sannapareddy, A Sivakumar, K Garrett, J McCormack

Presenting author: **Brenda Ramirez**, r.brenda235@gmail.com

The successful establishment of introduced species into urban areas is becoming more common due to anthropogenic change, often resulting in changes in niche dynamics and interspecific relationships within the novel ecosystem. It is still unclear how much of the success of introduced species can be attributed to pre-existing niche matching between native and introduced ranges or niche shifts into new environmental conditions. The Red-crowned Parrot (*Amazona viridigenalis*) and Lilac-crowned Parrot (*Amazona finschi*) are two endangered sister species from opposite coasts of Mexico that were introduced to Southern California through the illegal wildlife trade. These species are an ideal system to study niche shifts because they have established populations where they coexist and sometimes interbreed. To understand whether their introduction involved a niche shift, we compared the environmental conditions of both species' native and introduced ranges. Results from three methods suggest that both species have shifted into the same novel and narrower niche, which is different from their individual native ranges. This new niche is both significantly cooler and with less rainfall than their native ranges. To understand the genomic ramifications, we used SNPs mined from ultraconserved elements (UCEs) from museum specimens and modern parrots from Southern California to assess levels of hybridization. This study highlights that *Amazona* parrots can adapt to diverse environmental conditions, with cities offering a resource niche and potentially serving as refugia for threatened parrot species. However, understanding the role of hybridization between species emphasizes the need for ongoing monitoring and genetic investigations.

****Abundance, roosting, and breeding ecology of the Critically Endangered Hooded vulture *Necrosyrtes monachus* in four cities of Ghana**

S Boakye Yiadom, L Holbech, J Quartey

Presenting author: **Samuel Boakye Yiadom**, University of Ghana, boakyesy@gmail.com

The Hooded vulture has experienced a severe decline over the past three decades across most of its range and is currently listed as Critically Endangered owing to impact factors such as habitat destruction, persecution, trade in traditional medicine and ritual purposes. Despite its threatened status, there is still a lack of information on the population status, roosting, and breeding habitat characteristics of the species in Ghana. Therefore, this study sought to monitor the Hooded Vulture population and provide baseline data to enable researchers to identify and understand future trends and also provide baseline data for roosting and breeding habitat characteristics in urban Ghana. Data was collected from March to September 2023 covering wet and dry seasons in Ghana. Line transect distance sampling and variable

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circular plot methods were used in the data collection. Transects of 122 totalling 389km were covered using a bicycle and The transects were established between 153 Point count stations put under the following habitat categories; abattoirs, refuse collection points, refuse dump sites, filthy drains, compost and recycling plants, landfills, potential roost, poultry farms, roost and nesting sites spread across the four study sites. A total abundance of 9469 individuals of the species was documented with a mean encounter rate of 1.61, 1.57, 1.37, and 0 bird/km and a nest abundance of 2, 5, 11, and 0 recorded respectively in Accra, Kumasi, Takoradi, and Tamale. A relative abundance of 28.97% was recorded for Accra, 46.35% for Kumasi, 24.68% for Sekondi-Takoradi and 0% for Tamale. The mean count of vultures at the point count stations was statistically significant ($p < 0.05$). Abattoir, roost and landfill sites had the highest means. The Hooded vulture has undergone a severe decline in Ghana based on interviews conducted and to help mitigate the effects of human activities on the species, stakeholder engagement and public education are highly recommended.

How does translocated lesser prairie-chickens nest site selection affect nest survival?

E Teige, L Berigan, N Parker, C Aulicky, D Haukos, D Sullins, J Reitz, L Rossi, K Fricke, K Shultz

Presenting author: **Elisabeth Teige**, Cooperative Fish and Wildlife Research Unit, teigeel@ksu.edu

Understanding how habitat selection at multiple scales affects demographic outcomes is crucial for species conservation and is especially important for imperiled species subject to conservation efforts such as translocation to novel environments. The lesser prairie-chicken (*Tympanuchus pallidicinctus*) is a threatened and endangered prairie grouse species found in parts of five states (CO, KS, OK, TX, NM). As part of a larger translocation effort from 2016-2020 of 411 birds, 207 female lesser prairie-chickens were translocated to the U.S. Forest Service's Cimmaron and Comanche National Grasslands in southwest Kansas and southeast Colorado. Using 138 nest site locations and outcomes collected from radio- and GPS-marked birds, we used a hierarchical resource selection framework with remotely sensed environmental and field-collected vegetation covariates to model nest-site selection at multiple scales as well as nest survival. We found that Conservation Reserve Program grassland was the most selected cover type and held the majority of nest sites (65%), followed by the National Grasslands with a quarter of nest sites. Across the study site and at a local scale, females strongly selected sites with taller and thicker vegetation. Nest survival inference from vegetation covariates was weaker than nest-site selection, but nest survival increased for females nesting in areas with a greater variation in residual cover and vegetation heterogeneity. Our results encourage management that supports increasing areas of heterogeneous grassland such as the Conservation Reserve Program at the landscape scale and other similar programs that increase residual cover to benefit lesser prairie-chicken conservation.

Incorporating co-occurrence effects in Lotka-Volterra competition models improves model performance and suggests barred owl culling could save the imperiled northern spotted owl

V Srivastava, N Van Lanen, R Parshad

Presenting author: **Vaibhava Srivastava**, Iowa State University, vaibhava@iastate.edu

Robust estimation of wildlife populations represents a cornerstone of wildlife research and provides critical information to guide management, including identifying at-risk species, setting harvest rates, and evaluating predator and invasive species control programs. Efforts to enhance population estimation have long included influences one species may exert on another, beginning with direct effects of predation on prey populations. More recently, researchers have incorporated co-occurrence effects, such as fear of a competitor, into Lotka-Volterra competition models to generate more robust wildlife population estimates. Here we introduce two modified Lotka-Volterra competition models, which incorporate one- and two-way co-occurrence effects, to estimate populations of two competing species. Using the test case of northern spotted and barred owl populations in the Pacific Northwest region of the United States, we evaluate if

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these new co-occurrence models can generate more robust population estimates than previous models. We then evaluate if potential co-occurrence effects among barred and northern spotted owls are uni- or bi-directional. Lastly, we leverage the best-performing model to evaluate the degree to which a recently proposed barred owl culling program may help recover northern spotted owl populations. Our model results suggest incorporating co-occurrence effects improves model fit compared to classical Lotka-Volterra competition models. We found strong evidence for uni-directional co-occurrence effects of barred owls on northern spotted owls, but not vice versa. Lastly, our simulations of barred owl culling suggest barred owls would need to be culled from approximately 40% of all occupied barred owl territories each year to reverse ongoing northern spotted owl population declines. Other 'cost-effective' culling mechanisms are also explored.

Maximizing Translocation Success for Greater Sage-Grouse (*Centrocercus urophasianus*) Population Restoration

N Lindenauer, P Coates, M Milligan, S Mathews-Sanchez, G Patricelli

Presenting author: **Nicole Lindenauer**, nlindenauer@usgs.gov

Greater Sage-Grouse (*Centrocercus urophasianus*; hereafter, 'sage-grouse') populations have declined significantly across the western United States, including in the Bi-State Distinct Population Segment (Bi-State DPS), largely attributed to habitat loss, degradation, and fragmentation. For the Parker Meadows subpopulation in the Bi-State DPS, landscape changes combined with likely inbreeding depression resulted in steep population declines. Thus, translocations were initiated in 2017 to prevent local extirpation. As part of this translocation effort, from 2022 to 2023, this study compared the efficacy of two translocation methods to inform management decisions that optimize population restoration efforts. We compared whole-brood translocations, involving the relocation of females with their broods, against mixed-brood translocations, a novel approach where translocated broods were augmented with chicks from a different donor brood from the same source population. We evaluated initial chick retention rates within translocated mixed-broods, and compared survival estimates between translocated whole-broods and mixed-broods, as well as between donor and non-donor broods within the source population. We also compared habitat selection and survival between resident and translocated broods over the six-year period, which resulted in source-sink habitat maps that could be used to inform suitable future release site locations. By identifying the most effective translocation method and optimal release locations, we will provide valuable insights for conservation managers aiming to restore sage-grouse populations. This work will also have broader implications for translocation efforts in other threatened Galliformes species. These findings are preliminary, subject to change, and provided for best timely science.

Navigating the tides: Captive bred light-footed Ridgways rails respond differently to high tides than their wild-hatched counterparts

K Sawyer, C Conway, T Katzner

Presenting author: **Kimberly Sawyer**, kasawyer4@gmail.com

A thorough understanding of habitat selection is vital for making informed management decisions for recovery efforts of endangered species. Habitat selection is a dynamic process that varies temporally and spatially based on the requirements of a species and the ecosystem. Light-footed Ridgway's rails (*Rallus obsoletus levipes*) are a federally endangered species that relies on tidal marshes as habitat for its entire life cycle. We used solar-powered GPS transmitters to compare habitat selection of 46 captive-bred and 43 wild-caught juvenile rails at 3 marshes near San Diego, California. When all GPS data were considered, preliminary analyses did not detect differences in habitat selection between captive-released and wild-caught rails. However, we did detect differences in habitat selection when we refined our analysis by tidal stage. Wild-caught rails selected low marsh at low tides and moved up the marsh plain as water levels increased. Captive-released rails, however, selected low marsh and mudflats (inundated by water) during high tides, leaving them more exposed to the rising water levels and, potentially, increased predation risk. Our study emphasizes the relevance of designing habitat selection analyses around the ecological circumstances wildlife experience and of understanding potential differences in habitat selection between captive-bred and wild-hatched individuals.

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Importance of high-quality compensatory mitigation options for Golden Eagles and Bald Eagles

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The Bald Eagle (*Haliaeetus leucocephalus*) and Golden Eagle (*Aquila chrysaetos*) are managed in the United States to ensure the species are stable or increasing while allowing for potentially negative effects from anthropogenic sources like incidental take at wind, solar, or mining facilities. Compensatory mitigation for eagles is primarily through retrofitting high-risk power poles to reduce electrocutions but is expanding to non-lead ammunition distribution to reduce lead poisoning, and roadside ungulate carcass removal to reduce eagle-vehicle collisions. These mitigation methods provide population offsets and enable regulators to achieve their management objectives of species stability and persistence. Mitigation challenges abound for these species including ensuring high-quality, verifiable, and effective mitigation projects are completed to create eagle population credits that offset the debits incurred with federally permitted incidental take. Using electrocution mitigation as an example of current mitigation challenges, we compared conservation benefits among three power pole retrofitting project scenarios: 1) high-risk poles only, 2) a circuit of both low- and high-risk poles, and 3) low-risk poles only. We define high-risk poles in the context of compensatory mitigation as poles in high-quality eagle habitat with a relative risk index ≥ 0.40 . We estimate that the conservation benefit of retrofitting a high-risk pole is at least 5.25 times greater than the benefit of retrofitting a low-risk pole. These results stress the importance of publishing detailed guidance for those implementing electrocution mitigation to ensure all retrofitting projects successfully credit the eagle population as intended. Clear guidance is also needed for lead poisoning and vehicle collision mitigation methods to effectively identify high-risk areas for eagles, assess mitigation effort and costs, and secure compensatory mitigation funding to implement.

*Climate and Landscape Change Influence Bird Diversity and Community Composition Across Vancouver Island, B.C., Canada

J Berini, K Johnson, S Dubin, A Chen, G Casey, C Patterson, A Hund*Presenting author: John Berini, Carleton College, jberini@carleton.edu*

Nearly half of known bird species are exhibiting population decline. While much of this decline has been attributed to climate and landscape change, these drivers are multivariate in nature, making it difficult to define the mechanistic link between these drivers and local diversity. Here, we investigate the multivariate influences of both climate and landscape on bird communities across Vancouver Island, B.C., Canada. We deployed autonomous recording units for 72 hours at 48 lakes across the island during summer 2023 and used BirdNet to identify individual species. We then used spatial random forest to define our best-fitting model and a mixed-effects regression kriging approach to predict spatial variation in bird diversity and community composition. Preliminary results suggest that diversity and community composition are best predicted by a mix of covariates representing both climate and landscape, with covariates representative of timber harvest among them.

**Factors affecting terrestrial bird abundance in montane systems in Yukon, Canada: Topography or vegetation?

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Shrubs are expanding upslope and to higher latitudes as a result of increasing global temperatures, and bird species that breed in subalpine, alpine, and tundra habitats may be influenced by this increased 'shrubification'. A recent study in Alaska examined the implications of increasing shrub dominance across a latitudinal gradient on bird species abundance and found varying non-linear relationships between each bird species and different characteristics of shrub dominance (Thompson et al., 2016). Our project used similar concepts and methods, but examined the relationships between shrub height, shrub density, and

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topographical characteristics and predicted bird abundance along an elevational gradient at 10 montane sites in southwest Yukon, Canada. Results for 25 bird species suggest non-linear responses, indicating that some species are positively or negatively influenced by increasing shrub dominance and other species are influenced by topographic features. Our results identify: (1) which montane species may be of conservation concern with ongoing climate-induced shifts in shrub expansion, (2) which characteristics of shrub dominance and topography have the greatest influence on the distribution and abundance of montane species, and (3) how relationships across elevational gradients (high topographic complexity) in Yukon compare to those across latitudinal gradients (low topographic complexity) in Alaska.

****Estimates of bird distributional dynamics varied with grain sampling resolution****O Acevedo Charry, B Fricke, M Quinn, M Shuler, M Acevedo***Presenting author: Orlando Acevedo Charry, University of Florida, acevedocharry@gmail.com*

Species geographic distribution is dynamic, involving population-level processes of colonization (occupying previously unoccupied sites) and extinction (becoming extirpated from sites previously occupied) across different spatial scales. Although the spatial scale of these dynamics might affect the interpretation of any estimate, a more quantitative approach is needed. We sought to understand how differences in spatial resolution during spatio-temporal sub-sampling of a community science data set change - if so - the estimates of distributional dynamics of tropical bird species. Additionally, we evaluate if these estimates are related to the distributional range size of our studied species. Utilizing eBird data for seven *Thraupis* species with range sizes from 484,000 to 15,600,000 km², we applied a robust design assuming a closed population in 30-days primary periods over 12 secondary periods (years 2012-2023). We conducted spatio-temporal sub-sampling in hexagonal grid cells of 12 sizes (grain size of our sampling unit), from ~1 to ~517 km of diameter, and compared the estimates of colonization and extinction across these grain sizes within each species with the Akaike Information Criterion. Species with smaller range sizes require smaller grain sizes, while species with larger range sizes support larger grain sizes. Our results highlight that the ecological interpretation of spatially structured population dynamics is species-specific and depends on geographical range size. Over- or underestimation of distributional dynamics might occur if the 'scale of effect' is not considered when conducting species distributional dynamics modeling.

****Does species distribution model performance improve when habitat sampling is centered on bird locations instead of surveyor locations?****F Shen, F Stanley Jothiraj, T Hallman, R Hutchinson, D Robinson***Presenting author: Fang-Yu (Betty) Shen, Oregon State University, bettysheen@gmail.com*

Species distribution models (SDMs) help us understand and predict dynamics of avian distributions by combining bird detections with habitat information at sampling sites. Standard procedure when characterizing habitats occupied by birds detected during point counts is to center the habitat sampling on the surveyor location. However, birds are distributed away from the surveyor location and may be in habitats different from those the surveyor was in, potentially adding noise to bird-habitat relationships and reducing the predictive performance of SDMs. If distance and direction data for each bird detected during point counts are available, the location of each bird can be estimated. Habitat assessments can then be centered on birds instead of the surveyor. We compared SDMs built on 14,884 detections of American Robins during point counts in Oregon, 2006-2023, and assessed 7 Landsat spectral bands as our habitat information. We ran SDMs using boosted regression trees and compared area under the curve (AUC) of models centered on the surveyor locations (observer-centered) to those centered on bird locations (bird-centered). We assessed habitats at 3 levels: 30-m x 30-m pixel, 147-m radius (determined as effective strip width for robins from distance analyses) and 500 m. Model performance overall was better for the largest radius analyzed (0.765 for observer-centered vs 0.750 for bird-centered). Effective strip width radius had higher AUC (0.741) when centered on birds than on observers (0.737). American Robins are habitat generalists so additional evaluations should include species with more specialized requirements and smaller home ranges.

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***Assessing the abiotic and biotic predictors of the distribution of two Caprimulgids in the northern Blue Mountains of Oregon**

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Species distributions often depend on a combination of the habitat features and species interactions that characterize the abiotic and biotic environment. Large-scale sampling schemes and accurate species occurrence data are needed to understand how abiotic and biotic features interact to shape species distributions. Passive acoustic monitoring is an emerging and rapidly developing field wherein soundscapes are measured across broad spatial scales and soundscape recordings are analyzed, often using convolutional neural networks, to generate species detections. Occupancy models can then be used to examine support for hypotheses describing the processes mediating species distributions. Here, we apply a passive acoustic monitoring framework to understand the breeding distribution of two species of caprimulgids, the Common Nighthawk (*Chordeiles minor*) and Common Poorwill (*Phalaenoptilus nuttallii*), using large-scale monitoring data collected in the northern Blue Mountains of northeastern Oregon, a relatively understudied region that is subject to various land management practices and undergoing modification by global change processes. Over 100,000 hours of recordings from 350+ sites found across the Umatilla and Wallowa-Whitman National Forests were sampled during 2 consecutive breeding seasons and processed using BirdNet v2.4. We used remotely sensed habitat features and species co-occurrence data to understand how the abiotic and biotic environments interact to shape the distribution of both species. Viewed together, this work provides a robust quantification of the processes shaping the breeding distribution of two nocturnal insectivores, one of which is known to be experiencing significant population declines in parts of its range, in a relatively data-deficient region of North America.

Co-occurrence and behavior mediate interactions between sympatric nightjars exhibiting differential responses to landscape characteristics

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Nocturnal insectivorous birds such as the Eastern Whip-poor-will (*A. carolinensis*) have experienced steep population declines across North America since the mid-20th century, but standardized survey methods are biased against such species leading to uncertainty in trend assessments. Further, understanding of Eastern Whip-poor-will declines may be improved by considering the effects of the presence, or behavior, of the congeneric Chuck-will's-widow (*A. vociferus*). Identifying and understanding interspecific interactions that may influence species occupancy and detection is paramount, especially when synchronously monitoring multiple species. Between 31 May and 8 July of 2022 and 2023, we conducted 2,630 nocturnal surveys for both species at 584 sites across Eastern Oklahoma. We recorded 211 Eastern Whip-poor-will and 1,320 Chuck-will's-widow detections. Thereafter, we used single-season single-species models in combination with co-occurrence occupancy models to estimate the effects of observation-level covariates (e.g., moon illumination) on detection, and site-level covariates on occupancy probability of each nightjar species individually before testing for interspecific interactions. Both species responded similarly to changing synodic periods, especially in response to moon altitude. However, mean detection during the season was higher for Chuck-will's-widows (0.42 ± 0.01) compared to Whip-poor-wills (0.29 ± 0.03). Effects of land cover and topography on occupancy were species-specific and co-occurrence model results suggest detection of either species may depend on the presence and behavior of the other. Chuck-will's-widows were more likely to be detected in the presence of Whip-poor-wills, while detection of Whip-poor-wills varied in response to Chuck-will's-widow behavior.

Uncovering the Recurring Presence of Anthropogenic Debris in Nests of Urban Birds: A Coastal Investigation

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Birds build their nests using materials collected from their surroundings. Urbanisation have altered the

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environment for several birds and changed the type and abundance of available materials for nesting. Several birds are incorporating anthropogenic debris in their nests. Abundance of human produced debris (plastics and other solid wastes) and shortage of natural nesting materials are believed to be driving this behaviour. In Kollam, one of the most densely populated districts of India, a quick look has revealed the presence anthropogenic debris in the nests of 6 common bird species. Following the discovery of debris in nests in 2022 in the Vaddy fishing harbour area, the survey was repeated in 2023 and 2024 and debris were detected in varying amounts in more than 50% of the surveyed nests. The debris mostly pieces of derelict fishing gears ranged from fishing nets, fishing lines, ropes, baling straps, metal strips, wire mesh and cloth hangers. The observations in the nests of Black kites (*Milvus migrans*), Brahmini Kites (*Haliastur indus*), Little egrets (*Egretta garzetta*), Indian Pond herons (*Ardeola grayii*), House crows (*Corvus splendens*) and House sparrows (*Passer domesticus*) in the coastal urban area, around Vaddy fishing harbour in the heart of the city, reflects the type and amount of wastes in the surrounding area.

****Predicting bird responses to vegetation change in cities to guide urban greening initiatives**

S Safran*Presenting author: Samuel Safran, University of Minnesota, safra023@umn.edu*

Plants are crucial to the functioning of urban ecosystems and provide numerous benefits to human health and well-being, making efforts to green cities a growing priority. However, planning tools used to assess services provided by green infrastructure (e.g., street trees, parks) typically overlook the impact of vegetation on biodiversity, including the occupancy, abundance, or diversity of species. To bridge this gap, we developed a repeatable workflow to fit occupancy models with eBird data from cities to predict how hypothetical changes in vegetation would alter the local occupancy of birds. As an example of this approach, we applied the tools to New York City to assess the likely responses of 101 bird species to proposed changes in canopy cover at an active redevelopment site in Manhattan. The estimated effect of increasing vegetation cover (from 2% to 15%) varied by species, ranging from a 29 percentage point increase in occupancy probability for American Robin (95% CI, 24–32) to a 8 point decrease for American Kestrel (95% CI, 5–10). In total, the hypothetical change in vegetation would increase species richness by an estimated 3 species. In contrast, increasing vegetated cover to the same levels at another site in the South Bronx increased estimated richness by 7 species, illustrating how responses are not consistent across a city. Other variables, including site tree composition and proximity to non-urban areas, were found to mediate the responses of species to changes in vegetation cover. By advancing our ability to predict urban bird distributions, this work can help identify where new plantings would have the greatest biodiversity benefits, enable practitioners to set site-specific wildlife targets, and guide societal investments in urban greening to more equitably distribute the benefits of nature in cities.

Urban habitats impact the reproductive success and song of a migratory bird, the gray catbird (*Dumetella carolinensis*)

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Growing empirical evidence indicates that anthropogenic noise and urbanization affect birdsong and avian nesting success, but rarely do studies examine both. We investigated song features, body morphometrics, and reproductive success in populations of gray catbirds (*Dumetella carolinensis*) across an urban gradient. Model selection indicated both anthropogenic noise as well as male body size significantly predict song minimum frequency – with noisier habitats associated with higher minimum frequencies and larger males singing lower minimum frequencies. Nests were significantly more likely to successfully fledge and contain more nestlings in areas of higher impervious surface and less canopy cover, but with lower noise levels. Distances to roads or water sources explained little variation in nesting success. There was a significant interaction between habitat type and song minimum frequency on nesting success. In urban habitats, males that sang higher minimum frequencies were more likely to have successful nests, while males in suburban and rural habitats were more likely to fledge successful nests if they sang lower minimum frequencies. These results indicate urbanization not only influences song but

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also nesting success in gray catbirds with certain song features being more or less advantageous in different environments, which potentially represents shifts in sexual selection across the urban gradient.

Urban landscape: A potential refugia for the declining aerial insectivore*A Deshwal***Presenting author: Anant Deshwal, Bradley University, adeshwal@fsmail.bradley.edu*

Common Nighthawks are declining across their entire range in North America. This decline is attributed to several factors, such as habitat loss and degradation. The absence of Tallgrass prairies has resulted in the nighthawks nesting on flat gravel rooftops in the urban habitats. However, the absence of surveys focusing on crepuscular and urban birds has limited our ability to quantify the factors affecting Common Nighthawk populations. In this study, we used N-mixture Bayesian analysis to quantify the effects of landscape variables on the abundance of Common Nighthawks. We conducted surveys at dusk and dawn for nighthawks across the urban-rural-prairie gradient in Central Illinois. Our results show that the nighthawk abundance declined with the increase in cultivated land and pasture. The rate of decline in abundance was steeper for the pasture. Common Nighthawks prefer to nest on relatively flat lands in prairies. The advance of row crops in agricultural lands has resulted in fewer suitable nesting sites. Interestingly, the relationship between nighthawk abundance and developed areas was non-linear with quadratic response. Characteristics unique to urban landscapes, such as flat rooftops and light pollution, played an important role in determining their population abundance. Common Nighthawk abundance was not affected by other landscape characteristics.

Urban Northern Cardinals are bolder and less neophobic than rural birds**D Baldassarre, F Connors, T Faulkner, S Hernandez, J Niederhauser***Presenting author: Daniel Baldassarre, SUNY Oswego, dtbaldas@syr.edu*

Wildlife faces many challenges living alongside humans, but certain species can overcome these obstacles and succeed even in urban areas. Boldness and neophobia are two potential aspects of an individual animal's personality that could affect urban adaptation and, if correlated, may form a behavioral syndrome. If urban individuals are bolder and less neophobic than rural individuals, they may be able to exploit anthropogenic landscapes more fully. We tested this idea by conducting flight initiation distance and novel object experiments with urban and rural Northern Cardinals (*Cardinalis cardinalis*). Urban birds had shorter flight initiation distances and foraged near novel objects more readily than rural birds, and both behaviors were highly repeatable within individuals, suggestive of personality. We found a positive correlation wherein bolder individuals were also less neophobic, but only in the rural population. Thus, the urban environment may impose selective pressures that result in population-level differences in these two behaviors, while also decoupling them such that urban individuals can fine tune their behaviors in response to novel conditions. In contrast, the existence of a behavioral syndrome in rural birds may limit their behavioral evolutionary potential, and indeed may be an adaptive response to a more consistent environment. In total, these results help explain how Northern Cardinals can modify their behaviors, either plastically or via genetic evolution, to thrive in urban areas.

****The effects of urbanization on mobbing behavior at the community level in Los Angeles, California****Y Diaz, B Ewing, E Wood, C Whitcraft, A Martinez***Presenting author: Ynez Diaz, ynez.diaz@student.csulb.edu*

The effects of urbanization on species interactions have largely focused on urban-rural gradients, yet heterogeneity within urban ecosystems has received less attention. Variation in anthropogenic disturbances such as noise pollution, vegetation density, and impervious surface in urban areas, often covarying with socioeconomic patterns, can affect species interactions. Mobbing is an important species interaction that represents an antipredator defense response at the community level, yet hasn't been well studied in urban ecosystems. Whether group size of alarming individuals affects mobbing responses hasn't been well studied. We used playback of Bushtit (*Psaltirparus minimus*) alarm calls across Los

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Angeles County to test whether species interactions (mobbing responses) change across an urban and socioeconomic gradient, and whether the number of individuals alarming influences mobbing response. We evaluate 1) how species interactions are affected by noise, vegetation cover, and impervious cover, 2) how social factors can drive variation in these disturbances across an urban gradient, and 3) how the number of individuals alarming affects mobbing response. We found larger group size of alarming individuals may result in larger mobbing response at the community level at higher income sites of the socioeconomic gradient. In addition, we found migratory species respond to alarms more frequently than resident species across Los Angeles. Our results suggest there may be a threshold number of individuals needed to induce a significant antipredator response from the community. Understanding how specific species interact with abiotic changes due to urbanization will be important to maintain biotic processes in urban landscapes.

Nesting in urban areas affects American Kestrel home range size and adult female health

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Urbanization is happening at an unprecedented rate, and wildlife must adapt or face population declines. American Kestrels inhabit urban areas, however, whether human-dominated landscapes impact kestrel space-use, survival and health is largely unknown. We monitored American Kestrel nest boxes along a gradient of urbanization, measured using impervious surface area (ISA), and deployed GPS tags on breeding adults to examine the relationship between urbanization, home range size, and adult and nestling health. Male kestrel home ranges were 9.14 times larger than female home ranges, and home range size decreased as ISA increased for both sexes. Adult females lost weight at twice the rate over the breeding season than adult males, and females lost more weight as ISA increased. The effect of female home range size on overall nestling weight and the variation of weight within nests depended on ISA. Nestling weight was highest and within-brood weight variation was lowest with large home ranges in less urban areas, but this relationship was reversed in areas with more urbanization, where smaller home ranges led to higher nestling weight and lower variation than larger home ranges. Male home range size did not predict overall nestling weight but showed a similar, dependent effect on within-nest weight variation as the female home range size. Results suggest that smaller home range sizes in urban areas may be adaptive for kestrels. However, the effects of urbanization on adult female weight loss shows that while kestrels can successfully breed in urban areas, it could come at a cost to female health and potentially survival. Kestrels may not be as well-adapted to urbanization as previously reported.

Seasonal Urban Provisioning Changes Resource Selection of an Everglades Indicator Species, the American White Ibis

J Hepinstall-Cymerman, A Kidd-Weaver, C Teitelbaum

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Habitat selection varies by individuals with differences more common in heterogeneous environments. In urban areas, some individuals are more tolerant of human activity than others leading to populations that have developed specific behaviors to acquire resources from humans. However, these same individuals may have habitat requirements not provided in urban areas. We explored cross-season habitat selection in a nomadic wading bird, the American White Ibis (*Eudocimus albus*), which requires non-saline environments during the chick rearing. We determined resource use from GPS tracking data of 47 ibis captured in Palm Beach County, Florida between October 2015 June 2018. We used behavioral change point analysis to define breeding and non-breeding seasons and derived home ranges for each season using autocorrelated kernel density estimation. We classified ibis as non-breeding urban specialists or non-breeding generalists according to urbanization scores from a network analysis of habitat use. We quantified resources using 30-m resolution CCAP land cover and evaluated second-order resource selection for each bird-season-year. We modeled habitat selection using generalized linear mixed-effects models separately for breeding and non-breeding seasons including interactions with urbanization score. We collected 58,788 non-breeding season and 29,585 breeding season locations to define 96

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bird-season-years. Urban specialists clearly shifted their location, space use, and resource selection between seasons. The largest differences observed were in selection for medium-high intensity development where urban birds selected for these habitat types and generalists selected against them. As expected, generalists showed stronger selection for non-marine wetland habitat types in the breeding season than in the non-breeding season.

***Effects of Habitat Heterogeneity on Nestling Development Across an Urban and Rural Gradient**

S Garcia, I Joy, Q Adams, G Harker, Z Laubach, R Safran

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Understanding the environmental heterogeneity that underlies urbanization is incredibly important for exploring impacts of rapid environmental change on birds. Many urban-driven environmental changes have been found to have direct effects on avian life history traits, all of which can have profound effects on reproductive success. We used sensors to track multi-scale environmental data across 17 barn swallow nesting sites that lie across an urban-rural gradient. These measures along with tracking fine-scale growth of individual nestlings across the gradient, allowed us to explore direct effects of hierarchical nest-, site-, and regional- level environments on development. While these data are still currently being analyzed, we predict strong contrast in environmental fluctuations across the urban-rural gradient and effects on rate of growth across nestlings. Investigating the impacts of environment during a highly sensitive time of life in aerial insectivores is critical in the face of rapid climate change in urban ecoregions.

Behavioral, physiological and genetic adaptations to urbanization in American White Ibises (*Eudocimus albus*) and the potential for citizen science in urban ecology

D Chaussadas, S Hernandez, J Hepinstall-Cymerman

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Natural habitats are being converted in urban spaces to accommodate growing human populations' needs, thus forcing wildlife to adapt to urban conditions that are different from those they evolved with. For instance, urban diets are often composed of human handouts or refuse, known to be consistently abundant, which is associated with increased sedentarism, and could cause significant changes in their social structure. These food items are also typically rich in processed carbohydrates, which may be associated with increased amylatic activity and associated mutations in the amylase genes family.. However, in order to be able to access these resources, urban animals need to show fits of innovation, by which they can learn how to access forage on novel foods. We will use the urbanization of White Ibises (*Eudocimus albus*) to investigate: do urban populations adapt to urban diets by increasing their salivary amylase activity? Is this associated with markers of selection in their amylase genes? How does increased sedentarism impact flock structure in urban populations? Are successfully urbanized ibises more innovative than their non-urban counterparts? To do so, we are capturing 100 urban and 100 non-urban individuals and are individually tagging each. For each, we also collect blood and salivary samples. We will engage the local community in a resighting project in order to reconstruct the flock structure of these highly mobile birds. Indeed, urban ibises present us with unique opportunities to understand how animals can adapt to urban conditions and the various pressures the present, but also for human urbanites to find ways to connect with their non-human neighbors in ways that can contribute to scientific research.
