
vISEC2020
virtual International Statistical Ecology Conference
June 22-26, 2020
8-11am & 9pm-12am GMT

Abstracts

David Warton, Scott Foster, Otso Ovaskainen, Gordana Popovic and Skipton Woolley (UNSW Sydney / University of Helsinki / CSIRO)

Multivariate modelling in ecology and joint species distribution models

06/20-21/2020 8:00:00 AM-11:00:00 AM

Location: #short-course-jsdm *Short Course*

Multivariate analysis of abundance or presence/absence data in ecology is a challenging problem, for which analysis techniques have been developing rapidly in recent years. Historically these sorts of data were analysed using algorithms based on pairwise dissimilarity metrics, but a modern approach involves specifying a joint statistical model for the data, sometimes called a joint species distribution model. This approach has a number of advantages, including in statistical properties, interpretability, and functionality. This short course will give an introduction to a range of tools that have recently been developed for multivariate data in ecology, including methods for hypothesis testing, ordination, trait modelling, prediction, classification, and studying causes of co-occurrence.

Required software: R packages discussed include mvabund, HMSC, gllvm, SpeciesMix and ecoCopula

Nick Golding and Saras Windecker (Curtin University / University of Melbourne)

Level-up your R package

06/20-21/2020 8:00:00 AM-11:00:00 AM

Location: #short-course-R-packaging *Short Course*

It's easier than ever to write and distribute an R package to implement your new method. But it's much harder to make sure your new R package is bug-free, easy to use, and easy for you to maintain and extend. This workshop will teach you some tools and strategies for making your R package the best it can be.

We'll cover how to:

- Design and implement a simple and intuitive user interface
- Plan the internal architecture of your package code so it's easy to extend and maintain
- Create high-quality documentation, including vignettes, a website and forum
- Write good unit and integration tests to find and fix bugs
- Set up automated package testing, code style-checking, and documentation spell-checking

This will be a hands-on workshop. You'll gain experience reviewing other people's packages and working together to design new package interfaces. You're welcome to bring along your own package, work on it during the workshop, and get feedback on how to improve it.

Paula Moraga (University of Bath)

Spatial modeling and visualization of species distribution and disease risk using R and INLA

06/20-21/2020 8:00:00 AM-11:00:00 AM

Location: #short-course-spatial *Short Course*

In this course we will learn how to develop spatial geostatistical models using the R-INLA package to predict species distribution, estimate disease risk, and quantify risk factors. We will also learn how to create data visualizations such as static and interactive maps, and introduce presentation options such as interactive dashboards and Shiny web applications that facilitate the communication of insights to collaborators and policy makers. We will work through several fully reproducible examples of ecology and disease mapping applications using real-world data such as sloths in Latin America and malaria in The Gambia. The examples will provide clear descriptions of the R code for data importing, manipulation, modeling and visualization, as well as the interpretation of the results. We will cover the following topics:

- Manipulate and transform geostatistical and raster data using spatial packages

- Query and collect species occurrence data from several sources including the Global Biodiversity Information Facility (GBIF) and the Atlas of Living Australia (ALA) using the spocc package

- Retrieve high resolution spatially referenced environmental data using the raster package

- Model species distribution, disease risk, and risk factors in different settings

- Fit and interpret spatial models using Integrated Nested Laplace Approximations (INLA) and the Stochastic Partial Differential Equation (SPDE) approaches

- Create static and interactive visualizations using leaflet and ggplot2

- Communicate results with reproducible R Markdown reports, interactive dashboards and Shiny web applications

The course materials are based on the book 'Geospatial Health Data: Modeling and Visualization with R-INLA and Shiny' by Paula Moraga (2019, Chapman & Hall/CRC Biostatistics Series).

Jennifer Hoeting (Colorado State University)

A statistical view of deep learning in ecology

06/20-21/2020 9:00:00 PM-12:00:00 AM

Location: #short-course-deep-learning *Short Course*

The goal of this short course is to introduce neural networks and deep learning from a statistical viewpoint. The focus will be on explaining deep learning for statistical ecologists and ecological statisticians. Many conceptual explanations and cartoon sketches of deep learning are available, but deep learning is rarely translated into the mathematical framework required by most statisticians to understand the topic. In addition to presenting deep learning from a statistical viewpoint, we will consider where deep learning is useful in ecological applications. Students will gain experience with latest interface for deep learning programs within R (no Python required)!

Daniel Simpson and Andrew MacDonald (University of Toronto / Université de Montréal)

With great power comes great responsibility: Stan for modern ecological modelling

06/20-21/2020 9:00:00 PM-12:00:00 AM

Location: #short-course-stan *Short Course*

Contemporary ecological models are growing more complex, capturing not only ecological processes but also other sources of variation, such as sampling noise and measurement error. At the same time, ecological data is growing not only more available, but also more highly detailed. How can we create models that capture all this complexity, while confronting the unavoidable spectre of model misspecification? It is useful to turn to specialized programming languages like Stan, which aims to be a language for specifying probabilistic models.

Stan allows users to specify and infer complex, bespoke, statistical models that are built to appropriately represent the data and process at hand. While this extra power allows scientists to get the most out of their data, we must keep in mind the mantra of Spiderman: "With great power comes great responsibility".

In this course we will cover three main topics:

- Building bespoke models for ecological data in Stan, including appropriate prior modelling and model checking
- Inferring models using the Stan language
- Post-inference model checking, model criticism, and model selection

Required software: Participants are encouraged to bring their laptops with R and the RStan package installed.

Dianne Cook (Monash University)

Visualising data beyond 3D

06/22/2020 8:00:00 AM-9:15:00 AM

Location: #acacia *Skills Showcase*

This showcase will discuss using dynamic plots, called tours, to examine multivariate data spaces. There are several tour types, grand, guided, manual, local, and slice, that are useful and you will learn about. These can be helpful when conducting analyses involving dimension reduction, like principal component analysis and t-SNE, and machine learning methods, like supervised and unsupervised classification models. We hope to cover high-dimension, low-sample size problems, and compositional data.

Required software: R, tourr, spinifex, geozoo

Otso Ovaskainen (University of Helsinki)

Hierarchical modelling of species communities - accounting for environment, traits and phylogeny in space and time

06/22/2020 9:45:00 AM-11:00:00 AM

Location: #acacia *Skills Showcase*

Hierarchical Modelling of Species Communities (HMSC) is a joint species distribution modelling approach that enables one to integrate data on species abundances, environmental covariates, species traits, phylogenetic relationships, and the spatio-temporal context in which the data have been acquired (Ovaskainen et al. 2017, Ovaskainen and Abrego 2020). The Skills Showcase covers a brief introduction to HMSC, and shows with the help of worked out examples how to apply the R-package Hmsc (Tikhonov et al. 2020).

The Skills Showcase is run as a software demonstration. If you wish to repeat the analyses yourself, install the R-package Hmsc from CRAN and download the R-scripts and the data from https://www.helsinki.fi/en/researchgroups/statistical-ecology/hmsc (see HMSC book/executable scripts).

References:

Ovaskainen, O., Tikhonov, G., Norberg, A., Blanchet, F. G., Duan, L., Dunson, D., Roslin, T. and Abrego, N. 2017. How to make more out of community data? A conceptual framework and its implementation as models and software. Ecology Letters 20, 561-576

Ovaskainen, O. and Abrego, N. 2020. Joint Species Distribution Modelling – With Applications in R. Cambridge University Press.

Tikhonov, G., Opedal, Ø. H., Abrego, N., Lehikoinen, A., de Jonge, M. M., Oksanen, J. and Ovaskainen, O. 2020. Joint species distribution modelling with the R-package Hmsc. Methods in Ecology and Evolution 11, 442-447.

Required software: R package Hmsc

Len Thomas (University of St Andrews)

Inferences from passive acoustics: detection, classification, localisation, tracking and density estimation

06/22/2020 8:00:00 AM-9:15:00 AM

Location: #banksia *Skills Showcase*

In this showcase, we will take a tour through some methods for making ecological inferences by collecting data on the sounds animals make. We will very briefly mention data collection (microphone/hydrophones, recordings, positioning), but will focus on what to do with the data. A first task is to find sounds of interest (detection) and determine what they are (classification) – these tasks can be done manually (by listening to the sounds, or looking at spectrograms) or automatically using computer algorithms, or which there are very many. A second set of tasks involves determining where the sound came from in space, and potentially linking sounds from the same animal together to form tracks. Lastly, and this will be main focus, we may want to use the passive acoustic data to determine the density of animals in the sampled area. Key concepts here include estimating the area sampled by the acoustic sensors, and the additional information required to turn an estimate of acoustic density into animal density. For estimating the area sampled, we need to consider detectability; the way we can do that depends on the acoustic setup, and what other information we have available. Methods include auxiliary trials, distance sampling, spatial capture-recapture and acoustic propagation modelling. We will introduce all of these methods – no previous knowledge required. Throughout the skills showcase, we will refer to places where you can find out more, and available software for performing the analyses.

Florian Hartig (University of Regensburg))

A practical tutorial on residual diagnostics for hierarchical (multi-level/mixed) regression models with DHARMa

06/22/2020 9:45:00 AM-11:00:00 AM

Location: #banksia *Skills Showcase*

The interpretation of conventional (i.e. Pearson or deviance) residuals for generalized linear (mixed) and other hierarchical statistical models is often problematic. Distribution such as the Poisson or Binomial change their shape and variance with the mean, which results in non-homogeneous residual patterns even for correctly specified models, and discrete distributions often produce striped patterns that are visually confusing and difficult to handle with formal residual tests.

The ‘DHARMa’ package uses a simulation-based approach to create readily interpretable scaled (quantile) residuals for fitted (generalized) linear mixed models. Currently supported are linear and generalized linear (mixed) models from ‘lme4’ (classes ‘lmerMod’, ‘glmerMod’), ‘glmmTMB’ and ‘spaMM’, generalized additive models (‘gam’ from ‘mgcv’), ‘glm’ (including ‘negbin’ from ‘MASS’, but excluding quasi-distributions) and ‘lm’ model classes. Moreover, externally created simulations, e.g. posterior predictive simulations from Bayesian software such as ‘JAGS’, ‘STAN’, or ‘BUGS’ can be processed as well. The resulting residuals are standardized to values between 0 and 1 and can be interpreted as intuitively as residuals from a linear regression. The package also provides a number of plot and test functions for typical model misspecification problems, such as over/underdispersion, zero-inflation, and residual spatial and temporal autocorrelation.

In this Skills Showcase, I will demonstrate the functionalities of the DHARMa package using typical ecological regression analyses as examples. This will give us the opportunity to discuss how to test for common problems (over/underdispersion, zero-inflation, heteroskedasticity) in GLMMs, and check if those problems are resolved by modifying the analysis.

Required software: R package DHARMa

Shinichi Nakagawa (UNSW, Sydney)

An introduction to multilevel and phylogenetic meta-analysis using metafor

06/22/2020 8:00:00 AM-9:15:00 AM

Location: #corymbia *Skills Showcase*

You all have read a meta-analysis or two. But do you know how to do it? It is just a regression analysis without a slope although there is more to it. We will quickly cover the basics of meta-analysis and some advanced topics in meta-analysis just over an hour using the R package metafor. I will do this by going through this webpage (http://environmentalcomputing.net/meta-analysis/). Also, here is the relevant github repo (https://github.com/itchyshin/meta-analysis-demo).

Required software: metafor (R package)

Janine Illian (University of Glasgow)

Modelling ecological data as thinned point processes with inlabru

06/22/2020 9:45:00 AM-11:00:00 AM

Location: #corymbia *Skills Showcase*

Nick Golding (Telethon Kids Institute & Curtin University)

greta: simple and scalable statistical modelling in R

06/22/2020 8:00:00 AM-9:15:00 AM

Location: #darwinia *Skills Showcase*

General purpose MCMC software packages like WinBUGS, JAGS, and STAN enable users to define and fit almost any statistical model without having to worry about implementation details and have enabled significant progress in applied Bayesian modelling. However, these existing tools are largely unable to make use of recent advances in hardware and software for high performance computing so they often scale poorly to large datasets. In addition, the need to specify models using a compiled, domain-specific language is a significant hurdle to potential users and makes it hard for the wider community to extend and build upon these tools.

greta is a new software package for flexible statistical modelling that aims to overcome these limitations. greta uses Google's TensorFlow high-performance automatic differentiation library, so it scales well to massive data sets (millions of observations), can run across many CPUs or on GPUs. greta models can be fitted using efficient gradient-based MCMC samplers like Hamiltonian Monte Carlo or maximum likelihood/empirical Bayes methods. greta models are written directly and interactively in R, so greta is easy to learn and straightforward to extend with new R packages or use as a backend for more specific software.

I will demonstrate greta and some extension packages for modelling with Gaussian processes, generalised additive models and dynamical systems. If you want to know more now, see the website: https://greta-stats.org

Required software: just make sure you can log into the free RStudio Cloud instance: http://bit.ly/try_greta

Jennifer Hoeting (Colorado State University)

Deep learning: opening the black box

06/22/2020 9:00:00 PM-10:15:00 PM

Location: #acacia *Skills Showcase*

Deep learning algorithms are often presented as black box algorithms. Many cartoon sketches of deep learning are available, but deep learning is rarely translated into the mathematical framework required by most statisticians to understand the topic. In this lecture we will open the black box and explore neural networks and deep learning from a statistical viewpoint. In addition to an overview of the mathematics of deep learning, we will explore the types of problems when you might consider using a deep learning algorithm and when traditional inferential statistics may be preferred. We will briefly consider deep learning in ecology. We will offer links to recommended software as part of the lecture. Some deep learning algorithms are accessible to statisticians using R software. Python is even more widely used for deep learning. This lecture is intended for people who want to learn about neural networks and deep learning but have little previous exposure to it.
Required software: None - lecture only. Links to software provided for later use..

Vianey Leos Barajas (North Carolina State University)

Getting started with hidden Markov models

06/22/2020 9:00:00 PM-10:15:00 PM

Location: #banksia *Skills Showcase*

Hidden Markov models (HMMs) are ubiquitous across the field of ecology because they provide a mathematical framework to represent that an observed process over time is driven by a finite set of underlying latent ecological processes, e.g. observed movements of an animal are the result of its underlying behaviors (like resting vs traveling). HMMs are commonly applied in the analysis of animal movement in order to (i) identify a latent set of K ecological processes of interest, referred to states, where the states typically serve as proxies of animal behaviors, and (ii) understand how the state-switching dynamics evolve over time. However, HMMs are also commonly used in capture-recapture and occupancy modeling. A fundamental understanding of the basic HMM framework provides a foundation for the analysis of multiple types of ecological data and a manner to uncover novel insights from complex ecological data collected over time.

We will cover the basics of fitting a hidden Markov model in both the classical and Bayesian framework. We will use the R packages moveHMM and momentuHMM for likelihood-based inference and Stan for Bayesian inference. R Markdown files will be provided that cover all steps of the model building process along with a complete analysis of relevant ecological data examples.

Required software: Rtools, rstan, moveHMM, momentuHMM

Robin Aldridge-Sutton and Rachel M. Fewster (Department of Statistics, University of Auckland)

CaPow! Online simulation and power analysis for open-population capture-recapture

06/22/2020 9:00:00 PM-10:15:00 PM

Location: #corymbia *Skills Showcase*

CaPow! is a new Shiny web application for open-population capture-recapture models, with an emphasis on study design and model exploration as well as data analysis. The key features are an easy-to-use web interface for designing simulations and models, and efficient computation which enables thousands of simulated datasets to be fitted within seconds. Modelling follows the well-known POPAN style, including a superpopulation with time-varying population sizes, survival rates, and either free birth parameters or a constant population growth rate. Outputs include power analysis of proposed study designs, and diagnostic tools for exploring model precision and effects of model misspecification.

CaPow! runs online in a web browser and does not require any software to be installed. Sessions can be saved and uploaded again for future use.

In this workshop we will talk through the system and its functionality. Attendees can trial the system online during the session, or beforehand, at https://catchit.stat.auckland.ac.nz/apps/capow/. Datasets can be uploaded, but are not essential because the system simulates its own data.

Required software: Nothing but a regular web browser.

Christl A. Donnelly (Imperial College London / University of Oxford)

Real-time analysis of COVID-19: epidemiology, statistics and modelling in action

06/23/2020 8:00:00 AM-8:50:00 AM

Location: #acacia *Plenary (Chair: David Warton)*

The transmission and control of the pathogen responsible for COVID-19 have been in the headlines for months. It has created a global challenge unprecedented in our lifetimes. The epidemiological evidence base will be explored tracking how understanding improved month by month. Attention will then turn to current challenges and predictions for the short- and long-term future.

Margaret M. Mayfield (University of Queensland) with Malyon Bimler and Daniel Stouffer

An interaction network approach for applications in community ecology

06/23/2020 9:30:00 AM-9:45:00 AM

Session: Contributed talks *(Chair: Diana Cole)*

Location: #acacia

Network theory allows us to capture the complexity with which species, groups or individuals interact and clarify resulting emergent patterns. Though networks can be constructed using data from any set of interacting organisms, approaches for within trophic groups, such as plants, are less well-developed than for cross-trophic systems. Most of the interaction networks that have been developed for single-trophic levels rely on species associations rather than empirically measured outcomes of actual interactions. Building interaction networks of species-rich communities, where interactions are explicitly measured in the field allows us to incorporate their dependence on the environmental and biotic context giving a better reflection of the ecological processes underlying community diversity. I present a novel approach to building an interaction network based on competition coefficients measured in the field. Our approach applies two sets of population dynamic models of varying complexity to quantify observed interactions and then approximate the unobserved interactions occurring between rare species. In using a Bayesian statistical framework, our model can handle high levels of complexity and quantify the uncertainty around model estimates in a probabilistic way. In this talk I will show networks for diverse annual plant communities and compare them to networks developed from the same system but using association data only. I discuss what this approach offers over more traditional association-based networks for studying diverse communities. This exciting new network approach allows us to explore the structure of diverse natural communities in a mechanistic context while accounting for natural levels of complexity.

Keywords: Community ecology, Network ecology

Tianxiao (August) Hao (University of Melbourne) with Jane Elith, JosÃ© J. Lahoz-Monfort and Gurutzeta Guillera-Arroita

Testing whether ensemble modelling is advantageous for maximising predictive performance of species distribution models

06/23/2020 9:45:00 AM-10:00:00 AM

Session: Contributed talks *(Chair: Diana Cole)*

Location: #acacia *Student*

Predictive performance is important to many applications of species distribution models (SDMs). The SDM `ensemble’ approach, which combines predictions across different modelling methods, is believed to improve predictive performance, and is used in many recent SDM studies. We tested how these ensemble models perform, compared to single models, using a presence-absence tree dataset in New South Wales. We divided data into `internal’ and `external’ folds, using two spatial blocking strategies (blocks and slices).We trained and cross-validated all models on internal folds, using both repeated random cross-validation (CV) and spatially-blocked CV. We then built ensembles using the R package `biomod2’, with standard (`untuned’) settings. We also fitted boosted regression tree (BRT) models to the same data, tuned according to published procedures. We then compared the predictive performance of all models on external folds, using area under the receiver-operating characteristic curve (AUC) and log-likelihood as metrics. In all our tests, ensemble models performed well, but not consistently better than their component untuned individual models or tuned BRTs. Spatially-blocked CV estimates of predictive performance were better than repeated random CV, in terms of their match with external estimates of performance. The latitudinal slice test was only possible for four species but showed simple (e.g. regression models) or tuned models (i.e. tuned BRT) outperforming complex and untuned models (e.g. ensembles).

Keywords: Model assessment/validation, Species distribution modelling

MÃ¥ns Karlsson (Stockholm University) with Ola HÃ¶ssjer

Statistical species identification

06/23/2020 10:00:00 AM-10:15:00 AM

Session: Contributed talks *(Chair: Diana Cole)*

Location: #acacia

Correct identification of species, subspecies, sex and age are all of critical importance to get reliable time series of bird (and other taxa) population changes and migratory timings. Through a Bayesian latent variable approach, we present a way of obtaining aposteriori species probabilities based on measured traits, which generalizes to practically any group of species and any type of trait. One may also choose the degree of conservativeness through a parameter value determining the size of so called indecisive regions, which contain trait measurements that are not distinct enough to determine the species with acceptable confidence. In other words, our model does not only predicts species, it also predicts when the measured traits are not sufficient for reliable species identification.

Note that the method presented above is not only applicable to species identification, but also to subspecies, sex or age determination, or a combination thereof. We illustrate usage of the method on a data set of four Acrocephalus species.

Keywords: Classification, Population ecology, Software development, Trait based ecology

Thomas Frederick Johnson (University of Reading) with Nick Isaac, Agustin Paviolo and Manuela Gonzalez-Suarez

Handling missing values in trait data

06/23/2020 10:15:00 AM-10:30:00 AM

Session: Contributed talks *(Chair: Diana Cole)*

Location: #acacia *Student*

Trait data are widely used in ecological and evolutionary analyses, but often values are not available for all species of interest. Researchers traditionally have excluded species without data from analyses, but estimation of missing values using imputation has been proposed as a better approach. Here we evaluate the performance of different approaches for handling missing trait data. We simulated continuous trait data and separate response variables to test performance of nine imputation approaches and complete-case analysis (records with missing data excluded), given missing values under different biases. We characterized performance by estimating error in imputed trait values (deviation from the true trait value) and inferred trait-response relationships (deviation from the true relationship between a trait and response). Generally, imputation approaches outperformed complete-case analysis, but there were some cases were complete-case analysis was best, especially compared to `Mice’ imputation - a commonly used approach. Despite this, we still consider data imputation as the more effective approach for handling missing data. â€˜Rphylopars’ was the best performing imputation approach and could accurately predict a response-trait slope in all non-severe bias types. However, the estimates of missing data were still inaccurate e.g. for `Rphylopars’ in the best scenario (5% of values missing under no-bias), a 6,000kg Elephant could be predicted to weigh 10,000kg. Given these results, we recommend `Rphylopars’ imputation, but also encourage rigorous data checking for biases before and after imputation. Finally, we propose four variables that can assist researchers working with incomplete datasets to detect data biases and minimise errors.

Keywords: Trait based ecology

Benjamin R Fitzpatrick (Swiss Federal Research Institute WSL) with Andri Baltensweiler, Christoph DÃ¼ggelin, Lars Waser, Dirk Schmatz, Beat Wermelinger and Anita C Risch

Interpretable Machine Learning and Spatial Cross Validation applied to Species Distribution Modelling of IUCN Red Listed Red Wood Ants in Switzerland

06/23/2020 10:30:00 AM-10:45:00 AM

Session: Contributed talks *(Chair: Diana Cole)*

Location: #acacia

We use a random forest variant to predict the probability of red wood ant (Formica rufa group) occurrence across the forested areas of Switzerland. We address the class imbalance in red wood ant occurrence data and use a spatial cross validation scheme to tune the model for spatial interpolation. We partition our data into training, validation and hold-out sets with reference to the spatial dependence structure of our response variable, the class imbalance in our response variable and biogeographic regions of Switzerland. We validate our model through both prediction of hold-out sets and the use of techniques from interpretable machine learning. These techniques enable us to assess whether the main drivers of the predictive performance of our model are ecologically plausible in terms of existing knowledge regarding red wood ants. We also investigate the consequences of implementing a recently proposed method to include the effects of spatial position in random forests. This method involves the use of distances to each of a set of points in the study area as additional covariates. Other covariates trialed include summary statistics of climatic data, digital elevation model products, LIDAR derived descriptions of above ground vegetation structure and cover and predictions of woody vegetation composition from remotely sensed data. The map of the predicted probability of red wood ant occurrence across all Swiss forests provides a timely update on the distribution in Switzerland of this IUCN Red Listed group.

Keywords: Machine learning, Model assessment/validation, Species distribution modelling

David I. Warton (UNSW Sydney) with Arthur Huang, Thomas King and Gordana Popovic

Inference from the fossil record using bootstrap inversion: easier than ABC?

06/23/2020 10:45:00 AM-11:00:00 AM

Session: Contributed talks *(Chair: Diana Cole)*

Location: #acacia

Approximate Bayesian Computation (ABC), now widely used in stochastic modelling, pioneered the use of simulation for likelihood-free inference. However, implementing ABC has its challenges, many of which arise through the use of a Bayesian framework, which requires numerical techniques to reverse the order of conditioning. An alternative, available since the 1990's, is (parametric) bootstrap test statistic inversion. Bootstrap inversion can be applied in a similar setting to ABC - it just requires a simulation model and summary statistic, but makes less restrictive assumptions than ABC and typically returns more accurate results. For example, in the absence of nuisance parameters, the method is exact up to Monte Carlo error.

Ideas are illustrated on the problem of estimating extinction (or invasion) times from the fossil record, accounting for measurement error. This is a challenging inference problem because usual regularity conditions are not satisfied, and complex sources of measurement error should be accounted for that makes it difficult to specify a likelihood. It is evident that methods currently used in palÄ‡obiology underestimate uncertainty, by not appropriately accounting for sampling error.

Keywords: Hierarchical modelling, Paleoecology, Statistical inference

Naveed Richard Bhatti (James Hutton Institute / University of Aberdeen) with Ruth J. Mitchell, Jackie M. Potts and Thomas Cornulier

Estimating detection heterogeneity without covariates in occupancy modelling: validation experiments with a fully known population

06/23/2020 9:30:00 AM-9:45:00 AM

Session: Imperfect Detection *(Chair: Res Altwegg)*

Location: #banksia *Student*

Occupancy models can improve the accuracy of population distribution estimates by accounting for imperfect detection. However, different detection probabilities among sampling sites can lead to severely underestimating overall occupancy probability, unless this heterogeneity can be modelled. Predictors of detection probability at a given sampling site are not always available or sufficiently informative. In the absence of these, assumptions are needed about the distribution of detection probabilities across sampling sites.

Sessile organisms, such as lichens, show significant and unpredictable detection heterogeneity among sampling sites. In this study, multiple observers surveyed a set of trees with an experimental population of artificial lichens, thus providing an unusual opportunity to validate occupancy models in the field. Using the known realised detection rates, we evaluate the ability of a Bayesian hierarchical occupancy model to correctly recover the heterogeneity in detection probabilities between sites as well as overall occupancy. We investigate the sensitivity of parameter estimates to different prior distributions, and how sample size and the number of repeat surveys affect this sensitivity. We show the conditions in which site-detection heterogeneity can be successfully modelled, and conclude with general implications for the design and analysis of occupancy surveys.

Keywords: Hierarchical modelling, Occupancy analysis

Fabian Ketwaroo (University of Kent) with E.Matechou, X.Wang and C.Villa

Objective Priors from Scoring rules for N-mixture models

06/23/2020 9:45:00 AM-10:00:00 AM

Session: Imperfect Detection *(Chair: Res Altwegg)*

Location: #banksia *Student*

Estimating abundance of a population is a fundamental objective for many wildlife population monitoring programmes and ecological studies. N-mixture models are very commonly used to estimate the absolute abundance of a species based on survey sampling. They provide a simple and cost-effective way to estimate absolute abundance while accounting for imperfect detection. However, a number of issues with N-mixture models have been found when the models are fitted within a classical framework. In particular, parameter identifiability issues and cases where infinite estimates of abundance can arise have been found, while concerns about the considerably different estimates of absolute abundance under different model specifications have also been raised. Here, we consider fitting N-mixture models within a Bayesian framework. We develop new objective prior distributions for a number of existing and new formulations of N-mixture models. These objective prior distributions are obtained using scoring rules and are not model dependent. We compare the results of our objective priors to those obtained using standard priors, considering both simulated and real data. Finally, we present results on model selection using Bayes factors as well as other Bayesian tools.

Keywords: Abundance/richness/diversity estimation, Objective priors

Gurutzeta Guillera-Arroita (University of Melbourne) with Natalie J. Briscoe, Jane Elith, Damaris Zurell, Guillermo Fandos Guzman, Christian Koenig, Anne-Kathleen Malchow, Marc KÃ©ry and Hans Schmid

Can occupancy dynamics models improve predictions of species’ range dynamics? A test using Swiss birds

06/23/2020 10:00:00 AM-10:15:00 AM

Session: Imperfect Detection *(Chair: Res Altwegg)*

Location: #banksia

Predictions of species’ current and future ranges are required for many conservation and management decisions. Traditionally, these have been estimated using static, correlative distribution models. There is now increasing interest in methods that capture the dynamics that underpin range changes more explicitly, yet data required to build more complicated process-explicit models are often not available, and tests of whether these models improve predictive accuracy under current or future conditions are still relatively rare. Here we present an evaluation of performance using a large long-term multispecies dataset on Swiss breeding birds, spanning 14 years (2000-2013), 267 sites distributed across the country and 69 species. We test whether occupancy dynamics models, which describe changes in species’ occupancy through time via modelling site colonization and extinction events, can improve predictions of distribution changes over time. We compare their predictions to those obtained from standard static correlative models, fitted both using traditional regression methods and machine-learning techniques. We assess performance considering different amounts of data for model fitting (3, 5 and 10 years). We also explore how predictions of both static and dynamic models differ when imperfect detection is accounted for in the models.

Keywords: Model assessment/validation, Occupancy analysis, Range dynamics, Species distribution modelling

Maxime Fajgenblat (University of Leuven) with Kristijn Swinnen, Pieter Vanormelingen, Marc Herremans, Dirk Maes, Robby Stoks, Luc De Meester, Christel Faes and Thomas Neyens

Improving site-occupancy models for large-scale citizen science datasets

06/23/2020 10:15:00 AM-10:30:00 AM

Session: Imperfect Detection *(Chair: Res Altwegg)*

Location: #banksia *Student*

As the volume of citizen-science data on species occurrences rapidly increases, there is a need for modelling tools that properly address the many challenges that are intrinsically related to these data. Over the past few years, site-occupancy models have been advanced as a promising framework to draw inferences from opportunistically sourced occurrence data. Current approaches do not always fully capitalize on the information hiding in these datasets and leave several sources of bias unacknowledged. We developed a comprehensive spatio-temporal site-occupancy model that aims to mimic the data-generating process as closely as possible. We took a Bayesian approach using the probabilistic programming language Stan. We applied the model to a dataset containing over 1M butterfly records in Belgium, collected through the citizen science data portal Waarnemingen.be. By doing so, we obtained retrospective inference on the occurrence of species through time and space at high resolution, as well as inference on overall distributional trends, phenological patterns and habitat preferences. The proposed model can be used to increase the value of opportunistically collected data by volunteers, and can aid the understanding of spatiotemporal patterns of species distribution for which rigorously collected data are absent.

Keywords: Citizen science, Hierarchical modelling, Occupancy analysis, Spatio-temporal statistics

Kwaku Peprah Adjei (Norwegian University of Science and Technology) with Bob O'Hara

Diagnosis of model violations in N-Mixture models - A study of the interaction between accidental double counts and unmodelled variation in detection probability.

06/23/2020 10:30:00 AM-10:45:00 AM

Session: Imperfect Detection *(Chair: Res Altwegg)*

Location: #banksia

Model violations in the N-Mixture model lead to significant bias in abundance estimates, with potential non-detection with standard goodness of fit tests. Most studies have looked at the model violations independently with little focus on their interactions. However, simulation studies could be used when analysing data to identify potential model violations. Knowledge of the effects of the parameter choices for the prior distributions and interaction of model assumption violations would guide researchers in making inferences that is devoid of errors from the mis-specification of the prior distributions. The Bayesian framework with the Markov Chain Monte Carlo was used to study the effects on the bias of the abundance estimates, measures of overdispersion, quasi coefficient of variation and the caliberated Bayesian goodness of fit tests (Pearson-Chi square and Freeman-Tukey).

Keywords: Abundance/richness/diversity estimation, Hierarchical modelling

Jennifer L. Brazeal (Cornell University) with Angela Fuller

A multiscale multispecies occupancy model and its application to investigate spatial and temporal species use and interactions

06/23/2020 10:45:00 AM-11:00:00 AM

Session: Imperfect Detection *(Chair: Res Altwegg)*

Location: #banksia

Multispecies occupancy models examine the effects of both environmental conditions and species interactions on the distributions of species. If temporal avoidance enables coexistence of competing species at a site, however, species interactions might appear positive, while obscuring negative competitive interactions. To address this, we built upon a recent parameterization of a multispecies occupancy model to develop a multiscale multispecies occupancy model. We modeled species occurrence at a site as a multivariate Bernoulli (MVB) random variable, while at a secondary level, we modeled multispecies use of discrete periods during the day as a MVB random variable, conditional on site occupancy. We applied this model to examine multispecies occupancy of coyote (Canis latrans), red fox (Vulpes vulpes), and fisher (Pekania pennanti), using photos collected in the winter of 2015 from 608 camera stations in the Southern tier of New York. We partitioned days into diurnal (sunrise to sunset) and nocturnal (midnight to sunrise and sunset to midnight) periods. We found evidence that coyote and red fox avoided each other at the site level, but positively interacted during nocturnal periods, indicating similar daily activity patterns where they co-occurred. Meanwhile, fisher appeared to co-occur readily with other species, but there was evidence of negative interactions with other species during the nocturnal time period, suggesting temporal but not spatial avoidance. Our case study demonstrated a novel examination of species interactions at multiple scales, but more broadly, the multiscale multispecies model has similar utility to classical multiscale occupancy models, while also addressing multispecies questions and hypotheses.

Keywords: Camera trap data, Hierarchical modelling, Multivariate analysis/joint species distribution models, Occupancy analysis

Chenangnon Frederic Tovissode (UniversitÃ© d'Abomey-Calavi, Benin) with Romain GlÄ lÄ KakaÄ

Inference in flexible nonlinear models for repeated/clustered data: a Bayesian approach under scale mixture of skew normal distributions

06/23/2020 9:30:00 AM-9:45:00 AM

Session: Movement models *(Chair: Emiel van Loon)*

Location: #corymbia *Student*

Correlated data are generated in many application fields and their analysis often require mixed-effects models. Nonlinear mixed models are adequate for modeling phenomena following known nonlinear trajectories when repeated/clustered measurements are recorded. Unfortunately, the normal distribution usually assumed for random effects and residual errors in nonlinear mixed-effects models has been proved to be often restrictive in fields like ecology, agriculture, pharmacokinetics and economics among others. As a result, there has been increasing interest in allowing random effects and residual errors to have heavy tailed distributions. This work introduces an extension of the traditional nonlinear mixed-effects model considering the family of scale mixtures of skew normal distributions to account for skewness and kurtosis in both residuals and subject-specific parameters. A Bayesian estimation procedure is proposed to construct credible regions for fixed-effects and variance components. The procedure combines an accept-reject algorithm and an elliptical slice sampling algorithm within a Gibbs scheme. Model selection is achieved via Bayes factors, whereas residual and subject weights are provided for subject specific inference. Through a small Monte Carlo experiment, we showed that the proposed scale mixtures of skew normal nonlinear mixed modeling approach outperforms common competing Bayesian approaches to nonlinear mixed models when data exhibits skewness and kurtosis. An application to the temporal dynamics of vegetation moisture also proves the practical usefulness the new model in ecology.

Keywords: Accept-reject, Bayes factor, Bayesian nonlinear mixed models, Elliptical slice sampling, Hierarchical modelling, Model assessment/validation, Population ecology, Skew scale mixtures, Subject-specific weights

Theoni Photopoulou (University of St Andrews) with Karine Heerah and Lars Boehme

Using hidden Markov models to study the effects of environmental characteristics on the diving ecology of Weddell seals

06/23/2020 9:45:00 AM-10:00:00 AM

Session: Movement models *(Chair: Emiel van Loon)*

Location: #corymbia

Patterns of habitat use are often studied in horizontal space, but this does not capture the four-dimensional nature of ocean habitats. Especially at the poles, there is seasonal variation in vertical ocean structuring (i.e., in depth), governed by density, therefore deep-diving marine animals encounter a range of conditions that vary in density. We use hidden Markov models (HMMs) fitted to telemetry data to identify functionally different diving behaviours in an Antarctic top predator. We analyse the time series of dive variables, with environmental covariates acting on the probability of switching between states, to understand patterns of use of vertically distributed habitat. We present results from male and female Weddell seals in the Weddell Sea, in the Atlantic sector of the Southern Ocean. Weddell seals are found here all year round - as mammals, they breathe air but dive deeply to find prey at depth, offering an opportunity to study the relationship between behaviour and conditions found at depth, through their diving behaviour. We show that preference for different density regimes varies by sex. Males keep to the colder, on-shelf water masses, while females also venture off the continental shelf and visit warmer pelagic water masses. Both sexes exhibit a diurnal pattern in dive depth that persists from austral late summer into early winter. Our findings provide insights into the Weddell Sea shelf and slope ecosystem, suggesting the existence of a diel vertical migration of prey from late summer well into the months of reduced light availability.

Keywords: Behavioural ecology, Biologging, GPS data, Movement modelling

Jordan Milner (University of Sheffield) with Paul G. Blackwell and Mu Niu

Two’s Company, Three’s a Crowd: Modelling the Movement of Interacting Animals

06/23/2020 10:00:00 AM-10:15:00 AM

Session: Movement models *(Chair: Emiel van Loon)*

Location: #corymbia *Student*

The increasing availability of animal tracking data has enabled us to tackle more questions and develop more complex models. Typically though, these models have been developed for analysing the tracks of individuals and we lose sight of the impact animals have on each other with regards to their movement behaviours. Furthermore, this increase in data volume and model complexity gives rise to questions about model suitability and how to efficiently extract the desired information.

We aim to develop a model that captures the interaction in social animals’ movement in order to improve our understanding of their social structure, reproductive behaviour, etc. Our approach is based on the concept of social hierarchies, which is embedded in a multivariate diffusion process that models the movement of a group. Behaviour state switching facilitates dynamic social interactions and we augment the observed data with sampled switching times in order to model the animals' behaviour naturally in continuous time. In addition, this enables us to carry out exact inference in a Bayesian setting. All movement and behaviour parameters are estimated with Markov chain Monte Carlo methods.

Results from fitting the model to GPS locations of wild baboons will be presented, where we gain rich information on the groups social structure. Additionally, we will discuss some practical considerations we have investigated, such as if thinning the data provides the same insights whilst offering computational benefits and if our model formulation and assumptions are biologically sound.

Keywords: Behavioural ecology, Biologging, GPS data, Movement modelling

Laura Merritt (University of Reading / UK Centre for Ecology and Hydrology) with Tom Oliver, Justin Travis, Steven White, Rob Salguero-Gomez and James Bullock

An investigation into metrics to account for high model sensitivity to low values in dispersal kernel fitting

06/23/2020 10:15:00 AM-10:30:00 AM

Session: Movement models *(Chair: Emiel van Loon)*

Location: #corymbia *Student*

Species shift their ranges for a variety of reasons including climate change and introduction of invasive species. Modelling the movements of species allows us to target conservation and control measures where required. Dispersal kernels can be used in individual based models, species distribution models and integrodifference equations to indicate the likelihood of individuals moving certain distances across continuous landscapes. The issue is, during fitting, the tail of the kernel has been shown to be consistently underestimated. Integrodifference equations are especially sensitive to the number of individuals at the final measured distance, leading to underestimation of the speed at which species can shift their ranges. We compare different metrics designed to aid model selection, showing the limitations of current methods, and advancing research into novel approaches by accounting for the sensitivity to low values in the tail.

Keywords: Model assessment/validation

Katherine Whyte (University of St Andrews) with Stacy DeRuiter, Catriona Harris, Debbie Russell, Gordon Hastie, Carol Sparling, Bas Binnerts and Len Thomas

Detecting changes in movement behaviour in response to disturbance using Mahalanobis distance

06/23/2020 10:30:00 AM-10:45:00 AM

Session: Movement models *(Chair: Emiel van Loon)*

Location: #corymbia *Student*

The goal of behavioural response studies is to determine if a given noise disturbance caused a change in movement behaviour by comparing movements recorded before (baseline period) and during exposure (exposure period). Statistical methods are required to determine whether movement changed due to noise and if so at what noise level this occurred. A popular modelling framework to answer these questions centres around Mahalanobis distance, a univariate measure of how movement metrics change between moving-time windows. The method identifies responses using a randomization test and then estimates response probability for each noise level within a hierarchical Bayesian model, accounting for within and between individual variation. This approach has been widely applied to quantify cetacean response to navy sonar and we present a further application to quantify response of harbour seals to wind farm construction. However, despite wide application, there has been limited investigation into the reliability of this method.

In this talk, we present a simulation study to quantify both the false positive rate and statistical power of this approach for two relevant applications: detecting response of Cuvier's beaked whales to navy sonar using accelerometer tags and response of harbour seals to wind farm construction using GPS tags. In both cases, multi-state discrete-time correlated random processes with parameters estimated from real data are used to simulate realistic diving and horizontal movement patterns. Overall, we find the Mahalanobis method has high power to detect responses, but can also have a high false positive rate when baseline data is sparse.

Keywords: Behavioural ecology, Biologging, GPS data, Movement modelling

Leslie New (Washington State University) with Cheryl Schultz and Lori Babbick

Modelling butterfly movement using multi-scale hidden Markov models

06/23/2020 10:45:00 AM-11:00:00 AM

Session: Movement models *(Chair: Emiel van Loon)*

Location: #corymbia

A correlated random walk, summarized as a diffusion rate, has often proven to be a reasonable first approximation of large-scale butterfly movement behaviour. However, butterfly movement is occurring at multiple spatial and temporal scales, defined by broad-scale habitat types as well as local attractants on the landscape. Recent developments in animal movement modelling enable us to describe the mechanistic processes driving movement, as well as the more complex multi-scale behaviours. To test the efficacy of these approaches, we have applied a multi-scale hidden Markov model to data collected on Fender's blue butterflies (Icaricia icarioides fenderi). By de-coupling the larger-scale habitat-based parameters (e.g. edge habitat vs prairie) from the finer-scale features of the landscape that can be perceived by the butterflies (e.g. nectar sources), we able to build a more cohesive framework for the modelling of butterfly movement. At the larger scale, the butterflies' movement is affected by the type of habitat in which they are moving, particularly edge habitat, while at the smaller scale, individuals are attracted to nectar sources, in the form of Kincaid's lupine (Lupineus oreganus).

Keywords: Behavioural ecology, Movement modelling

Todd W. Arnold (University of Minnesota)

A flexible hierarchical model for estimating survival of unmarked group-living organisms

06/23/2020 9:30:00 AM-9:45:00 AM

Session: Acoustics and more *(Chair: Tiago Marques)*

Location: #darwinia

Field ecologists frequently acquire incomplete counts of unmarked individuals from discrete recognizable groups: examples include visual surveys of territorial group-living organisms, counts of unmarked offspring attended by marked parents, or citizen-science surveys of relatively sessile organisms from isolated habitat patches. Given replicated counts, N-mixture models provide a formal framework for estimating size of incompletely observed groups, but the assumptions of N-mixture models are often violated. Mortality of group members can occur between replicate surveys, and measuring survival between survey events might often be the primary ecological goal of the study. For group-living organisms, detection failure and mortality can impact the entire group, leading to zero-inflated detection and survival probabilities, thereby violating independence assumptions. I developed a flexible open-population N-mixture model that can accommodate incomplete counts (i.e., failing to detect some individuals within a group), missed counts (i.e., failing to detect any surviving group members), partial mortality (i.e., random loss of some group members), and complete group mortality (i.e., simultaneous mortality or emigration of the entire group). The model includes 4 parameters: group detection, group survival, individual detection, and individual survival. Simulations indicate that all 4 parameters are readily identifiable, although group detection and group survival exhibited fairly strong sampling covariance. Application to three real-world data sets suggests that the new model better accommodates violation of assumptions and leads to better ecological inferences about factors affecting survival and detection probability of group-living organisms.

Keywords: Abundance/richness/diversity estimation, Citizen science, Hierarchical modelling, Population dynamics

Eliza M. Grames (University of Connecticut) with Piper L. Stepule, Benjamin T. Ranelli, Susan Z. Herrick, and Chris S. Elphick

Separating acoustic signal patterns into underlying behavioral components with Hawkes self-exciting point process models

06/23/2020 9:45:00 AM-10:00:00 AM

Session: Acoustics and more *(Chair: Tiago Marques)*

Location: #darwinia *Student*

In animal communication, signals can arise both endogenously or in response to cues, such as signals by conspecific competitors. For species where the same signal serves dual functions, such as in some songbirds that use the same song for mate attraction and territorial defense, the underlying reason for a bird initiating a song at a specific time cannot be determined without direct behavioral observations, and even then may be hard to discern. Here, we present a flexible class of inhomogenous, self-exciting point process models (Hawkes process models) that can be used to estimate the underlying reasons for why an individual initiates an acoustic signal. In our application of Hawkes process models to acoustic signals, endogenous signals are assumed to arise at a constant background rate, but when a signal is initiated, it instigates (or *self-excites*) additional signals by conspecific individuals. When applied to time series of bullfrog (Rana catesbeiana) calls and ovenbird (Seiurus aurocapilla) songs, the Hawkes process models perform as well as a homogenous Poisson process model typically used to describe count data, while providing additional detail on the underlying motivations for signals. Because the structure of Hawkes process models can be fit in a flexible, hierarchical framework, the simple form can be extended to include spatiotemporal dynamics in signals. Although we apply the simple form to acoustic signals, the models can be applied to any class of behaviors that are self-exciting.

Keywords: Behavioural ecology

Sougata Sadhukhan (Wildlife Institute of India) with Bilal Habib

Counting wolves in a densely populated landscape: Can acoustic monitoring be the ultimate solution?

06/23/2020 10:00:00 AM-10:15:00 AM

Session: Acoustics and more *(Chair: Tiago Marques)*

Location: #darwinia *Student*

Population estimation of wolves is a decades-long challenge for scientists. Wolves are visually cryptic but vocally active species. Therefore, acoustics monitoring has long been identified as a possible solution for the wolf pack census. However, the difficulty of wolf population estimation lays on determining the animal distance and other factors associated with the detection function. Our newly adopted three observer-based howling survey method address both the difficulties hence will help standardise population estimation of other vocally active species.

The howling survey was conducted in the system-generated random grids based on potential wolf habitats in human-dominated arid landscapes of Maharashtra, India. The observer 1, played pre-recorded howls at different sound pressure and recorded the howl response and animal bearing. Observer 2 and observer 3 who were 200-400 meters apart recorded the bearing of playback and animal response along with their GPS location. The number of successful playback detection by observer 2 and 3 helped us to determine the area-specific acoustic detectability whereas the playback bearing enabled us to assess the accuracy of the responded animal’s position through binary regression using GLM. By determining the animal distance and the area-specific detectability, this model helps to improve the performance of density estimation of the wolf through a bioacoustics survey.

Our study is a significant addition in population study using bioacoustics. Since wolf howls also possess individuality information, incorporating this information will help to estimate wolf population using Spatially Explicit Capture-Recapture framework.

Keywords: Bearing, Howl Survey, Indian Wolf, Model assessment/validation, Population ecology, Population Estimation, Triple Observer

Nossaiba Baba (University of Hassan II) with I. Agmour, Y. El Foutayeni and N. Achtaich

Bioeconomic model of parapenaeus longirostris and small pelagic species with mortality rate

06/23/2020 10:15:00 AM-10:30:00 AM

Session: Acoustics and more *(Chair: Tiago Marques)*

Location: #darwinia *Student*

In the past few years, the parapenaeus longirostris population stock has seen a sharp reduction. In this work, we propose a bioeconomic model that represents the biomass evolution of this marine population in two moroccan maritime patches: protected area and unprotected area. In the model construction, we take in consideration the predation interaction between the parapenaeus longirostris population and the small pelagic species of moroccan coastal zones. We suppose the existence of coastal trawlers that exploit both the predator and prey populations. Our objective is to study the influence of the predator mortality rate variation on the evolution of prey biomass and the profit of coastal trawlers. It should be underlined that, coastal trawlers are constrained by the conservation of marine biodiversity. One of the key consequences of this is that the increase in the mortality rate of small pelagics leads to an evolution in the parapenaeus longirostris stock, and consequently to an increase in the profit of coastal trawlers after exploitation of this species. On the other hand, the level of fishing effort and catches of small pelagics is decreasing, which leads to a reduction in the profit of coastal trawlers after exploiting small pelagics.

Keywords: Dynamic state models, Ecological stability and resilience, Population dynamics, Predator-prey modelling

SÃ©bastien Roques (CEFE /Paul Sabatier University) with Pierre-Yves Henry, Daniel Turek, Emmanuelle Cam and Roger Pradel

A multi-species capture-recapture model to explore synchrony in departure from stopover sites

06/23/2020 10:30:00 AM-10:45:00 AM

Session: Acoustics and more *(Chair: Tiago Marques)*

Location: #darwinia *Student*

On their journeys between wintering and breeding sites, migratory birds usually alternate between migratory flights and stopovers where they refuel. With most of the time spent in stopovers, these stops are known to be crucial to allow birds to resume their entire journey. Correctly identifying the main drivers of departure decision from stopover sites is challenging because birds are often hard to detect (imperfect detection) and the true stopover duration is known to be larger than the observed stopover duration (days elapsed between first and last capture). Thus, capture-recapture models are required. In order to identify the main drivers of departure decision, we first used a single species state-space formulation of the Jolly-Seber model where we integrated weather variables and the estimated *Time Since Arrival* as covariates. However, on these stopover sites multiple species co-occured during their stopover but little is known on how these species synchronize or not their departure. Secondly, based on former studies on synchrony in survival, we extended the model to the multi-species level to explore synchrony in departure probability from stopover sites. Our new model allows quantifying synchrony in departure probability between species and also to disentangle the underlying processes generating synchrony in departure probability (weather or internal covariates). We applied our approach on a multi-species, multi-sites capture-recapture dataset about long-distance migratory passerines.

We implemented our model in a Bayesian framework using the Nimble R package resulting in a 80% reduction in running time when compared to Jags.

Keywords: Capture-mark-recapture, Hierarchical modelling, Population ecology

Sofia M. Gabriel (University of Tasmania) with Uffe Thygesen, Martin Waever, Paige Eveson, Russ Bradford, David Moreno, Jayson Semmens and Toby Patterson

Investigating the use of a novel state-space model prototype to analyse the fine-scale spatial use of marine species passively tracked in dense acoustic arrays

06/23/2020 10:45:00 AM-11:00:00 AM

Session: Acoustics and more *(Chair: Tiago Marques)*

Location: #darwinia *Student*

Acoustic telemetry uses ultrasonic transmissions from tags to be detected on arrays of fixed receivers. If receivers are in proximity and a single transmission is detected on multiple arrays, then the location of the animal can be inferred from triangulation. Without concurrent detections however, this method cannot be used. By grouping detections over a wider time interval, non-Gaussian state-space models (SSMs) can improve the location estimates of a tagged animal. This project investigates the use of a novel SSM prototype to analyse passive acoustic data collected on marine megafauna. An Ornstein-Uhlenbeck process model was used in discrete time with a binomial error model where probability of detection decays with distance from the receiver. The SSM prototype performed well in ideal simulated cases with varied array densities and detection functions. We present the results of investigating how varying number of receivers and detection functions influenced the model's ability to accurately estimate location. To determine how the model performed on real data sets, we applied it to data from case studies of marine fauna tagged with GPS and acoustic tags to investigate average error rates. We then investigated how the model might be used to explore the fine-scale spatial usage of beach areas in New South Wales, Australia by juvenile white sharks (Carcharodon carcharias) in an array of 26 receivers. This study provides an initial assessment of how an SSM could be used to increase understanding of localized movements of important marine species.

Keywords: Behavioural ecology, Model assessment/validation, Movement modelling

Di Cook (Monash University)

Making inference using data plots, with application to ecological statistics

06/23/2020 9:00:00 PM-9:50:00 PM

Location: #acacia *Plenary (Chair: Gordana Popovic)*

The statistical ecology community has been at the forefront of adopting and developing computational techniques for data analysis. Exploratory techniques that are popular in the field, such as ordination, have been equipped by ecologists with permutation tools for making inference. New high throughput techniques for data collection are being embraced by the community, posing new challenges for ecological data analysis.

Statistical graphics has always played an important exploratory role in ecological data analysis. This talk will describe using data plots to make inference, that leverages the modern computational toolbox and crowd-sourcing services. We will discuss the ideas, and methodology, that have been developed thus far, and how to apply them with the R package, nullabor. This will include an example of using visual inference in a high-throughput bioinformatics data analysis. With an eye to the future, crowd-sourcing might be supplemented with computer vision models using deep learning, to read data plots, which would be especially important for high throughput analyses.

Morgan W. Tingley (University of California, Los Angeles) with Christopher P. Nadeau and Manette E. Sandor

Multi-species occupancy models as robust estimators of community richness

06/23/2020 10:30:00 PM-10:45:00 PM

Session: Occupancy and multiple data sources *(Chair: Gurutzela Guillera-Arroita)*

Location: #acacia

Understanding diversity patterns is central to ecology and conservation, yet estimates of diversity are often biased by imperfect detection. In recent years, multi-species occupancy models (MSOM) have been developed as a statistical tool to account for species-specific heterogeneity in detection while estimating true measures of alpha, beta, and gamma diversity. Although the power of these models has been tested in various ways, their ability to estimate gamma diversity - or true community size, N - is a largely unrecognized feature that needs rigorous evaluation. We use both simulations and an empirical dataset to evaluate the bias, precision, accuracy, and coverage of estimates of N from MSOM compared to the widely applied Chao non-parametric estimator. We simulated 5,600 datasets across 7 scenarios of varying average occupancy and detectability covariates, as well as varying numbers of sites, replicates, and true community size. Additionally, we use a real dataset of surveys over 9 years (where species accumulation has asymptoted, indicating true N), to estimate N from each annual survey. Simulations showed that both MSOM and Chao estimators are generally accurate (i.e., unbiased and precise) except under unideal scenarios where average species occupancy is low (0.1). In such scenarios, MSOM bias frequently overestimated N. Across all scenarios, MSOM estimates were less certain than Chao, but this led to over-confident Chao estimates which showed poor coverage. Results from the real dataset largely confirmed the simulation findings, with MSOM estimates showing greater accuracy and coverage than Chao.

Keywords: Abundance/richness/diversity estimation

Amy J. Davis (National Wildlife Research Center, USDA, APHIS) with Richard B. Chipman, Kathleen M. Nelson, Jordona D. Kirby, Kim M. Pepin, and Amy T. Gilbert

A multi-method, dynamic occupancy approach to monitor wildlife disease distribution, elimination, and identify risk corridors

06/23/2020 10:45:00 PM-11:00:00 PM

Session: Occupancy and multiple data sources *(Chair: Gurutzela Guillera-Arroita)*

Location: #acacia

Wildlife diseases can pose a significant threat to humans, livestock, and wildlife. Effective disease control requires an integrated strategy of robust surveillance, coordinated management and program monitoring. Wildlife disease surveillance samples are typically collected from a variety of sources including opportunistic samples, public reports, and limited targeted surveillance, which are each constrained by inferences and biases. We used a multi-method approach to simultaneously examine several approaches to wildlife rabies surveillance and evaluate their relative biases to gain an overall understanding of detection probability. We analyzed 12 years of raccoon rabies virus (RABV) surveillance data to estimate the detection probabilities from different types of surveillance samples (e.g., strange acting reports, road kill, surveillance trapped animals, nuisance animals and public health reported animals) and evaluated the probability of raccoon RABV elimination in an enzootic zone with active oral rabies vaccination (ORV) management in progress using a dynamic occupancy approach adapted for multiple detection methods. We found that a combination of surveillance methods performed better than any single method. The public health surveillance method had a high detection probability, but was biased high in areas with active ORV management. Collection of strange acting animals also had high detection probability and was the least biased method, but only comprised ~6% of all samples. By using a multi-method occupancy approach we were able to capitalize on the advantages of different surveillance methods while reducing the overall bias from any given method.

Keywords: Hierarchical modelling, Occupancy analysis

Emy Guilbault (University of Newcastle) with Ian W. Renner, Olivier Gimenez, Julie Louvrier, Karine PrincÃ© and Christophe Botella

Combining datasets to improve predictions: data quality and dynamic processes.

06/23/2020 11:00:00 PM-11:15:00 PM

Session: Occupancy and multiple data sources *(Chair: Gurutzela Guillera-Arroita)*

Location: #acacia *Student*

Presence-only data is the most common type of species data as it can be obtained from opportunistic collections, surveys, and be reported by both specialists (researchers, museums) and the public. Presence-only locations represent a list of species' detected locations. Even if, presence-only data are widely available in ecology and used frequently in species distribution modelling, it can be delicate to work with due to uncertain accuracy of the information. More generally, ecological data present various quality in terms of error and bias. Some variability and mistakes in the citizen data science can be corrected or reduced through online filters, specialist opinion and verification. However, such strategies cannot take into account all aspect of data quality and data filtering can lead to some mistakes by erasing information. There is a need to integrate multiple aspects of data quality in statistical models to better integrate such data for species prediction.

In the literature, various models implement some aspects of data quality to improve models' predictions: observer recoding or sampling bias. Other methods involve combining different datasets to improve predictions. Nevertheless, no unifying framework exist that consider multiple datasets and various data quality aspects across years. We extend Renner et al. (2019) combined likelihood model by implementing different parameters to deal with data quality issues and by adding a dynamic framework to include colonization and extinction processes. This model combines Presence only data via Poisson point process models and occupancy data modelling in a discrete multi-year framework to improve species distribution predictions.

Renner, I. W., Louvrier, J., & Gimenez, O. (2019). Combining multiple data sources in species distribution models while accounting for spatial dependence and overfitting with combined penalised likelihood maximisation. bioRxiv, 615583.

Keywords: Citizen science, Occupancy analysis, Point process models, Spatio-temporal statistics, Species distribution modelling

Kayla L. Davis (Michigan State University) with R. Randy Wilson, Emily D. Silverman, Allison L. Sussman, James E. Lyons and Elise F. Zipkin

Flock counting error in aerial seabird surveys

06/23/2020 11:15:00 PM-11:30:00 PM

Session: Occupancy and multiple data sources *(Chair: Gurutzela Guillera-Arroita)*

Location: #acacia *Student*

Characterizing marine bird species' composition, distribution, and abundance is necessary for assessing the impacts of changing environmental conditions and for guiding management practices. However, developing predictive models is challenging because it can be difficult to locate and count bird flocks and individuals in the vast marine environment. The typical study design consists of aerial surveys in which observers count individuals within flocks and attempt to identify seabird species from planes moving at 150-200 km/h at an altitude of 50-100 m. Inherent to this study design are issues not considered explicitly in subsequent analyses including species misidentification, imperfect detection, and flock size counting error. Marine bird count data are often modeled using a negative binomial or zero-inflated negative binomial distribution due to marine birds' tendency to aggregate and their patchy distribution throughout the marine environment. However, this approach models the recorded count data as truth, yet previous work and our own study show that counts, particularly for large groups (flock sizes greater than 100 individuals), can be severely biased, and this may negatively affect the strength of our inferences from such models. We investigate counting error and its potential for biasing estimates with a case study examining seabirds in the Gulf of Mexico as a part of the ongoing Gulf of Mexico Marine Assessment Program for Protected Species (GoMMAPPS). Using these data, we evaluate the strength of our inferences under the typical, negative binomial approach versus an ordinal modeling approach, which incorporates some uncertainty around the recorded counts into our data. We compare these approaches and suggest using an ordinal modeling approach when confidence in recorded count data is low.

Keywords: Abundance estimation, Study design

Christopher T. Rota (West Virginia University) with Kenneth F. Kellner, Arielle W. Parsons, Roland Kays, and Joshua J. Millspaugh

A multispecies occupancy model with a continuous-time detection process reveals spatial and temporal interactions

06/23/2020 11:30:00 PM-11:45:00 PM

Session: Occupancy and multiple data sources *(Chair: Gurutzela Guillera-Arroita)*

Location: #acacia

Detection/non-detection data are increasingly collected in continuous time, e.g. via camera traps or acoustic sensors. Application of occupancy modeling approaches to these datasets typically requires binning detection / non-detection data over coarse time-scales, which precludes analysis of fine-scale temporal interactions between species. We developed a multi-species occupancy model that assumes a temporal point process detection model, which permits simultaneous analysis of species interactions in space and time. We applied the model to detections of white-tailed deer (Odocoileus virginianus) and coyote (Canis latrans) collected via camera trapping. We modeled temporal interactions by allowing daily patterns of deer detection probability to vary as a function of latent coyote presence. We modeled spatial dependency by allowing deer and coyote occupancy probability to vary in the presence or absence of the other species. We found evidence of both spatial and temporal interactions between deer and coyote. Coyotes were most likely to occur at sites where deer were also present. At sites where coyotes were present, deer detection probability was lower and deer were more nocturnal relative to sites where coyotes were absent, suggesting deer may shift activity patterns at sites with and without coyotes. Our example highlights how multi-species occupancy models with a continuous time detection process can be used to simultaneously infer spatial and temporal interactions. Our approach extends to any data collected in continuous time and broadens the set of questions ecologists can ask regarding both spatial and temporal interactions between species.

Keywords: Camera trap data, Hierarchical modelling, Multivariate analysis/joint species distribution models, Occupancy analysis, Spatio-temporal statistics

Eugene Seo (Oregon State University) with Xiao Fu, Justin Clarke, Andrew R. Moldenke, Julia A. Jones and Rebecca A. Hutchinson

Link Prediction Under Imperfect Detection: Collaborative Filtering for Ecological Networks

06/23/2020 11:45:00 PM-12:00:00 AM

Session: Occupancy and multiple data sources *(Chair: Gurutzela Guillera-Arroita)*

Location: #acacia

Matrix completion based collaborative filtering is considered scalable and effective for online service link prediction (e.g., movie recommendation) but does not meet the challenges of link prediction in ecological networks. A unique challenge of ecological networks is that the observed data are subject to systematic imperfect detection, due to the difficulty of accurate field sampling. In this work, we propose a new framework customized for ecological bipartite network link prediction. Our approach starts with incorporating the Poisson N-mixture model, a widely used framework in statistical ecology for modeling imperfect detection of a single species in field sampling. Despite its extensive use for single species analysis, this model has never been considered for link prediction between different species, perhaps because of the complex nature of both link prediction and N-mixture model inference. By judiciously combining the Poisson N-mixture model with a probabilistic nonnegative matrix factorization (NMF) model in latent space, we propose an intuitive statistical model for the problem of interest. We also offer a scalable and convergence-guaranteed optimization algorithm to handle the associated maximum likelihood identification problem. Experimental results on synthetic data and two real-world ecological networks data are employed to validate our proposed approach.

Keywords: Network ecology

Skipton N. C. Woolley (CSIRO) with Scott D. Foster, David Warton and Piers K. Dunstan

Multiple species modelling of presence-only datasets with mixture-of-regressions models

06/23/2020 10:30:00 PM-10:45:00 PM

Session: Point event and citizen science data *(Chair: Trevor Hefley)*

Location: #banksia

Describing the distributions of species is a fundamental line of scientific enquiry, and is needed for conservation, social, economic and political decisions. The need to understanding how species are distributed based on sparse collections of biological data, has seen the development and implementation of species distribution models (SDMs). Often, information on where the species was not seen (absences) is lacking for many SDM applications. In these contexts, there has been much use and development of presence-only species distribution models (POSDMs), which aim to estimate the distributions of species when species' absences are not explicitly recorded.These approaches can be viewed as inhomogeneous Poisson point process models (IPPMs). In this paper we present a novel multiple-species approach for understanding how multiples are species distributed based on presence only datasets. We present an approach which jointly models the distributions of multiple species simultaneously using finite mixture-of-regressions, referred to as Species Archetype Models (SAMs). We extend SAMs to be an inhomogeneous Poisson point process (IPP-SAMs). We demonstrate that our method can accurately recapture mean and variance of parameters from simulated data sets, and provide better estimates than those generated from multiple single species IPPMs. We applied our approach to a multiple species Myrtaceae presence-only occurrence dataset from New South Wales, Australia. We demonstrate that IPP-SAMs are more reliable at estimating distributions of multiples species compared to single species IPPMs. We demonstrate show that our IPP-SAM approach provides statistical precision and interpretation by grouping multiple species. In addition, IPP-SAM allow for the transfer of variance and uncertainty from the data through to predictions, improving inference made on multiple species presence-only data sets.

Keywords: Community ecology, Ecosystem ecology, Species distribution modelling

Ian Flint (University of Melbourne) with Peter Vesk, Nick Golding, Yan Wang, Aihua Xia and Janine Illian

Point process models to account for interactions across different ranges in joint species distribution models

06/23/2020 10:45:00 PM-11:00:00 PM

Session: Point event and citizen science data *(Chair: Trevor Hefley)*

Location: #banksia

A complex combination of abiotic and biotic mechanisms are known to drive species' spatial distribution, and it can often be difficult to disentangle the effects of any of these competing ecological drivers on the actual observed spatial distribution. One of the aims of joint species distribution models (JSDM) is to explain why species are found where they are, and how they interact with other species in a given ecosystem.

In this project, we propose a JSDM model that accounts for environmental effects and interactions between organisms (both positive and negative) on different scales. More precisely, we propose a multivariate point process model that allows for different types of interactions, both within a species, and across species. The model accounts for environmental effects, and can exhibit attraction and repulsion between any two organisms. This means that it can be fitted to large datasets without presuming anything about the species, thereby giving some important insights into the biological mechanisms driving the distribution. As an illustration, our model was fitted to a dataset of hundreds of species located across twenty rainforest plots spanning environmental gradients in Queensland, Australia. Our model gives some important insights into interactions between individuals that presence-absence based JSDMs are not able to capture.

We have also implemented our multivariate point process model in an R package in order to allow ecologists to use it on their own datasets.

Keywords: Multivariate analysis/joint species distribution models, Species distribution modelling

Janine B Illian (University of Glasgow)

Flexible point process modelling with inlabru -- new methodology

06/23/2020 11:00:00 PM-11:15:00 PM

Session: Point event and citizen science data *(Chair: Trevor Hefley)*

Location: #banksia

inlabru is an R-package that aims to provide flexible and computationally efficient fitting tools for spatial and spatio-temporal models based on integrated nested Laplace approximation (INLA). It is a wrapper around the well-known package R-INLA, but provides additional features that are of particular interest to ecological modelling. In particular, it facilitates point processes modelling for log Gaussian Cox processes, accounts for complex observation processes that are common in ecological data and allows for non-linear functional relationships.

This talk will provide a short introduction to the background of inlabru. However, it will mainly focus on recent method development available through inlabru. Specifically, it will focus on methods for model assessment as well as on appropriate result communication, illustrated by a case-study data set

Keywords: Spatio-temporal statistics

Meridith L. Bartley (Pennsylvania State University) with Ephraim M. Hanks, Autumn-Lynn Harrison, Jay Carlisle, David Bradley, Stephanie Coates, and David Newstead

Integration of citizen science eBird abundance data with individual animal tracking data

06/23/2020 11:15:00 PM-11:30:00 PM

Session: Point event and citizen science data *(Chair: Trevor Hefley)*

Location: #banksia

Understanding migratory patterns provides vital insights into the ecology, evolution, and conservation of birds . Massively successful citizen science efforts, such as eBird (www.eBird.org), have informed species-level abundance estimates of birds throughout their range and annual cycles. However, these observations, usually presence/absence records or bird counts, are unable to answer questions about population-level variation because the breeding population of origin is often unknown to observers. To understand this, it is necessary to know which breeding populations migratory species came from and how they are connected in space and time. Individual-level movement data that can be scaled up to populations and species could help separate species-level citizen science based abundance estimates into biologically meaningful sub-populations. We develop methods for formally pairing individual level tracking data with population level eBird abundance estimates. We consider Long-Billed Curlew (Numenius americanus), a shorebird species of conservation concern in North America, tagged with ARGOS satellite transmitters that were duty-cycled every 48 hours. We developed novel methods to combine individual bird tracking data with spatio-temporal eBird abundance data to understand subpopulation variation in abundance and migratory patterns throughout birds' annual cycles. We characterized spatial movement of each subpopulation using a potential function approach to animal movement, and formally link this potential function approach to an SDE model for the population-level observations over space and time. This knowledge is invaluable for policy, management, and conservation decisions across the entire distributional range of migratory birds.

Keywords: Biologging, Bird migration, Citizen science, Data integration, EBird, GPS data, Hidden Markov Model, Hierarchical modelling, Individual-based models, Integrated population models, Movement modelling

Corey T. Callaghan (UNSW Sydney) with Shinichi Nakagawa and William K. Cornwell

Estimating global abundance for 10,000 bird species with multiple imputation

06/23/2020 11:30:00 PM-11:45:00 PM

Session: Point event and citizen science data *(Chair: Trevor Hefley)*

Location: #banksia

The abundance of a species in a given area at a given time is key baseline data for ecology and biodiversity conservation. But such data range from high quality with limited spatial and temporal resolution to low quality but massive spatial and temporal coverage. Gap filling imputation methods may be useful in this situation. We developed an approach leveraging big citizen science data (i.e., >400 million observations), using the global citizen science dataset eBird. First, we statistically assessed the relationship between estimated populations, from a number of disparate sources, and the number of individuals observed per unit effort derived from eBird for ~ 700 bird species. This statistical relationship was then treated as a measure of â€˜detectability’ specific for the eBird data resource - accounting for the myriad biases associated with citizen science data (e.g., spatial biases, temporal biases, observer skill). We then used life history traits (e.g., color, body size, flock size) with multiple imputation methods to estimate density throughout the world for our training species. Finally, we used eBird to calculate, for the majority of the world’s bird species (~10,000 species), observation rate per unit effort to abundance based on imputed detectability estimates, along with associated uncertainty. As citizen science data continue to increase in quantity, we believe our method of integrating seemingly disparate datasets to train citizen science data will be critical to quantify biodiversity in the future.

Keywords: Abundance/richness/diversity estimation, Citizen science, Community ecology

Casey Youngflesh (University of California, Los Angeles) with Morgan W. Tingley

A hierarchical Bayesian framework for modeling large-scale phenological dynamics of North American birds

06/23/2020 11:45:00 PM-12:00:00 AM

Session: Point event and citizen science data *(Chair: Trevor Hefley)*

Location: #banksia

In seasonal environments, the timing of ecological events (known as phenology) plays a critical role in ecosystem functionality. Phenological changes have been observed across a number of bird species in recent years, however the degree to which these changes vary over space has been largely unaddressed.

Using large-scale observational data from both eBird, a community science platform, and MAPS, a continental-scale bird banding program, we estimated phenological metrics for forest dwelling passerine birds across eastern North America over the last several decades. We applied Generalized Additive Models in conjunction with spatial autoregressive models in a Bayesian framework to derive phenological estimates and associated uncertainty while leveraging spatial information inherent in the data. We then used hierarchical models to investigate how changes in both migration and breeding phenology varied over a latitudinal gradient and the role that plasticity to environmental phenology (namely vegetation green-up) plays in these dynamics.

Across the assemblage, we find that bird phenology is generally advancing and that the rate of change often varies across a species' range. We also find that migration and breeding phenology are changing at different rates, which has effectively led to a compression of the interval between these events over time. Work presented here represents a framework for modeling large-scale phenological dynamics across space and time while propagating uncertainty through the analysis. Results have implications for better understanding phenological responses under global change and what this might mean for phenological mismatch dynamics, whereby species are temporally out of sync with favorable environmental conditions.

Keywords: Citizen science, Hierarchical modelling

Fay Frost (University of Sheffield) with P.G.Blackwell, Mu Niu, and Anna Skarin.

Modelling the Collective Movement of Reindeer

06/23/2020 10:30:00 PM-10:45:00 PM

Session: Animal movement *(Chair: Henry Scharf)*

Location: #corymbia

With the continuing evolution of GPS tracking systems, animal movement models are growing in accuracy and more interesting ecological questions can be answered. High resolution data can now be accessed remotely and we have the ability to mass tag individuals, thus generating large data-sets of simultaneous locations.

Learning about animal interactions with the environment can have significant applications for conservation, food and disease spread. However, many current movement models and statistical techniques are inadequate, especially when considering the collective movement of a species. Most techniques focus on individual-level behaviour without a coherent model of movement across all individuals.

I will present novel methodology for modelling collective animal movement in continuous time with behavioural switching. Each individual in the group can switch between behavioural states representing 1following the group' and `independent movement' which are modelled via an Ornstein-Uhlenbeck or a Brownian motion process respectively. This builds on previous literature, namely Langrock et al (2014) and Niu et al (2016).

I will give an application of these methods to the real location data of reindeer (Rangifer tarandus) obtained from Anna Skarin (University of Uppsala). I will discuss the implementation of covariates such as climatic data which is often a major driver in behavioural switching.

References

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Langrock, R., Hopcraft, J. G. C., Blackwell, P. G., Goodall, V., King, R., Niu, M., Patterson, T. A., Pedersen, M. W., Skarin, A., and Schick, R. S. (2014). Modelling group dynamic animal movement. Methods in Ecology and Evolution, 5(2):190-199.

Keywords: Movement modelling, Theoretical ecology

Joshua Hewitt (Duke University) with Robert S. Schick and Alan E. Gelfand

Discrete models for discreet whales: Modeling deep whale dives with coarse data

06/23/2020 10:45:00 PM-11:00:00 PM

Session: Animal movement *(Chair: Henry Scharf)*

Location: #corymbia

Beaked whales are cryptic animals that spend little time at the ocean's surface and dive to extreme depths over 1,000m for long periods of time to forage. Naval sonar can disturb beaked whales and cause lost foraging opportunities. Scientists study deep dives with telemetry devices to better understand the potential physiological impacts that sonar and other disturbances may cause (e.g., on descent rates, depths, and durations). In particular, satellite-linked telemetry devices monitor diving behaviors over several weeks, but such data have coarse resolution: tags record depths in one of 16 bins (e.g., 0-100m) every five minutes. Satellite tag data for dives are naturally described through continuous-time discrete-space (CTDS) models for animal movement (Hanks et al., 2015). However, computational techniques for estimating CTDS models rely on an approximate data augmentation step that cannot be used in our application. Continuous-space models for animal movement use a similar approximation, which introduces bias when an animal's position is uncertain and sparsely observed (Scharf et al., 2017). Instead, we use distribution theory for continuous time Markov chains to enable approximation-free estimation of a CTDS model for deep dives. We also model structural breaks in dive characteristics across dive phases (e.g., descending, foraging, ascending) with a latent semi-Markov model, and use out-of-sample techniques to demonstrate model fit. Lastly, we discuss model extensions, including potential avenues for constructing approximation-free CTDS models for terrestrial movement.

Keywords: Movement modelling

ThÃ©o Michelot (University of St Andrews) with Richard Glennie, Len Thomas and Catriona Harris

Spline-based diffusion models for accelerometer and other movement data

06/23/2020 11:00:00 PM-11:15:00 PM

Session: Animal movement *(Chair: Henry Scharf)*

Location: #corymbia

Accelerometers collect high-resolution movement data on animals. Statistical time series offer a rigorous framework to link this new type of data to biological inferences about behaviour. We propose a new time series approach, wherein the level of activity of the animal is formulated as a flexible function of temporal covariates using splines. We use this method to analyse accelerometer data of a Cuvier's beaked whale, from a behavioural response study. The animal was equipped with an accelerometer, and exposed to controlled sounds, to observe its response and infer the impact of sonars and other anthropogenic noises on whale behaviour. More generally, I will describe how the drift and diffusion terms of a stochastic differential equation can be specified using splines, to define a flexible model for animal movement data. The drift can capture attraction to a point in space or habitat selection, while the diffusion measures the scale of the variability in the movement. Time-varying drift and diffusion functions allow us to model heterogeneity in the behaviour of animals more flexibly than the widely-used state-switching movement models.

Keywords: Biologging, GPS data, Movement modelling

Kim Whoriskey (Dalhousie University) with Ethan Lawler, Chris Field, W. Don Bowen, Mike O. Hammill, Cornelia den Heyer, and Joanna Mills Flemming

Iteratively fitting switching state-space models to animal tracks via maximum likelihood estimation

06/23/2020 11:15:00 PM-11:30:00 PM

Session: Animal movement *(Chair: Henry Scharf)*

Location: #corymbia *Student*

The hidden Markov model framework is a powerful and popular tool for inferring the underlying features of animal movement. When locations are sampled with error, which is often the case in the marine realm, an additional equation is required in the model hierarchy to account for the differences between the observed locations that are measured by the tag and the unobserved true locations of the animal. State-space models that predict both location and behavioural states are often fitted within a Bayesian framework where an estimate of the posterior likelihood is generated via a sampling algorithm. Alternatively, within a maximum likelihood (ML) framework the optimization can be broken into two steps - one for predicting the discrete behaviours and another for the continuous locations. We expand current research within the ML realm by developing and testing a procedure that iteratively optimizes the parameters related to the movement of the animal, and those related to the measurement error. To enable fast computation of the parameters and the random effects, we employ the Laplace approximation and Automatic Differentiation through the R package TMB for model fitting. We validate this new iterative procedure through simulation and by analyzing tracks with substantial measurement error to compare the foraging ecology of grey seal herds in the Northwest Atlantic Ocean. We find that our method can fit multiple popular movement models, including those based on correlated random walks on the locations as well as those based on step lengths and turning angles.

Keywords: Behavioural ecology, Hierarchical modelling, Individual-based models, Movement modelling

Wanchuang Zhu (University of Sydney) with Yanan Fan

New Approaches for Markov Random Field With Intractable Normalizing Constant on Large Lattices

06/23/2020 11:30:00 PM-11:45:00 PM

Session: Animal movement *(Chair: Henry Scharf)*

Location: #corymbia

Potts model is a classic method which models spatial correlation between individuals. Its application fields cover geo-statistics, image analysis, social network and so on. In this work,Â new methods were proposed to tackle the intractable normalizing constant problem of the Potts model.

The first method takes advantage of conditional independence of the Potts model and recursively decomposes the original Potts model on large regular lattice into many small tractable sublattices. Doing so completely avoids the need to compute the troublesome normalizing constant. The computational complexity is O(N), where N is the number of pixels in the lattice, making it computationally attractive for very large lattices. We show through simulations, that the proposed method performs well, even when compared with methods using exact likelihoods.

To handle with Potts models defined on irregular lattices, a synthetic likelihood approach was developed. The new approach utilizes synthetic likelihood which is product of many similar small and tractable terms. A Monte Carlo method is then adopted to approximate each of the small terms, which then forms a tractable synthetic likelihood. The method is scalable with respect to lattice size and can be used to problems with irregular lattices.

Extensive simulation studies indicate that our method performs at least as well as existing methods, whilst providing significant computational savings. Up to 10 times faster than the current fastestÂ method.

Finally, we include two real data applications for illustration: remote sensing satellite image analysis and texture analysis.

Keywords: Potts model, Spatio-temporal statistics

Brett T. McClintock (NOAA-NMFS Alaska Fisheries Science Center, Seattle)

Worth the effort? A practical examination of individual-level random effects in hidden Markov models, with an emphasis on animal movement

06/23/2020 11:45:00 PM-12:00:00 AM

Session: Animal movement *(Chair: Henry Scharf)*

Location: #corymbia

The use of individual-level random effects in hidden Markov models (HMMs) of animal movement behaviour has been promoted in recent years. These "mixed HMMs" can include continuous- or discrete-valued random effects, but mixed HMMs with continuous random effects have rarely been used in practice because model fitting typically requires computationally-intensive numerical integration techniques, such as quadrature or Monte Carlo methods. Discrete random effects can be appropriate for explaining individual heterogeneity attributable to latent categorical factors, but are also advocated as a practical alternative to continuous random effects. However, to our knowledge, the performance of mixed HMMs has not yet been sufficiently explored to justify their widespread adoption in movement models for telemetry data. Compared to mixed HMMs for other types of individual- or site-level time series data (e.g. capture-recapture or species occurrence), an important distinction for animal telemetry data is that they often consist of long time series from relatively few individuals. Under sampling scenarios more typical of animal telemetry studies, we performed an extensive simulation study comparing a suite of fixed- and random-effect models for individual-level state transition probabilities in a 2-state HMM. We generally found: 1) mixed HMMs did not improve behavioural state assignments under any scenario; 2) reliable estimation of continuous random effect parameters required a larger number of individuals than is typically feasible in telemetry studies; 3) in terms of state transition probability estimation, continuous random effect models were fairly robust to data generated from a discrete random effect model, but not vice versa; and 4) models with fixed individual-level effects performed well in all cases, albeit with somewhat less precision than the random effects models. We discuss the implications of our findings in the context of a previous application of mixed HMMs to long-finned pilot whale telemetry data.

Keywords: Behavioural ecology, Biologging, Dynamic state models, GPS data, Hierarchical modelling, Individual-based models, Movement modelling

Robert L. Emmet (University of Washington) with Ben Augustine, Briana Abrahms, Lindsey N. Rich, J.W. McNutt, Alan M. Wilson, Brett T. McClintock, and Beth Gardner

A spatial capture-recapture model for group-living species

06/23/2020 10:30:00 PM-10:45:00 PM

Session: Spatial capture-recapture and genetics *(Chair: Beth Gardner)*

Location: #darwinia *Student*

Spatial capture-recapture (SCR) models have been applied to many species, including those considered group-living species. Standard SCR models applied to group-living species assume that group members move independently, though this is not often the case. Recently, SCR models that include a group component have been proposed, allowing researchers to estimate density and home range sizes of individuals and groups. However, these models do not include group movement dynamics. Group dynamics are an important part of the detection process, as individuals within groups likely have correlated movements, which may bias density estimates in group-living species. We developed a new SCR model for group-living species with an unknown number of groups. The model estimates the number of individuals and groups using data augmentation, assigning individuals to groups based on proximity to group activity centers. The model allows for the estimation of the density and home range sizes of both individuals and groups. We examined the performance of this model through a simulation study and applied the model to an empirical case study of African wild dogs in the Okavango Delta of Botswana. In this well-studied population, there is a known number of groups and group sizes. Standard SCR models were previously applied to this dataset and shown to perform well for estimating abundance. However, in our simulation study, we found that group movement dynamics can bias density estimates from standard SCR models. Thus, the new group SCR model promises to advance understanding of group movement dynamics and better estimate density of group-living species.

Keywords: Abundance/richness/diversity estimation, Hierarchical modelling, Spatial capture-recapture

Alissa J. Brown (Morton Arboretum) with Adam Smith, John Robinson, Allan Strand, Sean Hoban, and Andria Dawson

Estimating North American tree migration patterns after the last glacial maximum using Bayesian hierarchical modeling

06/23/2020 10:45:00 PM-11:00:00 PM

Session: Spatial capture-recapture and genetics *(Chair: Beth Gardner)*

Location: #darwinia *Student*

After the last glacial maximum (c. 21k years ago), rapid global warming led to retreating ice sheets, opening new areas for colonization and forcing species to migrate or adapt to new climates. Sedimentary deposits contain a timeline of tree taxa occurrences at a particular location from tens of thousands of years ago to present. Burgeoning online repositories of fossil pollen data allow us to compile sites to look at tree occurrences over large geographic areas and time scales. Pollen vegetation models (PVMs) attempt to construct a relationship between relative pollen abundance and local vegetation composition. Some practitioners do not model pollen abundance, working with raw or smoothed values, and traditional PVMs use simple linear or additive modeling approaches. But to accurately model tree relative abundance using pollen counts, we need to account for spatial and temporal autocorrelation and formally quantify uncertainty. For example: ages of sedimentary deposits contain error; pollen is often only identifiable to the genus level, leaving species-level variation unknown; and long-distance pollen dispersal can lead to false occurrences. We use a Bayesian hierarchical modeling framework to construct a PVM that explicitly incorporates different sources of uncertainty. Our model estimates responses of North American trees to shifts in climate over the past 21,000 years. We show that tree ranges shifted contemporaneously with climate changes and that these shifts occurred individualistically for different genera. Understanding these patterns can help us predict tree response to modern climate change, allowing us to improve conservation strategies.

Keywords: Hierarchical modelling, Paleoecology, Spatio-temporal statistics

Matthew W. Rees (University of Melbourne) with Jack Pascoe, Mark Le Pla, Brendan Wintle, Alan Robley and Bronwyn Hradsky

Using spatial mark-resight and generalized additive models to infer predator interactions

06/23/2020 11:00:00 PM-11:15:00 PM

Session: Spatial capture-recapture and genetics *(Chair: Beth Gardner)*

Location: #darwinia *Student*

Inferring species interactions from monitoring data is difficult, particularly for cryptic and low-density predators. This partly explains why evidence for the mesopredator release theory - that smaller-bodied mesopredators are *released* from top-down control following apex predator suppression - is mixed. Mesopredators may avoid apex predators in space and/or time, and this might impact their population density, but we lack integrated methods to measure this effect. My research is working towards this by aiming to combine spatial patterns of activity/density with daily temporal activity patterns.

Research partners and I have been experimentally surveying the response of feral cats Felis catus to the lethal control of red foxes Vuples vuples, mainly through camera-trapping. After identifying individual cats through unique natural coat markings, I am using spatial mark-resight models to investigate how their density changes at both fine and broad-scales due to fox activity. Additionally, using longer-term datasets which lack individual identification, I have been building spatio-temporal generalised additive models of fox and prey activity, which, along with other environmental covariates, can be used to test drivers of cat activity. This hierarchical model structure makes it easier to distinguish how cats are avoiding foxes or whether they are simply more interested in tracking prey species. This will be key to resolving contention around the control of invasive predators in Australia. This method is highly transferrable to other potentially interacting species and camera-trap datasets - being particularly beneficial when spatial and temporal autocorrelation is present.

Keywords: Camera trap data, Population dynamics, Population ecology, Spatial capture-recapture

Pedro G. Nicolau (UiT The Arctic University of Norway) with Sigrunn H. SÅ™rbye and Nigel G. Yoccoz

Incorporating sampling error in the estimation of autoregressive coefficients of animal population cycles using capture-recapture data

06/23/2020 11:15:00 PM-11:30:00 PM

Session: Spatial capture-recapture and genetics *(Chair: Beth Gardner)*

Location: #darwinia *Student*

The estimation of density-dependence in population dynamics models requires addressing sampling uncertainty. State-space model approaches (SSMs) appear as a way to integrate sampling error and population process modelling, but rarely include an explicit link between the sampling procedures and the true population size. This happens because many of the models proposed to estimate population size, in the presence of heterogeneity, lead to incomplete likelihood functions which cannot be straightforwardly included in SSMs. Such is often the case with capture-recapture data. We assess the performance of an intermediate approach between ignoring uncertainty in population size estimates, and fully specified state-space models, in second-order autoregressive (AR(2)) population cycles. First, we estimate individual capture probabilities, using a conditional Multinomial likelihood, followed by a Horvitz-Thompson estimate for population size. Then, we estimate autoregressive parameters for the log population size. Inference is performed using the integrated nested Laplace approximation (INLA) methodology. We perform an extensive simulation study to compare our approach with density-dependence estimates which disregard sampling error. The methods are then applied in a real dataset of gray-sided voles Myodes rufocanus from Northern Norway, to understand the spatial population variation with climatic conditions. We find that density-dependence estimation is indeed important when explicitly modelling uncertainty, although this is parameter-dependent. Particularly, in AR settings with low variance, it is especially beneficial to incorporate uncertainty information. Furthermore, by considering a realistic sampling model, the bias appears to be reduced when compared to more simplistic models, such as the Poisson or log-Normal distributions, commonly assumed in SSMs.

Keywords: Capture-mark-recapture, Integrated population models, Population dynamics, Population ecology, State-space models

Ben C. Augustine (Cornell University) with J. Andrew Royle, Dan W. Linden, and Angela K. Fuller

Estimating Animal Density Using Genetic Markers Observed with Error

06/23/2020 11:30:00 PM-11:45:00 PM

Session: Spatial capture-recapture and genetics *(Chair: Beth Gardner)*

Location: #darwinia

Standard methods for estimating wildlife population parameters such as abundance and survival from noninvasive genetic samples are inefficient because lower quality samples cannot be used, and these methods do not allow for errors in individual identification, which cannot be completely eliminated. We address these problems by introducing the Genotype Spatial Partial Identity Model (SPIM) that propagates the uncertainty in inferring individual identity from genetic samples observed with error to the population parameters of interest and allows all samples to be used, thereby increasing precision and removing bias. This model replaces the subjective decision-making process of the geneticist, subject to strict constraints on the number of errors allowed and informed only by the information contained in the genotyping replicates, with a spatially-explicit statistical classification model that leverages information from the ecological, capture, and genotype observation processes to probabilistically assign individual identities. We apply this model to data from a study of fishers where 48% of the samples were originally discarded due to their low certainty in individual identity. The Genotype SPIM density estimate using all collected samples was 25% more precise than the original density estimate and the model identified and corrected 2 errors in the original individual identity assignments. Further, a simulation study demonstrates that the Genotype SPIM model parameters are identifiable with only one PCR per sample and that accuracy and precision are relatively insensitive to the number of PCRs for high quality samples, suggesting genotyping protocols could be more efficient by devoting more resources to low quality samples.

Keywords: Abundance/richness/diversity estimation, Capture-mark-recapture, Hierarchical modelling, Population dynamics, Population ecology, Spatial capture-recapture

Elizabeth Thompson (University of Washington)

Detecting selection through realized relatedness in natural populations

06/23/2020 11:45:00 PM-12:00:00 AM

Session: Spatial capture-recapture and genetics *(Chair: Beth Gardner)*

Location: #darwinia

Genetic marker data have long been used to detect close relatives or validate putative relationships in natural populations, thus providing measures of population structure, migration, and variance in reproductive success. Modern genetic data provide much greater power to understand the causes of genetic variation among individuals and across genomes. However, many methods estimate only a genome-wide average, and only estimate pairwise relatedness. In fact, SNP data provide information to estimate the precise location-specific segments of genome shared by individuals, and thus to assess realized descent in specific genome regions. Additionally, joint inference among individuals is necessary for accurate inference of shared genome segments. We present a method to infer location-specific shared realized descent jointly in a small set of relatives. The constraints imposed by joint relationship in close relatives such as a set of litter-mates or a parent-offspring trio provide sufficient power to detect genome regions where the realized sharing deviates significantly from the expectation given the known or clearly inferred pedigree relationships. Such regions may indicate selection. Using the example of data on the Soay Sheep population of St Kilda, we show how estimation of segments of genome shared between parents inferred jointly with regions of autozygosity in surviving offspring may be used to detect regions of the genome potentially involved in inbreeding depression.

Keywords: Population ecology, Population genetics

Mark V. Bravington (CSIRO)

Kinship, death, and life on the cutting edge

06/24/2020 8:00:00 AM-8:50:00 AM

Location: #acacia *Plenary (Chair: Rachel Fewster)*

Close-Kin Mark-Recapture takes advantage of modern genotyping techniques to identify pairs of close relatives from tissue samples. These kinships can be embedded into a mark-recapture population-dynamics framework for estimating demographic parameters such as survival and absolute abundance. CKMR has attracted attention first through CSIRO's successful application to a high-profile commercial fish--- Southern Bluefin Tuna--- and now to numerous other species. While we have used CKMR successfully for "pure conservation" settings with live biopsies, its greatest potential is for large-scale "renewable-resource management" where animals are being killed anyway: fisheries, by-catch, hunting. CKMR can be cheap and reliable in such cases for three reasons: first, it can be done just with samples from dead animals; second, the bigger the population, the smaller the proportion of dead ones that need sampling; third, the data are largely immune to human actions.

CKMR is certainly powerful, but also challenging to get right. Aside from logistics, there are many statistical steps in going from tissue samples to abundance-etc-estimates, requiring expertise in distinct domains. After introducing the basics, I will explain our whole-of-problem approach to CKMR--- "engineering with statistics"--- and in particular why we decided for and against certain modelling approaches. Then I will somehow segue into a more general discussion of statistics in renewable-resource work, also highlighting which statistical techniques I personally have, and haven't, found most useful over three decades. Finally, I'll return to CKMR, its challenges, and the great opportunities that it presents for conservation and sustainable management.

Natalie J. Briscoe (University of Melbourne) with Jane Elith, Gurutzeta Guillera-Arroita and Roberto Salguero-GÃ³mez

How well do process-explicit models predict species range dynamics?

06/24/2020 9:30:00 AM-9:45:00 AM

Session: Competition and demography *(Chair: Margie Mayfield)*

Location: #acacia

Species distribution models are widely used to forecast species responses to climate change and inform conservation decisions. Models are typically based on correlations between species occurrence data and environmental predictors, with underlying mechanisms captured only implicitly. However, there is a growing interest in approaches that explicitly model processes such as physiology, dispersal, demography, and biotic interactions that underpin species range shifts. A wide array of these process-explicit modelling approaches are now available, but it is not clear which methods are best for which types of problems or scenarios. In addition, data to parameterise and build these models are often limited, which could reduce their ability to accurately forecast range dynamics. To evaluate the promise of these emerging methods, we developed novel integrated models that link eco-physiological models with individual-based models, which can simulate responses of real species to climate change and landscape dynamics. We coupled these models with a sampling module that recorded data required to fit different methods (e.g. vital rates, dispersal distances, population abundances) under different sampling regimes. Using these simulated datasets, we then tested the ability of different process-explicit distribution models such as occupancy dynamics models, coupled SDM-population models and demographic distribution models to capture and predict range dynamics. Using this simulation approach, we gain insight into what drives performance of different process-explicit methods, mechanisms that they do and do not capture and how to best allocate efforts to improve the reliability of range dynamics predictions under climate change.

Keywords: Mechanistic models, Population dynamics, Species distribution modelling

Andrew O'Reilly-Nugent (University of Canberra) with Elizabeth M. Wandrag and Richard P. Duncan

Inferring the competition from community data: reconciling field and experimental results

06/24/2020 9:45:00 AM-10:00:00 AM

Session: Competition and demography *(Chair: Margie Mayfield)*

Location: #acacia *Student*

Community data is often complicated by a large number of species absences. Joint species distribution models (JSDMs) that model zero-inflated abundance data need to carefully account for the cause of species absences when separating absences that occur from competitive or environmental exclusion.

We fitted a JSDM to data from an Australian temperate grassland to identify non-native grasses that had significant competitive impacts on local communities and validated our inferences in a glasshouse experiment. We grew three non-native grasses that had varying competitive effects in the field (Avena fatua, Bromus diandus and Eragrostis curvula) to with a representative grass community (Bromus hordaceuous, Poa labillardieri, Rytidosperma caespitosum) using a response surface study design replicated at three levels of nutrient addition. We fitted yield density curves at each fertility level to estimate the effects of intra- and interspecific competition, then compared our results with the residual covariation between species abundances estimated in the JSDM.

Our JSDM underestimated the effects of interspecific competition by incorrectly predicting that some species would be absent from high fertility sites due to environmental unsuitability rather than competitive exclusion. We show through simulation that JSDMs will be less prone to this problem when patterns of observed abundance are sufficiently noisy to decouple species abundance from environmental factors. Our results show that JSDMs have the potential to identify competitive interactions in field data but, like other phenomenological models, they need to be validated against ecological knowledge and experimental tests.

Keywords: Abundance/richness/diversity estimation, Community ecology, Hierarchical modelling, Model assessment/validation, Multivariate analysis/joint species distribution models

Nick Golding (University of Melbourne)

Fitting demographic models to species distribution data

06/24/2020 10:00:00 AM-10:15:00 AM

Session: Competition and demography *(Chair: Margie Mayfield)*

Location: #acacia

Correlative species distribution models are good at describing species' current distributions, and inferring their environmental drivers. However they are pretty bad predicting what will happen if we change something, like fragmenting habitat, introducing other species, or implementing a control or conservation action. Replacing the statistically convenient (but ecologically meaningless) internal structure of these models with demographic models should enable us to make much better predictions of how distributions will change.

I will present recent work developing demographic species distribution models that extend matrix population models to explicitly consider how vital rates vary through space (like spatial integral projection models) but are fitted to commonly available species distribution data (like dynamic range models). Combining these approaches enables us to fit ecologically-realistic species distribution models without the need for detailed demographic data. We can include density dependence, dispersal, biotic interactions and prior knowledge of species' population dynamics and ecology.

Asking for more information from the same data means we have to deal with a number of potential issues, including poorly-identified parameters and more computationally intensive statistical inference. I'll argue that non-identifiability is actually a good thing (in this context) and show how the computational issues can be resolved using the Bayesian inference package greta, and some new extensions for modelling dynamical systems.

Keywords: Abundance/richness/diversity estimation, Population dynamics, Software development, Species distribution modelling

Catherine Helen Bowler (University of Queensland) with Lauren G. Shoemaker, Christopher Weis-Lehman and Margaret M. Mayfield

Improving coexistence modelling with demographic stochasticity and facilitation

06/24/2020 10:15:00 AM-10:30:00 AM

Session: Competition and demography *(Chair: Margie Mayfield)*

Location: #acacia *Student*

Statistical modelling techniques aid ecologists in predicting the long-term coexistence of species. Coexistence models rely on calculating competition coefficients; parameters which are based on measurements of the competitive effect of one species on another. However, these parameters are typically a stylized version of nature in that no variation such as that from demographic stochasticity is incorporated. Demographic stochasticity arises from the probabilistic nature of demographic events and has typically been dismissed as noise disguising an underlying deterministic skeleton and has been ignored in coexistence modelling to date. We propose that predictions of species coexistence could be dramatically improved by utilising the inherent variability in nature from demographic stochasticity. We provide a hierarchical Bayesian framework to incorporate demographic stochasticity from field-based assessments of plant-plant interactions into species interaction models. These models are used to estimate the interaction coefficients that parameterize our coexistence models, where we use the invasibility criterion to predict species coexistence. To add further biological realism, we allow for facilitation in these species interaction models and then utilise a lottery model framework to realistically restrict simulated population growth based on competition for space in the community. The inclusion of demographic stochasticity and facilitation revealed flexibility within species' responses to neighbours, and carrying this through to calculating coexistence provided us with a probability of coexistence, which is more informative than the classic approach. These distributions provide a quantification of the flexibility in species interaction outcomes and help capture the inherent unpredictability of dynamics in diverse communities.

Keywords: Community ecology, Hierarchical modelling, Theoretical ecology

Marie-Josee Fortin (University of Toronto)

Ecological Networks in Dynamics Landscapes

06/24/2020 10:30:00 AM-10:45:00 AM

Session: Competition and demography *(Chair: Margie Mayfield)*

Location: #acacia

Species are a suite of simultaneous direct and indirect threats from climate change and land-use change that homogenize ecosystems. Such global change results in the uncoupling of trophic links due to phenological change and species range shifts resulting in species non-analog interactions. Hence, the fabric of species persistence and the ecosystem services that they provide is precarious to say the least. Yet, the vulnerability of ecological networks will vary depending on the magnitude of the mismatches between changes in habitat (e.g. amount, quality, configuration) and species biotic responses to those changes (e.g. species' abilities to acquire resources, the stability of species interactions, and the pace of thermal niche tracking). To mitigate these rapid changes, several conservation strategies have been proposed such as the establishment of protected areas and connectivity among them. Unfortunately, there is a conundrum about the positive (rescue effect through dispersal and gene flow) and negative (increased risk of species invasion, predation, and disturbance spread) effects of connectivity and how to implement such connectivity to optimize species persistence. Here, I will show that ecological networks can be organized into a unifying typology to disentangle their complexity. A series of network analytical methods and case studies will be presented to depict how the spatio-temporal dynamic of landscapes that affect ecological network topology and the rewiring of species interactions in response to global change.

Keywords: Community ecology, Network ecology

Shinichi Nakagawa (UNSW Sydney)

Credibility Revolution in Ecology and Evolution

06/24/2020 11:00:00 PM-11:30:00 PM

Session: Reproducible Science in Ecology and Evolution *(Chair: Peter Vesk)*

Location: #acacia

Psychologists dominate the movements against the replicability crisis, followed by medical scientists. However, there is a less well-known credibility revolution in the fields of ecology and evolution. This is a story of the credibility revolution from the fields closer to the home where many researchers study different species and systems. So our studies are highly heterogeneous and replication seems impossible. Consequently, our story does differ in several ways from ones in the social and medical sciences. For example, we are among the first field to mandate data archiving. And what else is different? Or what’s similar? Pherpahs, more interesting to this audience. What does it mean by "replicating" statistically? It is more difficult than we initially think, as we want to replicate the real effect not necessarily the original estimate of that effect. I hope to facilitate some discussion on how we can make our ecological research more open, robust and reproducible.

Hannah Fraser (University of Melbourne) with Ashley Barnett, Timothy H. Parker, Shinichi Nakagawa, Fiona Fidler

Questionable Research Practices in Ecology and Evolution

06/24/2020 11:30:00 PM-12:00:00 AM

Session: Reproducible Science in Ecology and Evolution *(Chair: Peter Vesk)*

Location: #acacia

Psychology, economics and some areas of medicine are in crisis due to the low reproducibility of their research findings. In psychology, researchers find contradictory results around half of the time when they redo studies. In ecology, it is more difficult and expensive to redo studies and we expect far more variation in results due to environmental stochasticity, so we are unsure of how reproducible results are. However, in other fields low reproducibility has been attributed to a number questionable research of practices that increase the chances of finding a significant result where no relationship exists. By comparing the prevalence of Questionable Research Practices in ecology and psychology, it is possible to judge whether low reproducibility is something we should be concerned about.

Responses from 652 ecologists and evolutionary biologists suggest that ecologists use Questionable Research Practices just as often as psychologists. For example, 64% of our participants choose not to present all the variables they evaluated if they weren’t significant as compared with 63% of psychologists.

With such similar rates of Questionable Research Practices it seems highly likely that ecology has just as big a problem with reproducibility and psychology. What would it mean if half (or fewer) of the results in our literature were false positives?

Jonathan F. Jupke (University Koblenz-Landau) with Ralf B. SchÃ¤fer

Should ecologists prefer model- over distance-based multivariate methods?

06/24/2020 9:30:00 AM-9:45:00 AM

Session: New Methods and Applications for Community Level Modeling *(Chair: Francis Hui)*

Location: #banksia *Student*

A typical data set in ecology contains the abundance of multiple species at multiple sites. Multivariate statistical methods are optimal to analyze such data and are commonplace in ecological studies. Typically, a distance matrix of the site - species table is analyzed instead of the raw abundances. This contrasts with univariate analyses, where typically raw data is fit assuming data models with specific distributions. However, through advances in statistical theory and computational power, methods relying on data models for multivariate data have gained traction. Systematic simulation-based evaluations and comparisons of these methods are important to guide practitioners, but are scant. Here, we compare two model-based methods, multivariate generalized linear models (MvGLMs) and constrained quadratic ordination (CQO), with two distance-based methods, distance-based redundancy analysis (dbRDA) and canonical correspondence analysis (CCA). We compared the methods’ ability to differentiated between casual and noise variables in 190 simulated data sets varying in distribution and sample size.

In data sets where all species share the same maximal abundance, MvGLM and dbRDA differentiated accurately between causal and noise variables. The former had the lowest false-positive rate, whereas the latter had the lowest false-negative rate. CQO and CCA had the highest false-negative rate and false-positive rate, respectively, where these error rates were high for data sets with linear responses. In data sets with varying maximal abundances, dbRDA had the highest false-positive rate. Our results show that model- and distance-based methods have their place in the ecologist's statistical toolbox. However, across all data sets MvGLM exhibited the highest performance.

Keywords: Multivariate analysis/joint species distribution models

Martin Ingram (University of Melbourne) with Damjan Vukcevic and Nick Golding

Variational Multi-output Gaussian Process Models for Species Distribution Modelling

06/24/2020 9:45:00 AM-10:00:00 AM

Session: New Methods and Applications for Community Level Modeling *(Chair: Francis Hui)*

Location: #banksia *Student*

Gaussian Processes (GPs) provide a way of defining prior distributions over functions, making them a popular approach to non-linear regression. Multi-output GPs (MOGPs) extend them to vector-valued observations by modelling each dimension of the observations as a linear combination of GPs. Gaussian processes are attractive for the modelling of species distribution for multiple reasons: their preference for smooth functions is plausible from an ecological point of view, they are able to capture complex interactions while avoiding overfitting, and MOGPs model correlations between species, allowing them to borrow strength across species. However, GPs are notoriously hard to scale to large datasets, and fitting to multiple species at once using MOGPs further exacerbates this issue. As a result, MOGPs have usually only been applied to small datasets.

We build on variational inference techniques developed in the machine learning literature to scale MOGPs to large presence / absence datasets containing observations for hundreds of species at thousands of sites. We use six datasets to evaluate the resulting model against GPs fit separately to each species, as well as tree-based and linear models. We find that both independent GPs and MOGPs significantly outperform these models (+2.5% AUC on average across species and datasets), and that the MOGP further improves on single GPs when modelling species with fewer than 50 observations in the training set (+1.6% AUC), giving evidence for its ability to borrow strength. Finally, we explore approaches to extend MOGPs to presence-only data and to incorporate correlations among the residuals of the model.

Keywords: Hierarchical modelling, Machine learning, Multivariate analysis/joint species distribution models, Species distribution modelling

Marti J. Anderson (New Zealand Institute for Advanced Study) with Daniel Walsh, Winston Sweatman and Andrew Punnett

Nonlinear models of species-environment relationships, with modern tools for misbehaving errors

06/24/2020 10:00:00 AM-10:15:00 AM

Session: New Methods and Applications for Community Level Modeling *(Chair: Francis Hui)*

Location: #banksia

Species are being destroyed faster than they are being discovered. Despite growing repositories of global ecological data, current models of species' responses to broad-scale spatio-environmental gradients (such as temperature, latitude, depth, nutrients, moisture, or elevation), are either overly simplistic (Gaussian), or they are a "black box" without meaningful interpretable parameters. Furthermore, real ecological data messy. Raw counts of individuals or biomass from broad-scale field surveys have no upper bound, and typically display large residual variance, over-dispersion and zero-inflation. In this lecture, I will outline a novel class of flexible models that combine new nonlinear mathematical functions for mean species' response curves with an array of modern statistical error distributions tailored to accommodate abundance, biomass or functional traits. Enhancing this even further, we can use flexible copulas to model multi-species associations in either their mean response along a given gradient, or in their (quite disparate types of) error distributions. From coniferous forests on mountain-tops to fishes in the deep blue sea, I will show a variety of key examples to demonstrate how this unique statistical framework can successfully capture and quantify global-scale responses of ecological communities to environmental change. The aim is to provide radical clarity on species' joint responses (through time and space), for important decisions that can change our world.

Keywords: Community ecology, Multivariate analysis/joint species distribution models, Species distribution modelling

Maximilian Pichler (University of Regensburg) with Florian Hartig

Scalable and accurate Joint Species Distribution Modeling using the GPU

06/24/2020 10:15:00 AM-10:30:00 AM

Session: New Methods and Applications for Community Level Modeling *(Chair: Francis Hui)*

Location: #banksia

Joint Species Distribution models (jSDMs) explain spatial variation in community composition by contributions of the environment, biotic interactions, and possibly spatially structured residual variance. They show great promise as a general analysis method for community ecology and macroecology, but current jSDMs scale poorly on large datasets, limiting their usefulness for novel community data, such as datasets generated using metabarcoding and metagenomics.

Here, we present the R package sjSDM, which implements a scalable method to estimates joint Species Distribution Models (jSDMs) based on the multivariate probit model through Monte-Carlo approximation of the joint likelihood. The numerical approximation is based on PyTorch and reticulate and can be calculated on CPUs and GPUs alike. sjSDM is orders of magnitude faster than existing jSDM packages, can be scaled to very large datasets, and can be flexibly regularized. Despite the dramatically improved speed, sjSDM produces the same predictive error and more accurate estimates of species association structures than alternative jSDM implementations.

We will show benchmarks of sjSDM, demonstrate its simple and intuitive programming interface, and highlight other features, such as modeling spatial effects, separating the different contributions of the effects (variation partitioning), and the ability to switch easily between statistical and machine-learning models for the different model components, as well as between CPU and GPU computing.

Keywords: Joint species distribution modelling, Software development

Alain Franc (INRAE - France) with Nathalie Peyrard, Sourakhata Tirera, Benoit de Thoisy, Damien Donato and Anne Lavergne

Statistical methods for ecoviromics of rodent reservoirs of zoonoses in French Guiana

06/24/2020 10:30:00 AM-10:45:00 AM

Session: New Methods and Applications for Community Level Modeling *(Chair: Francis Hui)*

Location: #banksia

The role of wildlife reservoir and environmental drivers on the spread of tropical zoonoses is a key issue, with new perspectives provided by metagenomics. A question is the relative weight of host species and environment variables in shaping viral diversity. We adress it in the case of the virome of several wild rodents in French Guiana, observed along a gradient of anthropisation of the habitat. We combine viral metagenomics and statistical ecology in an â€˜ecoviromics’ approach to study the structure and diversity of the viromes of seven rodent species captured in different environments . We have built a count array by allocating 73,013,622 reads to 137 virus genera and 12 samples. Among the 137 virus genera, two subsets are of particular interest: 32 genera associated to vertebrates/invertebrates and 67 genera associated to bacteria.We have selected several complementary statistical methods for the identification of patterns in the distribution of viruses among the hosts and habitats and in the composition of the samples. We show that some structure patterns appear systematically whatever the method and the subset of genera, comforting their significance and indicating that the host species seems to have more impact than environment on shaping virus diversity. These methods also exhibit different patterns, probably because they do not emphasize the same components of the diversity. With this study, we promote the use of more than one statistical tool in order to avoid method bias and to strenghten ecological conclusions by their convergence.

Keywords: Abundance/richness/diversity estimation, Metagenomics, Multivariate analysis/joint species distribution models, Viral ecology

Bert van der Veen (Norwegian Institute of Bioeconomy Research) with Francis K.C. Hui, Knut A. Hovstad, Erik B. Solbu and Robert B. O'Hara

Quantifying the ecological niche with unequal tolerances

06/24/2020 10:45:00 AM-11:00:00 AM

Session: New Methods and Applications for Community Level Modeling *(Chair: Francis Hui)*

Location: #banksia *Student*

For any species in an ecological community, the conditions it can occur at are represented by the width of the fundamental niche. Niche width is synonymous to environmental tolerance, i.e. a species sensitivity to change in environmental conditions. An early niche model was the species packing model, which assumes that the shape of the fundamental niche is quadratic, and species tolerances are equal. Assuming niche width to be equal across all species is equivalent to assuming all species are generalists or specialists to the same degree, which is biologically unrealistic. This assumption is also made in Correspondence Analysis. Here we relax the equal tolerances assumption and use the Generalized Linear Latent Variable Models (GLLVM) framework to fit quadratic niches with unequal tolerances to common data types in community ecology. GLLVMs can be understood as Joint Species Distribution Models, or alternatively as a model-based ordination method. Our model captures species associations using fewer latent variables than a GLLVM with linear latent variables and lets us visualize species distributions in latent space in the form of an ordination diagram, to be able to show tolerances and how they vary between species.

Keywords: Abundance/richness/diversity estimation, Community ecology, Ecological niche, Model-based ordination, Multivariate analysis/joint species distribution models, Species distribution modelling, Theoretical ecology

Sam Nicol (CSIRO) with Hannah Lloyd, James Brazill-Boast, Emma Gorrod and Iadine Chades

Using adaptive management to demonstrate success in threatened species management

06/24/2020 9:30:00 AM-9:45:00 AM

Session: Contributed talks *(Chair: Erin Peterson)*

Location: #corymbia

The outcomes of intervention actions to manage threatened species are uncertain, making it difficult to predict or attribute success or failure of actions designed to protect species. Despite this uncertainty, species continue to decline and funding for threatened species is decreasing globally, creating an urgent need to rigorously determine which actions best protect species. Although the effectiveness of an action could be determined by repeated applications over long periods of time, this approach incurs an opportunity cost if the wrong action is taken. Instead, a dynamic approach is needed that learns the best approach from regular experimentation and feedback. Adaptive management, or `learning by doing' is a dynamic optimisation approach that can determine the optimal management action based on current knowledge while simultaneously maximising learning to improve future management. Although the theory of adaptive management is well-developed, the complexity of the approach means that it has had limited uptake by practitioners.

In collaboration with New South Wales (NSW) government's flagship threatened species program, we developed a general adaptive management approach that can be used to demonstrate management success over time. We applied two key design principles to overcome the implementation challenges faced by previous adaptive management studies: simplicity (minimal number of states) and generality (a model structure that is applicable to any species-threat combination). We demonstrate our approach using a case study of fox impacts on two threatened marsupial species in NSW. Our approach provides a general method to demonstrate success in threatened species management while maximising learning.

Keywords: Adaptive management, Decision science, Dynamic state models, Markov decision processes, Measuring effectiveness, Model assessment/validation, Occupancy analysis, POMDP, State-transition models

P. Solano Solano.P (Universidade Federal do Rio de Janeiro)

Hierarchy for Time-Dependent Quantile regression model to predict coral cover

06/24/2020 9:45:00 AM-10:00:00 AM

Session: Contributed talks *(Chair: Erin Peterson)*

Location: #corymbia *Student*

Some data are not adequately modeled by its mean trajectory, as the longitudinal measurement's distribution might be skewed or heavily tailed. Quantile regression (QR) is used as a way to reduce vulnerability to these issues, while maintaining the dynamic structure. This particular approach shows one advantage of this procedure by developing the prediction of coral cover, which can be achieved due to the natural forecasting feature of dynamic models. An additional advantage of the model is presented by exploring two different loss functions. We exemplify the model using two marine ecology data sets.

Keywords: Abundance/richness/diversity estimation, Asymmetry, Behavioural ecology, Community ecology, Dynamic state models, Environment variables, Hierarchical modelling, Interdisciplinary ecology, Loss function, Model assessment/validation

Kadambari Devarajan (University of Massachusetts Amherst) with Prabhu Ramachandran

View eXtract aNnotate (ViXeN) Multimedia Projects

06/24/2020 10:00:00 AM-10:15:00 AM

Session: Contributed talks *(Chair: Erin Peterson)*

Location: #corymbia *Student*

Ecological monitoring is increasingly dependent on multimedia data such as photos/videos from camera traps and audio files from amphibian/bird call recorders. This has resulted in a need for computational tools that aid in the access and processing of such multimedia data, especially in order to manage projects that have more than one type of media. ViXeN (https://vixen.readthedocs.io), an acronym for View eXtract aNnotate media data, is a general-purpose, free and open-source media metadata management tool that is easy to install and use. ViXeN facilitates managing the metadata associated with media files such as images and videos from trail cameras. This media manager can currently support media such as images, videos, audio files, text, and portable document format (PDF) files. It was originally designed to handle several thousand trail camera videos for an ecological study on mammalian carnivores and can accommodate large datasets of the order of a million files. Subsequently, ViXeN has been used to conduct literature reviews and for projects involving images, and can be applied to projects involving different kinds of media files and data types. The package is portable and intuitive to use since it has a web browser-based user interface (UI) to view the media in different file formats and simultaneously edit the user-defined custom metadata tags. Researchers can create and assign a number of arbitrary metadata tags with the media. These tags can then be exported as a comma separated value (CSV) file using ViXeN for further processing and analysis.

Keywords: Biologging, Camera trap data, Data science, Interdisciplinary ecology, Software development, Wildlife monitoring

Jock C. Currie (South African National Biodiversity Institute/Nelson Mandela University) with James T. Thorson, Kerry J. Sink, Lara J. Atkinson, Tracey P. Fairweather and Henning Winker

A novel approach to assess distribution trends from fisheries survey data

06/24/2020 10:15:00 AM-10:30:00 AM

Session: Contributed talks *(Chair: Erin Peterson)*

Location: #corymbia

Understanding and predicting changes in marine population distributions is important for the management of fishery resources and biodiversity. Identifying such trends is challenging, however, given the variability inherent in biological field data. To assess distribution trends from fisheries trawl survey data, we applied a novel two-step approach: First, species-specific locations (latitude and longitude centre of gravity) and extent (effective area occupied) were estimated within a spatio-temporal delta modelling framework. The resulting time series and associated variance estimates were then passed to a multivariate Bayesian state-space model to estimate average trends over the study period. In this way, the uncertainty in mean location (or extent) is appropriately propagated to the trend estimate, which also takes into account interannual variability. We applied this approach to three decades (1986-2016) of trawl research survey data from South Africa's Agulhas Bank to quantify distributional changes in 44 common demersal fishes. Average trends across the assemblage showed a westward (alongshore) shift in location and a reduction in the extent of populations. At the species level, six taxa showed a location trend towards the west or south-west and three shifted towards the east or north-east, while two taxa reduced their spatial extent and one species expanded it. The mean westward and contracting trends of the assemblage were interpreted as likely signals of climate forcing, whereas the eastward shift of three species may be linked to fishing impacts. We recommend additional research regarding causal drivers of distribution shifts, specifically to attribute observed changes to climate and fishing.

Keywords: Species distribution modelling

Amelia S C Hood (University of Cambridge) with Phil A Martin and Gorm E Shackelford

A new method for ecological evidence-synthesis: dynamic meta-analysis on metadataset.com

06/24/2020 10:30:00 AM-10:45:00 AM

Session: Contributed talks *(Chair: Erin Peterson)*

Location: #corymbia *Student*

This talk introduces a new method for ecological evidence-synthesis: dynamic meta-analysis. Traditional meta-analyses answer a particular question, such as “what is the effect of intercropping on biodiversity”. The effect of such farming practices depends on many things (e.g. intercrop species, crop age or soil type) because ecological systems are highly complex and unique. Traditional meta-analysis methods do not allow users to filter the evidence based on their specific circumstances and, because of this, land managers are forced to make decisions based on evidence that may not be relevant to them. This is a major issue if we are to make informed decisions about how to manage our existing landscapes.

We are building a *dynamic meta-analysis* on a web application (www.metadataset.com) that allows users to filter evidence that is relevant to their needs. Users first decide which farming practice (e.g. intercropping) or outcome (e.g. biodiversity) they would like to know about. The web app then calculates the effect of this practice (e.g. it may show that there are 150 studies on the effect of intercropping on biodiversity, and that there is a weighted average increase of ~10% in biodiversity following intercropping). Then users can set filters (e.g. soil type), and the web app will automatically recalculate the results. In this talk, I will take you through an example.

Our ecosystems all unique and highly valuable. We need to be making properly informed and tailored decisions about how to manage them sustainably, and this new tool provides a means to do that.

Keywords: Evidence synthesis, Meta-analysis

Andrew E Seaton (University of St Andrews) with David Borchers, Ben Stevenson, Janine Illian and Richard Glennie

A new point pattern model for spatial capture-recapture

06/24/2020 10:45:00 AM-11:00:00 AM

Session: Contributed talks *(Chair: Erin Peterson)*

Location: #corymbia *Student*

Spatial capture-recapture methods aim to estimate the abundance and spatial distribution of populations of wild animals. At their heart, they contain a point process model for the distribution of individual animals' activity centres. Typical applications use either homogeneous Poisson processes or inhomogeneous Poisson processes with spatial covariates to model spatially varying intensity. Here we present a method that uses a log-Gaussian Cox process instead. This generalisation of the inhomogeneous Poisson process includes a spatially-structured Gaussian random field with MatÃ©rn covariance, implemented using a computationally efficient stochastic partial differential equation approach. The random field models heterogeneity that is unaccounted for by available spatial covariates. We describe how the model can be implemented in TMB and show results from a simulation study and an analysis of real data.

Keywords: Abundance/richness/diversity estimation, Camera trap data, Capture-mark-recapture, Hierarchical modelling, Spatial capture-recapture, Species distribution modelling

Maud Queroue (CNRS) with Christophe Barbraud, FrÃ©dÃ©ric Barraquand, Daniel Turek, Nathan Pacoureau, Karine Delord and Olivier Gimenez

Multispecies integrated population models reveal the relative contribution of interspecific relationships and climate fluctuations on seabirds demography.

06/24/2020 9:30:00 AM-9:45:00 AM

Session: Population modelling *(Chair: Len Thomas)*

Location: #darwinia *Student*

Assessing the effect of climate and interspecific relationships on populations of different species is challenging because of the complex dynamic of species in interaction and the need to integrate information over several biological levels (individuals - populations - communities). There is therefore a need to combine all available sources of data to understanding the extent to which interactions between species can mitigate or exacerbate the effects of climate fluctuations.

For single-population studies, Integrated Population Models (IPMs) combine population counts and capture-recapture data to inferring on demographic parameters. IPMs have recently been extended to the community level with the development of multispecies IPMs to fit multispecies nonlinear matrix models to multiple data sources. However, the approach has never been applied to real data and parameters have so far been considered as being independent of environmental conditions.

Here, we extend multispecies IPMs by accommodating the effects of climate conditions on demographic parameters. Our new model allows quantifying the relative contribution of climate vs. species interactions on demographic parameters such as survival and breeding success. We apply our new approach on a stage-structured predator-prey system combining 22 years of capture-recapture data and population counts on two seabirds, namely the Subantarctic skua (Catharacta skua lÃ¶nnbergi) and its main prey the Blue petrel (Halobaena caerulea) both breeding on the Kerguelen Islands in the Indian Ocean.

We implemented our model in a Bayesian framework using the Nimble R package which allowed us to greatly maximize efficiency (speed and quality of convergence) when compared to Jags.

Keywords: Capture-mark-recapture, Integrated population models, Population dynamics, Predator-prey modelling

Marianna Chimienti (Aarhus University) with Floris M. van Beest, Larissa Teresa Beumer, Jean-Pierre Desforges, Lars H. Hansen, Mikkel Stelvig, and Niels Martin Schmidt

Quantifying ungulates' behavior and life history events from year-long continuous accelerometer data using Hidden Markov Models

06/24/2020 9:45:00 AM-10:00:00 AM

Session: Population modelling *(Chair: Len Thomas)*

Location: #darwinia

Three-dimensional accelerometer data can provide extremely detailed multi-channel information on individuals' activity. However, management and analysis of such complex data challenge ecologists and statisticians, especially in applications where accelerometer data have been recorded over sufficiently long timescales and show seasonal structures. We continuously collected accelerometer data, over a full year, at 8 Hz on seven muskox females (Ovibos moschatus) with variable reproductive status. Individual-specific Hidden Markov Models (HMM) were built based on Overall Dynamic Body Acceleration (ODBA) and pitch. Seasonality and habitat heterogeneity influence animal movements, energetics, and critical demographic events such as reproduction and mortality. Hence, snow depth was included as a dependent structure in the HMM to incorporate the dominant environmental constraint on muskox activity. We used GPS and Vaginal Implant Transmitter (VIT) data to further clarify the behavioral partition and to validate calving and mortality events. Time budgets and behavioral switching showed seasonal patterns, with distinct signatures depending on individuals' survival and reproductive status. As confirmed by GPS collar retrieval and VITs, accelerometers can detect changes in behavioral patterns related to mortality and reproductive events. Lower ODBA recordings during deeper snow depth periods suggests that snow influences animal velocity, possibly adding an additional cost to movement. Long-term high-resolution accelerometer data within HMM frameworks can successfully detect environmental dependent behavioral plasticity leading to demographic events. Such information opens novel opportunities to study life history events in more detail, and will facilitate integration of data at both individual and population level, which is critical for species' management and conservation.

Keywords: Accelerometers, Behavioral variation, Biologging, Demographics, Movement modelling

Saskia Schirmer (University of Greifswald) with FrÃ¤nzi Korner-Nievergelt, Jan A. C. von RÃ¶nn and Volkmar Liebscher

Modelling continuous spatial survival using dead recovery data

06/24/2020 10:00:00 AM-10:15:00 AM

Session: Population modelling *(Chair: Len Thomas)*

Location: #darwinia

The knowledge of how mortality rate varies in space and time is crucial for understanding demography of migrating animals. But even though there is a huge amount of methods for estimating survival locally or globally from capture-recapture related data, little is known how to generate valid maps of spatially resolved survival. The latter faces problems created by the observation process and migratory connectivity.

Here, we show how to estimate spatially continuous yearly survival from dead recoveries using mixed binomial point processes. We derive the density function of this process by normalizing with the explicit formulation of the density of not recovered individuals. Survival, migratory connectivity and recovery probability can be seen as derived parameters using local linear models. By inspection of the formula the estimate of the survival function is robust with respect to time independent spatial covariates including migratory connectivity and recovery probability. The product of migratory connectivity and recovery probability can be divided in a constant and a spatial component. We propose the former to be interpreted as recovery probability and the latter as migratory connectivity if the observation process is roughly constant over the observed area.

The talk will give insights into the mathematical model, explain the parameter estimation process and show the performance of the model on simulated data. There will be some preliminary results on real world data of European robins and ospreys, followed by a discussion what else needs to be done to also make the spatial variance of the observation process identifiable.

Keywords: Spatial capture-recapture, Spatio-temporal statistics

Daniel W. Linden (NOAA Fisheries) with William J. Rayment

A hierarchical robust design model with 2nd order Markovian temporary emigration and reproductive state uncertainty for southern right whales

06/24/2020 10:15:00 AM-10:30:00 AM

Session: Population modelling *(Chair: Len Thomas)*

Location: #darwinia

Population estimation can be a challenge for wide-ranging migratory taxa such as baleen whales. High visibility during aggregations on breeding grounds can allow for individual identification and capture-recapture methods, yet individual availability can be quite low and vary non-randomly according to reproductive state. Extended breeding intervals and uncertainty in the reproductive state complicates the typical approaches to modeling temporary emigration. Here we used a hierarchical Bayesian form of Pollock's robust design model to estimate demographic parameters, including temporary emigration, for southern right whales (SRW; Eubalaena australis) in the Auckland Islands breeding area from sightings data collected during 2006-2013. Importantly, our temporary emigration was formulated as a 2nd order Markovian process to account for the 3-yr breeding interval (on average) of mature females, since individuals raising calves successfully would be unlikely to return to the breeding area for 2 years. We also modeled sex and maturity as partially latent states, given that individuals could only be identified as a breeding female once they were first sighted with a calf. Model results indicated that the annual probability of a mature female being present in the breeding area was much higher for those individuals that had been absent the previous two years (0.31; 95% CRI: 0.17, 0.49) than those that had visited (0.04; 95% CRI: 0.02, 0.08). While the number of other individuals (e.g., males) fluctuated in the breeding area across the years, the greater population had an annual growth rate (~8 %) consistent with other recovering SRW populations globally.

Keywords: Capture-mark-recapture

Lisa V. Gecchele (University of Edinburgh) with Amy B. Pedersen and Matt Bell

Determining the impact of urbanisation on parasite infection of European red foxes: a large-scale, spatio-temporal meta-analysis using R-INLA.

06/24/2020 10:30:00 AM-10:45:00 AM

Session: Population modelling *(Chair: Len Thomas)*

Location: #darwinia *Student*

The presence of red foxes living in urban environments is now a common occurrence across Europe, living urban environment can impact their behaviour and ecology, but also their parasite and pathogen community.

Many studies have investigated the effect of urbanisation on fox disease ecology at a local scale, but efforts to produce a comprehensive analysis of the overall effect of urbanity level on parasite prevalence is difficult. The lack of a unique definition of what urbanisation mean is one of the main reasons for this, as most studies relies on subjective classification of the urban landscape, which is inherently study-specific and cannot be generalised.

We collaborated with 35 research groups from across Europe, to assemble a georeferenced dataset of parasites and pathogens infection status of red foxes across 27 European countries and spanning 20 years.

Using a remote-sensing dataset of built-up space extent (HBASE) as a measurement of urbanity, we developed a spatio-temporal model to determine the effect urbanisation level on the probability of infection of wild red foxes. We classified the parasites taxa according to functional traits (such as transmission method and parasite type) and modelled the response of each trait to urbanisation level. We found that microparasites respond strongly to urbanity, showing a highest prevalence at medium levels of urbanisation, following closely observed fox population density patterns.

This is the most comprehensive study on the effect of urbanisation on the disease ecology of foxes to date, and will help advance our understanding of the effect of urbanisation on the infection dynamics of wildlife.

Keywords: Disease ecology, GPS data, Hierarchical modelling, Spatio-temporal statistics, Trait based ecology, Urban ecology

Saudamini Venkatesan (University of Edinburgh) with Amy R. Sweeny, Andy Fenton and Amy B. Pedersen

Context-dependent sex differences in parasite prevalence and intensity in populations of wild wood mice

06/24/2020 10:45:00 AM-11:00:00 AM

Session: Population modelling *(Chair: Len Thomas)*

Location: #darwinia *Student*

In vertebrate host populations, males generally exhibit higher parasite prevalence and infection intensity compared to females. Evidence for this male-bias in parasitism comes primarily from meta-analyses of cross-sectional studies lacking spatio-temporal replicates of parasite prevalence and intensity. Additionally, these studies are often limited to a single parasite species infection per host and do not consider other important host factors such as body mass and reproductive condition that could be co-predictors of sex differences in parasite infection. Here, I present results from a 6-year, longitudinal study on wild wood mouse (Apodemus sylvaticus) populations and their parasite community (15 species), trapped every 3-4 weeks from 7 different sites in the UK. We show that there is significant annual and spatial variation in both the magnitude and direction of sex-bias in infection. We also find that the magnitude and direction of sex-bias varies across the different parasite species and importantly, that these relationships are impacted by including host body weight, reproductive condition and season as additional predictors within our statistical models. Our results demonstrate that considering other host characteristics in addition to host sex can reveal the biological contexts under which sex-differences in infection are observed, thereby shedding light on the possible mechanisms underlying this phenomenon.

Keywords: Disease Ecology, Hierarchical modelling, Host-parasite ecology, Population ecology, Sex-differences

Kyuhan Kim (Victoria University of Wellington) with Nokuthaba Sibanda, Richard Arnold and Teresa A'mar

A novel life stage-structured density-dependent biodynamic model in a state-space framework for fish stock assessment

06/24/2020 9:00:00 PM-9:15:00 PM

Session: Fish *(Chair: Brett McClintock)*

Location: #acacia *Student*

Data poor fisheries make up the majority of the world's catch. Such data often consist only of a total annual catch and catch-per-unit-effort (CPUE) from more than one commercial fishery, with no information on age or length at catch that can inform life stage dynamics assessment. With such data poor fisheries, scientists have limited options for stock assessment, such as biodynamic models. An important assumption of biodynamic models is that a relative abundance index, such as CPUE, is proportional to the size of the entire population (or vulnerable population). However, in practice, such an assumption is often problematic mainly because commercial CPUEs often merely represent the abundance of specific size groups. Instead, if one has information of which size groups are specifically targeted by each fishery, one may incorporate life stage dynamics in a biodynamic model which include the commercial CPUEs. In this study, we developed a state-space, two stage-structured biodynamic model, based on Jensen's density-dependent matrix model (Jensen, 1995). This new method not only provides estimates of parameters for each life stage, but also incorporates both process and observation errors. One key advantage of our model is the ability to utilize the prior information available for the standard Schaefer model, as our model shares approximately the same biological parameters with the standard one. This new model was applied to the Korean pollock stock (Gadus chalcogrammus), which has been heavily exploited by targeting both juveniles and adults for more than two decades.

Keywords: Population dynamics

Eric J. Pedersen (Concordia University) with Darrell Mullowney and Krista Baker

Modelling fishing gear with functional responses: a new approach to depletion estimates of fisheries abundance with saturating gear

06/24/2020 9:15:00 PM-9:30:00 PM

Session: Fish *(Chair: Brett McClintock)*

Location: #acacia

Accurately estimating the abundance of benthic populations is vital for both fisheries management and for understanding the dynamics of a species. One of the most popular methods of estimating heavily fished populations is to use a depletion estimator, which relies on how quickly catch per unit effort declines with fishing effort to infer how large the population was when fishing started. Depletion estimators depend on the assumption that the fishing gear has the same catchability at all population sizes. However, many benthic species are fished with traps which can saturate at high population densities. This can result in substantially over-estimating population sizes, and overestimating both rates of population decline and increase. We have developed a new Bayesian dynamic state model that allows simultaneously estimating trap saturation, gear catchability, and initial population size, by modelling trap catchability using predation functional responses. We demonstrate how this method can be used to measure spatially and temporally varying biomass dynamics in spatially structured populations and illustrate how it can be used to improve estimates of rapid declines in Snow Crab across a large-scale metapopulation on the Newfoundland Shelf. We also discuss how this method can be extended to multi-gear fisheries, and to incorporate spatially or temporally varying catchability.

Keywords: Abundance/richness/diversity estimation, Dynamic state models, Fisheries management, Population dynamics

Mollie E. Brooks (Danish Technical University)

Bootstrapping binomial GLMMs in fisheries

06/24/2020 9:30:00 PM-9:45:00 PM

Session: Fish *(Chair: Brett McClintock)*

Location: #acacia

Individual fish in gear selectivity experiments are counted in ways that lead to binomial data. Each unit of replication (i.e. a haul of a net from the sea) could be considered as a random effect in a regression model because outcomes of multiple fish collected in a haul may be correlated. A bootstrapping procedure was developed by Millar (1993) to account for variation among units of replication to allow for predicting outcomes with appropriately wide confidence intervals (CIs). Obtaining the most relevant predictions from GLMMs is notoriously challenging due to the complication of marginalizing over random effects. Given that statistical methods and computational power are improving, the best methods for bootstrapping predicted CIs of GLMMs in general is a topic to investigate going forward. I will introduce a new R package (selfisher) developed for statistically modeling data collected from fisheries gear selectivity experiments, but the bootstrapping methods may be more widely applicable.

Keywords: Hierarchical modelling

Philip Michael Dixon (Iowa State University)

Model-based dissimilarity measures for continuous species composition data

06/24/2020 9:00:00 PM-9:15:00 PM

Session: Multivariate abundances *(Chair: Marti Anderson)*

Location: #banksia

Model-based dissimilarity measures compute the dissimilarity between two vectors of species composition data. These measures provide graphical displays and sample-level diagnostics that are based on the same distributional assumptions about data that are made in model-based analyses. Frequent practice has been to use negative binomial distributions to fit models to data and Bray-Curtis dissimilarity and nMDS to visualize the patterns in species composition. These two approaches make different assumptions about the data, so they are inconsistent. Model-based dissimilarities use the same assumptions for the modeling and the visualization.

Model-based dissimilarities are currently available only for presence/absence and count data. I extend them to continuous species composition data using Tweedie distributions. These are a common choice of distribution for continuous data with frequent zero values. I illustrate the characteristics of the Tweedie dissimilarity using data from the ParkGrass experiment and alpine meadows in Colorado. The ParkGrass samples have relatively similar species composition while the alpine meadow data represent a long gradient from dry ridges to wet meadows.

Keywords: Multivariate analysis/joint species distribution models

Maeve McGillycuddy (UNSW Sydney) with David Warton and Gordana Popovic

Adding latent variables to glmmTMB for parsimonious high dimensional modelling

06/24/2020 9:15:00 PM-9:30:00 PM

Session: Multivariate abundances *(Chair: Marti Anderson)*

Location: #banksia *Student*

Generalised linear mixed models provide a flexible approach to model data, including multivariate data, with clustered or correlated outcomes via random effects. The variance-covariance matrix of the random effects may require estimating many parameters which is problematic with high dimensional random effects and few observations. This often happens when modelling multivariate abundance data in ecology. Another way to model correlation is to use a factor analytical approach, sometimes called a generalised latent variable model (GLVM). A latent variable can be understood as a reduced rank covariance structure for the random effects, with potentially many fewer parameters. While there are several software packages available that can fit a multivariate GLVM, they are not very flexible when it comes to adding additional random effects. We have extended the flexible package, glmmTMB, to include latent variables to create a reduced rank covariance structure to account for correlation across observations.

We apply this model to a study investigating the effect of an offshore wind farm on fish abundance with 10 fish taxa. Instead of accounting for correlation across taxa using an observation-level multivariate random effect, which would have 55 parameters, to be estimated from a sparse dataset with only 179 observations, we have 2 latent variables which only requires 20 parameters. Additionally, we make inferences about the size of treatment effects via inference on the variance of the relevant random effect terms.

Keywords: Hierarchical modelling, Multivariate analysis/joint species distribution models, Software development

Gordana Popovic (UNSW Sydney) with David I. Warton

Fast model-based ordination with copulas

06/24/2020 9:30:00 PM-9:45:00 PM

Session: Multivariate abundances *(Chair: Marti Anderson)*

Location: #banksia

Ordinationis a common way to visualize multivariate data in ecology. It aims to reduce data from many response variables (species/orders) to just two, which may represent an underlying ecological gradient. Sites can then be plotted on a scatterplot so that patterns can be uncovered.

Ordination is traditionally done using algorithmic methods, most commonly non-metric multidimensional scaling (nMDS). In the last decade model based methods for unconstrained ordination have gained popularity. These are based on generalized linear models, with latent variables estimating the underlying ecologicalgradients.

A major advantage of algorithmic methods over model based methods is their speed, with model based methods traditionally taking much longer to return a result, especially for large sample sizes.

We introduce copula ordination, a fast model based method for unconstrained ordination. This method has all the properties of model based ordination methods, and it is fast, with consistently quicker computation than other model based methods, and faster computation than nMDS for large sample sizes.

Keywords: Community ecology, Multivariate analysis/joint species distribution models, Ordination, Software development

Harlan Campbell (University of British Columbia)

The consequences of checking for zero-inflation and overdispersion in the analysis of count data

06/24/2020 9:45:00 PM-10:00:00 PM

Session: Multivariate abundances *(Chair: Marti Anderson)*

Location: #banksia

Count data are ubiquitous in ecology and the Poisson generalized linear model (GLM) is commonly used to model the association between counts and explanatory variables of interest. When fitting this model to the data, one typically proceeds by first confirming that the data is not overdispersed and that there is no excess of zeros. If the data appear to be overdispersed or if there is any zero-inflation, key assumptions of the Poison GLM may be violated and researchers will then typically consider alternatives to the Poison GLM. An important question is whether the potential model selection bias introduced by this data-driven multi-stage procedure merits concern. In this paper, we conduct a large-scale simulation study to investigate the potential consequences of model selection bias that can arise in the simple scenario of analyzing a sample of potentially overdispersed, potentially zero-heavy, count data.

Keywords: Individual-based models, Model-selection bias, Model assessment/validation, Multivariate analysis/joint species distribution models

Imane AGMOUR (Hassane II University) with Meriem Bentounsi, Naceur Achtaich and Youssef El Foutayeni

Mathematical modelling for the sustinble developement of marine resources

06/24/2020 11:00:00 PM-11:15:00 PM

Session: Landscapes and ecosystems *(Chair: Kiona Ogle)*

Location: #banksia

In our work, we propose a bioeconomic model of marine populations exploited by purse seiners in the maritime zones of Morocco. We calculate the fishing effort and the amount of catch that allows seiners to have a maximum annual profit taking into account changes of wind speed in the reporting year and the sustainability of the marine populations stocks. We compare our results with those obtained by the" Institut National de Recherche Halieutique (INRH)" (National Institute of Fisheries Research). One of the key results of this study is the great difference seen between the monthly fishing efforts, the catches and the profits calculated under the two constraints: wind speed changes and biodiversity conservation, and those calculated under the only constraint of the biodiversity.

Keywords: Bioeconomic modelling, Nash equilibrium problem, Population dynamics, Predator-prey modelling, Problem of maximization, Stability analysis, Wind speed

Gerard E Ryan (University of Melbourne)

How much modelling is enough to manage biodiversity in your forests, should you bother with population viability analysis, and should you use new PVA tool STEPS to do that bothering?

06/24/2020 11:15:00 PM-11:30:00 PM

Session: Landscapes and ecosystems *(Chair: Kiona Ogle)*

Location: #banksia *Student*

This talk is about accounting for uncertainty to manage biodiversity in forests and demonstrates the use of a new population viability analysis tool in doing so.

There is an inequality among species about the variety and quality of information we have about them - some are well studied, others poorly. Information affects our ability to model species' response to management actions, and in-turn make good management decisions. Does it matter and how much?

To understand the impact of timber harvest and fire management in forest biodiversity in Victoria, Australia, we compare a suite of increasingly complex models, with increasingly complex informational needs: species distribution models, metapopulation capacity models, and population viability analyses.

We also illustrate the use of a new, spatially explicit, population viability analysis tool "STEPS", which is available as an R package.

Keywords: Abundance/richness/diversity estimation, Population dynamics, Population ecology, Species distribution modelling

Ismael V. Brack (Federal University of Rio Grande do Sul) with Andreas Kindel, Douglas O. Berto, AndriÃ©li R. Garcia, JosÃ© L. P. Cordeiro, JosÃ© J. Lahoz-Monfort, and Luiz Flamarion B. Oliveira

Spatio-temporally replicated drone flights for estimating marsh deer abundance in Pantanal Wetland

06/24/2020 11:30:00 PM-11:45:00 PM

Session: Landscapes and ecosystems *(Chair: Kiona Ogle)*

Location: #banksia *Student*

Abundance estimates from aerial surveys are subject to two main detection errors: perception and availability, the latter commonly being addressed using ancillary data or not even addressed. Recent rise of drones for population studies and monitoring has allowed exploring novel approaches for designing and analyzing aerial surveys. Here, we apply hierarchical N-mixture models to spatio-temporally replicated drone flights reviewed by multiple observers in order to investigate how marsh deer (Blastocerus dichotomus) abundance varies according to green biomass and water bodies in Northern Pantanal Wetland (Brazil). We conducted 24 fixed-wing drone flights in six transect missions (32-42km long) replicated from two to six times each, and flight images were reviewed by either one or two observers. We obtained 66 records of marsh deer in 25,000 images from a total of 763 km flew. Mean marsh deer abundance was 0.3 (95%CI=0.1-0.5) individuals/km and local abundance presented a positive relation with green biomass (NDVI) and a negative relation with distance to water bodies. The use of a double observer protocol in the revision of only 20% of the flights decreased the 95%CI of total abundance from 42-332 to 43-243 individuals. The choice of segment length to define the sites (sampling units) did not affect abundance estimates. The versatility of drones for spatio-temporally replicated sampling designs allows reliably estimating abundance, while accounting for both perception and availability errors without resorting to ancillary data. The use of multiple observers in image review permits to model both observation processes separately, and improve precision in abundance estimates.

Keywords: Abundance/richness/diversity estimation, Aerial surveys, Hierarchical modelling, Population ecology, Spatio-temporal statistics

Cristina Barber (Boise State University) with Trevor Caughlin

A Bayesian framework to link remote sensing and field data to predict natural regeneration at the landscape scale.

06/24/2020 11:45:00 PM-12:00:00 AM

Session: Landscapes and ecosystems *(Chair: Kiona Ogle)*

Location: #banksia *Student*

Calls to restore forest cover to hundreds of millions of hectares of degraded land have led to a demand for spatially-targeted reforestation projects, including maps of where forest will return with minimal intervention. However, forecasting rates of forest recovery in heterogeneous landscapes has proven a difficult task, with high variability in natural regeneration outcomes between sites. Recruitment, the establishment of new trees, represents the first step in successful forest recovery and many have attempted to predict recruitment rates by linking landscape-scale seed sources with seedling abundance. However, results from these studies are highly variable, including strong to weak relationships between landscape context and recruitment. We address uncertainty in modeling drivers of recruitment in the landscape by applying a Bayesian modeling framework to link field data on recruit abundance with aerial remotely sensed data on tree crown locations. Our recruit abundance model provides insight into how recruit abundance could be predicted by fusing data sources. First, we found that modeling recruit abundance as a zero-inflated distribution, representing a combination of negative binomial and bernoulli processes, was essential to achieve predictive accuracy, even without covariates. Second, our models suggest that accounting for species-level differences in a hierarchical framework results in large improvements in predictive accuracy. Third, our results provide strong evidence that distinguishing species-identity of potential tree crown seed sources can improve predictive accuracy, at least for some recruit species. Our modeling work provides an example of how spatial models could provide decision support tools for large-scale restoration projects, including the value of hierarchical Bayesian approaches for accounting for variability across landscapes.

Keywords: Spatial predictions by combining field data and remote sensing

Fernando P. Mayer (UFPR) with Paulo J. Ribeiro Jr.

Spatio-temporal Bayesian biomass dynamics models

06/24/2020 9:00:00 PM-9:15:00 PM

Session: Contributed talks *(Chair: Alison Johnston)*

Location: #corymbia *Student*

A two-stage approach was developed for the estimation of parameters (r, q, K) from fisheries biomass dynamic models (e.g. Schaefer model). This approach allows for both process and observation equation errors. Moreover, the parameters of interest (r, q, K) are allowed to vary in space and time. In the first stage, a linearized form of the catch equation is used, allowing for spatial, temporal and/or spatio-temporal random effects. The estimated parameters are then used in the second stage, where estimates of (r, q, K) are obtained. This approach was developed in a fast Bayesian context, through the Integrated Nested Laplace Approximation (INLA) framework. Simulations where the parameters (r, q, K) vary in space and time were developed. Results showed that when the spatio-temporal structures are considered, parameter estimates are unbiased and consistent. Allowing for space-time varying parameters should bring more realistic population dynamics models, improving decision-making in management of exploited fish populations.

Keywords: Abundance/richness/diversity estimation, Dynamic state models, Hierarchical modelling, Spatio-temporal statistics

Taylor Jon Hamlin (University of Otago) with Matthew Schofield, Dean Anderson and Phil Seddon

Linking foraging with reproductive success among AdÃ©lie penguins (Pygoscelis adeliae) at Cape Bird, Antarctica.

06/24/2020 9:15:00 PM-9:30:00 PM

Session: Contributed talks *(Chair: Alison Johnston)*

Location: #corymbia *Student*

Movement is a feature of almost every aspect of life, underpinning the interactions an organism has with the biotic and abiotic elements of the surrounding world. The study of animal movement is used increasingly to unpack the complex lives of animals. But, many movement-based studies lack the mechanistic links between movement and the ecological process they describe. This is particularly evident in research that attempts to infer the reproductive and/or demographic implications of variation in movement parameters. Motivated by a study of AdÃ©lie penguins (Pygoscelis adeliae) from Cape Bird Antartica, we show how Bayesian hierarchical modelling can be used to jointly model reproductive and demographic outcomes. The AdÃ©lie data includes information on foraging movement, foraging success, survival, weight change, and fledging success of ten breeding pairs during the breeding period in each of two years. We will present preliminary results and discuss how the model can be generalized to other organisms and systems.

Keywords: Behavioural ecology, Biologging, GPS data, Hierarchical modelling, Model assessment/validation, Movement modelling, Population dynamics, Population ecology

Perry de Valpine (University of California Berkeley) with Daniel Turek, Christopher J. Paciorek, Benjamin R. Goldstein, Sally Paganin and Wei Zhang

Recent developments and future directions for NIMBLE

06/24/2020 9:30:00 PM-9:45:00 PM

Session: Contributed talks *(Chair: Alison Johnston)*

Location: #corymbia

NIMBLE (R package nimble) is a hierarchical model and algorithm programming system that is being used by many ecological researchers. It is distinct from other tools in its flexibility and efficiency. Its MCMC system is highly customizable. Its programming system supports new algorithms, new samplers for MCMC, and new functions and distributions for models. Efficiency is achieved by C++ code-generation. One design goal of NIMBLE is a one-model-many-method workflow, so that users do not have to switch packages, re-coding models each time, to try different methods.

This talk presents several advances that increase NIMBLE's usefulness for ecologists. First, NIMBLE's code-generation system is extended to create automatic differentiation (AD) code using the CppAD package. AD has enabled development of fast Laplace approximation, Hamiltonian Monte Carlo (HMC), and other derivative-enabled MCMC methods such as Metropolis-adjusted Langevin (MALA) samplers. Second, a macro system for the model language will provide tools for more easily writing complex models and code-generating complex models from R, supporting development of high-level packages that use NIMBLE models internally. Third, NIMBLE's C++ code-generation and compilation system is undergoing an overhaul, which will make it easier to re-use code, save and load compiled objects, generate code into packages, and parallelize algorithms. Finally, I will briefly touch upon methods newly implemented in NIMBLE, including tools for occupancy, capture-recapture and abundance models in the nimbleEcology package; reversible jump sampling for variable selection; Bayesian non-parametric distributions; cross-validation; and calibrated posterior predictive checks.

Keywords: Hierarchical modelling, Software development

Audrey Beliveau (University of Waterloo) with Joe Thorley

simcases: a new R package to facilitate model comparisons and simulation studies with JAGS

06/24/2020 9:45:00 PM-10:00:00 PM

Session: Contributed talks *(Chair: Alison Johnston)*

Location: #corymbia

Research in statistical ecology frequently involves simulation studies and/or data analyses requiring multiple model comparisons. Nowadays, such analyses are commonly conducted in a Bayesian framework with BUGS software, i.e. JAGS, WinBUGS and OpenBUGS which are prized for their flexibility in model implementation and the convenience of their MCMC samplers. However, modern statistical ecologists still face challenges with regards to runtime, organization of results, reproducibility and simplicity of coding when it comes to running a large number of analyses. simcases is a new collection of R packages designed to address these issues, with a particular focus on simulation studies with JAGS.

In this paper, we will demonstrate the capabilities of simcases using a simulation study of a capture-recapture experiment. We will show how - using a small number of concise lines of code with simcases' functions - the user can specify the various scenarios, simulate data with BUGS code, distribute the computations across CPUS, save the results in an organized manner, automatically ensure convergence of the MCMC chains (and thin as needed), and choose between different analysis modes, including a quickmode which simply runs the code quickly for testing and a paper mode which ensures convergence of the chains for a paper publication. We will also demonstrate that the results of simulation studies with simcases are perfectly reproducible even when changing between the parallel vs sequential computation mode and whether or not saving results to files.

Keywords: Capture-mark-recapture, Hierarchical modelling, Integrated population models, Population dynamics, Software development

Nels G. Johnson (USDA Forest Service) with Erin C. Riordan and Matthew R. Williams

A generalized nonlinear modeling approach can solve the prediction problem for data from species-stratified use-availability designs

06/24/2020 11:00:00 PM-11:15:00 PM

Session: Citizen science and opportunistic data *(Chair: Skipton Woolley)*

Location: #corymbia

Habitat suitability modeling methods for presence-only species data are limited in their ability for making true predictions and are therefore often misused in ecological applications. A use-availability design--also known as a case-control design with contaminated controls--combines presence only species data with a background sample of covariates where the species presence/absence is unknown. Assuming a log link-function for the true probability of presence/absence, the use-availability data then can be analyzed as a logistic regression model with a biased estimate of the intercept. Due to the biased intercept, the model is unable to make true predictions. Instead, ranking the "pseudo predictions" from the model with biased intercept provides a viable alternative for making predictive inference in single-species models. We show that when such a single species model is extended to multiple species the ranks are no longer conserved across species, limiting predictive inference. Alternatively, by assuming a logit link-function for the true probabilities of the presence/absence data, the resulting model allows for predictive inference even when extended to multiple species. We provide theoretical details justifying both fully Bayesian and large background sample asymptotic Bayesian generalized nonlinear model approaches. We illustrate how multiple species can be analyzed using these approaches in R and Stan using presence-only data for foundational shrubland taxa occurring in California, USA. Predictive inference highlights differences in habitat suitability rankings among individual species and among infraspecific taxa within a single species, improving the application of habitat suitability models for ecological restoration of southern California shrublands.

Keywords: Species distribution modelling

Timothy D. Meehan (National Audubon Society) with Sarah P. Saunders, William V. DeLuca, Jill L. Deppe, and Nicole L. Michel

Inferring Avian Migration Corridors Using Probabilistic Least Cost Path Analysis of Predictions from Weekly, Hemispheric Species-Distribution Models

06/24/2020 11:15:00 PM-11:30:00 PM

Session: Citizen science and opportunistic data *(Chair: Skipton Woolley)*

Location: #corymbia

Identifying likely migration corridors is critical for conserving migratory bird populations across their full annual cycle. Our current understanding of North American migration corridors primarily comes from bird banding and tracking data, but is limited by low band re-encounter rates, heavy and expensive tracking technology, and spatial bias in banding and tracking locations. An alternative approach to describing migration corridors uses species distribution models (SDM) based on observations collected across the full annual cycle. Here, we describe a novel corridor analysis method that uses weekly, hemispheric, SDM relative-abundance predictions produced for hundreds of species by the Cornell Laboratory of Ornithology using data from the eBird community science program. The method uses probabilistic least cost path analysis to connect neighboring locations of high relative abundance across weekly time steps. Weekly paths are aggregated over a given migration season per species, and then aggregated over multiple species to describe probabilistic migration corridors for a suite of North American wood warbler species. We compare corridor probabilities to banding and tracking data for different species to explore the validity of the approach under a variety of data-availability circumstances. The modeling framework provides a means for ascertaining likely migratory corridors for many species that lack banding or tracking data, and offers a possible solution for identifying areas along migratory routes where conservation actions should be targeted.

Keywords: Movement modelling

Richard J. Camp (University of St Andrews / U. S. Geological Survey, Pacific Island Ecosystems Research Center) with Andrew E. Seaton, David L. Miller, Len Thomas, Stephen T. Buckland, Janine B. Illian, David L. Borchers and Steve J. Kendall

Species distribution modelling: insights from modelling using one- and two-stage methods

06/24/2020 11:30:00 PM-11:45:00 PM

Session: Citizen science and opportunistic data *(Chair: Skipton Woolley)*

Location: #corymbia

Conducting analyses that account for spatial correlation can help policy makers and managers make informed decisions based on precise population estimates. Two common statistical approaches to model spatial correlation are (1) penalized spline-based smoothing, and (2) point process models. We compare the density and SE estimates produced using the two approaches applied to a survey of Hawai`i `akepa (*Loxops coccineus*), an internationally and federally endangered Hawaiian honeycreeper. For our first approach, we used a two-stage model-based analysis to model counts, with an estimated offset to allow for imperfect detection, using a generalized additive model (hereafter, DSM). In our second approach, we modelled the data as a thinned log-Gaussian Cox process using Gaussian Markov random field approximations to Gaussian random fields. Both the detection function and log-intensity of points were modelled using a stochastic partial differential equation approach (hereafter, INLA). We drew 1000 samples from the posterior of each approach and computed differences among realisations. Both the DSM and INLA approaches produced similar density spatial patterns and estimates. The SE values were greater for the DSM than for the INLA approach, although they had similar spatial patterns of high and low uncertainty. While both approaches produce comparable density estimates, the INLA approach better modelled the spatial inhomogeneities, edges and textures in counts across the domain to produce more precise density estimates. Our results indicated that we should select either the penalized spline-based smoother or point process approach if we believe the surface to be more smooth or wiggly, respectively.

Keywords: Abundance/richness/diversity estimation, Model assessment/validation, Species distribution modelling

Joe Watson (University of British Columbia) with Marie Auger-MÃ©thÃ©, Ruth Joy, Dominic Tollit and Sheila Thornton

Combining citizen science and survey data in a log-Gaussian Cox process framework to estimate the monthly space-use of Southern Resident Killer Whales

06/24/2020 11:45:00 PM-12:00:00 AM

Session: Citizen science and opportunistic data *(Chair: Skipton Woolley)*

Location: #corymbia *Student*

Species distribution models (SDMs) are useful tools to help ecologists quantify species-environment relationships, and they are being increasingly used to help determine the impacts of future climate and habitat changes on species. Estimating SDMs can be tricky from a statistical point of view since the effects of spatial and temporal autocorrelations, land cover and environmental covariates and detectability functions all need to be considered and inherently modeled. Furthermore, such models often assume that data have been collected from well-designed surveys and/or studies. In practice, data are often of the form of presence-only sightings collected from 'citizen scientists' and other sources whose 'search effort' can be difficult to quantify. Furthermore, search effort from such sources is often concentrated in areas in which the expected count of the species under study is high, and/or where population density is high. Ignoring the search effort can lead to severely biased estimates of the species distribution.

We look at data collected on Southern Resident Killer Whales (SRKWs), an ecotype with designated 'species at risk' status found off the coast of Vancouver Island. Data from from a variety of 'citizen science' sources and government surveys are considered. We present a method to combine the different data sources and estimate the monthly SRKW space-use in a statistically-rigorous manner using spatio-temporal log-Gaussian Cox processes within the R-INLA and inlabru packages. Improved (effort-corrected) estimates of the SRKW distribution will hopefully help ecologists and policy-makers safeguard the future of the SRKW.

Keywords: Citizen science, Effort correction, Hierarchical modelling, Spatio-temporal statistics, Species distribution modelling

Alexandru M. Draghici (University of Western Ontario) with Simon J. Bonner and Wendell O. Challenger

Accounting for Dependence within Mating Pairs in the Cormack-Jolly-Seber Framework

06/24/2020 9:00:00 PM-9:15:00 PM

Session: Capture-recapture challenges *(Chair: Richard Chandler)*

Location: #darwinia *Student*

Many ecological studies focus on estimating the demographics of wildlife populations by modeling the mechanisms governing their behavior. For example, survival rates can be studied using mark-recapture data. Mark-recapture data is collected by capturing individuals from a population of interest at several given time points, marking untagged individuals with a unique identifier, recording the marked individuals, and then releasing them back into the study region.

The Cormack-Jolly-Seber (CJS) model, developed in 1965, has been widely applied to the study of animal survival rates in open populations. For animals that form monogamous long-term pair bonds, the model assumption about independence between individuals can often become unrealistic. It is unlikely that a pair of animals which have formed a long-term pairing have disassociated fates. We propose an extension which allows pair-bonded animals to have correlated survival and recapture rates. Furthermore, we account for the possibility that pair-bonded individuals may go through periods of temporary separation where they act independently.

Using the proposed extension to generate data, we conduct an in-depth simulation study where we explore the impact that correlated fates has on the CJS model. Specifically, we address the issues of underestimated standard errors, failings of goodness-of-fit tests for nested models, and finally the ability of the ? correction (an omnibus variance inflation factor meant to deal with goodness-of-fit issues) to address the problem of correlated fates within mark-recapture data.

Keywords: Capture-mark-recapture, Cormack-Jolly-Seber, Hierarchical Modelling, Model Assessment/Validation, Pair-Bonds, Statistical Dependence

Simon J. Bonner (University of Western Ontario) with Jiaqi Mu and Wei Zhang

On the Identifiability of Open Mark-Recapture Models with Continuous Covariates

06/24/2020 9:15:00 PM-9:30:00 PM

Session: Capture-recapture challenges *(Chair: Richard Chandler)*

Location: #darwinia

Several variants of the classic Cormack-Jolly-Seber model have been developed to study the impacts that individual, time-varying covariates (like mass per unit body size or other measures of fitness) may have on the survival of marked animals. The main challenge with such covariates is that they cannot be observed when individuals aren't captured. The first methods proposed to address this problem considered models in the Bayesian framework and employed Markov chain Monte Carlo (MCMC) sampling to explore the joint posterior distribution of both the missing values and the model parameters. While this approach provides exact inference, it is computationally intensive. This makes it difficult to analyze large data sets or to compare the fit of multiple models to the same data. Several alternative models have been developed that essentially employ partial likelihoods obtained by removing pieces of the full likelihood to simplify the computation. We consider the identifiability of these models when the survival probability is linked to the covariate through a scaled logistic function which reaches an asymptote at some value less than 1. We examine the models theoretically by applying Bayesian methods for partial identification (in the statistical sense) based on construction of the limiting posterior distribution -- the hypothetical posterior distribution arising from an infinite sample size. We provide further results from a simulation study and the analysis of data collected to examine the effect of parasite load on the survival of spiny lizards (Sceloporus sp.).

Keywords: Bayesian methods, Capture-mark-recapture, Individual-based models

Han-Na Kim (University of Western Ontario) with Simon J. Bonner

H-likelihood for Fitting Closed Capture-Recapture Models with Unobserved Heterogeneity

06/24/2020 9:30:00 PM-9:45:00 PM

Session: Capture-recapture challenges *(Chair: Richard Chandler)*

Location: #darwinia *Student*

Incorporating random effects into capture-recapture (CR) models allows for the estimation of the size of a population in which individuals are nested within clusters having different capture probabilities. Through the approach of conditional likelihood, all closed CR models described by Otis et al. (1978), including those with heterogeneity in the capture probabilities, can be regarded as generalized linear mixed models (GLMMs) or vector GLMMs (VGLMMs). Building on this connection, we propose to fit these models by applying the H-likelihood procedure described by Lee and Nelder (1996) to fit GLMMs and VGLMMs. In essence, the H-likelihood procedure derives inference for both the fixed and random effects from maximizing the extended likelihood function (i.e., the joint density of the data and the random effects) and consequently avoids the need to compute the intractable integrals that arise in the marginal likelihood of the data alone. This feature of the H-likelihood procedure can reduce high computation times frequently caused by the need to conduct numerical integration through sampling (e.g., MCMC) or methods such as quadrature. Surprising as it seems at first glance, the H-likelihood procedure provides valid inference for both the fixed and random effects provided that certain conditions are met. We show that the closed population CR models do satisfy these properties and demonstrate our proposed methodology by a simulation study and analysis of an example from ecological data.

Keywords: Capture-mark-recapture, Generalized linear mixed models, H-likelihood, Heterogeneity

Matthew R. Schofield (University of Otago) with Heloise Pavanato, William A. Link and Richard J. Barker

Estimating abundance: binomial vs Poisson

06/24/2020 9:45:00 PM-10:00:00 PM

Session: Capture-recapture challenges *(Chair: Richard Chandler)*

Location: #darwinia

When modeling mark-recapture data it is common to assume that the total number of individuals observed is the realization of a binomial distribution. The index is of this distribution is the abundance, and is often the parameter of interest. Alternatively, one can assume that the number of individuals observed is the realization of a Poisson with interest in the rate parameter. It is commonly thought that the estimators for these two models are similar. Indeed they have been shown to be equivalent if a scale prior is assumed, asymptotically equivalent otherwise, and been labeled as `remarkably close' due to differing by O(1). Motivated by a mark-recapture distance sampling example of humpback whales off the coast of Brazil, we show that there are realistic situations where the choice of models is important and the estimators can differ substantially. In this talk we will reconcile the differences, explaining how and why the estimators differ. We demonstrate these differences in terms of the motivating application.

Keywords: Abundance/richness/diversity estimation, Capture-mark-recapture

Andrea M. Havron (University of Washington) with Carey R. McGilliard

A Gaussian Markov random field approach to the spatial finite mixture model

06/24/2020 11:00:00 PM-11:15:00 PM

Session: Populations in time and space *(Chair: Rahel Sollmann)*

Location: #darwinia

Spatial clustering via finite mixture models is frequently used in ecological analysis to account for discontinuities in spatial heterogeneity, such as in landscape classification, population genetics, and patch analysis of ecological communities. Previous studies have demonstrated the effectiveness of using a Gaussian Markov random field (GMRF) within a Gaussian Mixture Model to inform both spatial clustering within the mixture component and continuous spatial residual pattern in the response (Fernandez and Green, 2002).

We develop a new spatial finite mixture model approach within the framework of Template Model Builder (Kristensen et al, 2016). TMB allows for fast likelihood computations of geostatistical random effects by applying sparse matrix algorithms to approximate the GMRF of a spatial process; after which, the marginal likelihood is specified using the Laplace Approximation. Our method incorporates spatial effects in both the group membership probability using logistic regression and the response density. Models are fit using the EM algorithm where the Laplace Approximation is implemented in the maximization step. Given the inherent flexibility of TMB, this approach can be extended to more complex models, such as non-Gaussian response distributions. Examples will be provided using simulated data and a case study that aims to identify fishery fleet clusters, or mÃ©tiers, in the multispecies Bering Sea fishery.

Fernandez, C., Green, P.J. 2002. Modelling spatially correlated data via mixtures: a Bayesian approach. Journal of the Royal Statistical Society. 64: 805-826.

Kristensen, K., Nielsen, A., Berg, C.W., Skaug, H., Bell, B. 2016. TMB: Automatic Differentiation and Laplace Approximation. 70: 1-21.

Keywords: Finite mixture models, Multivariate analysis/joint species distribution models, Spatio-temporal statistics

Beth Gardner (University of Washington) with Nathan J. Hostetter, Briana Abrahms, Richard Chandler, Paul Conn, Sarah J. Converse, Robert Emmet, Devin Johnson, and Brett McClintock

Moving forward: Integrating animal movement into spatial capture-recapture models

06/24/2020 11:15:00 PM-11:30:00 PM

Session: Populations in time and space *(Chair: Rahel Sollmann)*

Location: #darwinia

Spatial capture-recapture (SCR) models have become widespread in ecological and wildlife studies, with continual new developments that provide more flexibility in SCR. The underlying observation model in SCR defines how an animal's encounter rate is a function of the distance between its activity center and a trap, which can often be related to the assumption of animals having a Bivariate Normal (BVN) home range. SCR models appear to be resilient to violations of this movement assumption for estimating density. However, the BVN home range assumption limits the ecological questions related to space use, habitat selection, behavior, and their interactions with demographic rates that can be addressed by SCR. Here, we conducted a simulation study to explore the power of SCR to estimate density under different movement processes and provide a framework for how to integrate more complex movement models into SCR. We simulated movement trajectories of animals (under the BVN, random walk, correlated random walk, and state-switching models with and without central tendency) and conditional on these tracks, encounter data were simulated based on locations of animals relative to proximity detectors. We simulated 200 datasets per scenario and fit standard SCR models to each; similarly finding minimal bias in density estimation across the different scenarios (generally 3-8%), but the detection parameters not easily interpretable and provide little information on animal movement in these cases. We develop a method for integrating movement into SCR and apply the novel model to the simulated datasets described above. Incorporating greater movement realism into SCR models is an important step in advancing both SCR and movement modeling.

Keywords: Abundance/richness/diversity estimation, Capture-mark-recapture, Movement modelling, Spatial capture-recapture

Rishika Chopara (University of Auckland) with David Borchers, Ian Durbach, Ben Stevension, Rachel Phillip, and Koustubh Sharma

That's not the Mona Lisa!: how to interpret spatial capture-recapture density surface estimates

06/24/2020 11:30:00 PM-11:45:00 PM

Session: Populations in time and space *(Chair: Rahel Sollmann)*

Location: #darwinia *Student*

Non-uniform density surfaces obtained from spatial capture-recapture analyses are quite often misinterpreted. Spatial variation in how much is known about activity centre locations is confused with spatial variation in activity centre density. There is also often a lack of clarity about what the estimated surface is.

We consider three surfaces: (1) the expected activity centre density, (2) the realised activity centre density, and (3) the realised usage density. For easy visual interpretation, we use a greyscale image of the Mona Lisa as the true activity centre density surface and illustrate correct and incorrect inferences from simulated surveys of populations with this density as well as from a real camera trap survey.

We show that treating the realised activity centre density surface as a realised usage density or expected activity centre density surface results in misleading ecological inferences. Very different realised activity centre density surfaces can be obtained by surveying exactly the same animals with different detector placements. Valid activity centre density surfaces are obtained by estimating the intensity of a point process model for activity centres, which may depend on spatially-referenced covariates. Realised usage density surfaces are obtained by extending methods used for realised activity centre density surfaces.

To avoid misinterpretation, practitioners should state explicitly what kind of density surface they are estimating and should be careful to draw inferences appropriate to that kind of surface. In particular, misleading inferences are obtained if realised activity centre density estimates are interpreted as if they were expected activity centre density estimates.

Keywords: Spatial capture-recapture, Species distribution modelling

David K. Chan (University of Auckland) with Ben C. Stevenson, Regina A. Guazzo and Tyler A. Helble

Spatial capture-recapture applications to acoustic surveys of cetacean populations

06/24/2020 11:45:00 PM-12:00:00 AM

Session: Populations in time and space *(Chair: Rahel Sollmann)*

Location: #darwinia *Student*

Acoustic surveys are rapidly becoming one of the most common ways to assess cetacean populations, and can be vastly cheaper than other alternatives, like visual surveys. This is because visual surveys have low detection rates, even under ideal conditions. However, acoustic surveys can detect large numbers of vocalising individuals, if the monitoring devices and survey design are appropriate for the target population. Acoustic spatial capture-recapture (ASCR) can estimate call density from these surveys. ASCR has not been widely applied to acoustic surveys of cetacean populations although it is acknowledged in the literature.

In this talk I describe an application of ASCR to estimate call density of eastern North Pacific gray whales, Eschrichtius robustus, and how it varies with environmental covariates like ocean depth and distance from coast. Our findings are broadly consistent with those of Guazzo et al. (2017), who described the data set and estimated homogeneous call density within the hydrophone array using a method that analysed a subset of calls that could be accurately localised. Our analysis highlights two considerable advantages of ASCR over other established methods in the literature: calls do not have to be localised to be included in the analysis, and it allows estimation of an inhomogeneous call density surface.

Reference

Guazzo, R. A., Helble, T. A., Gerald, L. D., Weller, D. W., Wiggins, S. M., & Hildebrand, J. A. (2017). Migratory behavior of eastern North Pacific gray whales tracked using a hydrophone array. PloS one, 12(10), e0185585.

Keywords: Acoustic survey, Call density, Passive acoustic monitoring, Spatial capture-recapture

Mahdieh Tourani (Norwegian University of Life Sciences)

Landscape-level patterns in wolverine home range size using non-invasive monitoring and hierarchical modelling

06/25/2020 8:00:00 AM-8:15:00 AM

Session: Genetics and broad-scale assessment *(Chair: Ben Stevenson)*

Location: #acacia *Student*

Of perennial interest in ecology is the study of home range, the area within which an individual does its routine foraging, mating and parenting while avoiding risks. Identifying landscape-level correlates of home range size has usually been performed using a patchwork of telemetry studies. Animal welfare as well as logistic and economic considerations limit the scale at which telemetry studies can be implemented, both in terms of spatial extent and the proportion of the population tracked. Non-invasive monitoring methods, such as camera trapping and genetic sampling, offer opportunities to obtain information about animal space-use at the scale of populations and landscapes. In this study, we analyze non-invasive genetic monitoring data of wolverine (Gulo gulo) in Scandinavia using spatial capture-recapture models. We quantify the effect of landscape level covariates on home range size variation at an unprecedented spatial extent. The biological (population) and spatial (landscape) scale at which non-invasive monitoring allows investigators to operate, could in many cases compensate for the reduced spatiotemporal detail (observations per individual) when compared with contemporary GPS-based telemetry.

Keywords: Hierarchical modelling, Population ecology, Spatial capture-recapture

Robin Aldridge-Sutton (University of Auckland) with Rachel Fewster and Emma Carroll

New methods for estimating population size based on close-kin genetics and extensions

06/25/2020 8:15:00 AM-8:30:00 AM

Session: Genetics and broad-scale assessment *(Chair: Ben Stevenson)*

Location: #acacia *Student*

Close-kin genetics is an emerging approach to estimating population size and demographics, based on family relationships elicited from samples of genotyped animals. The field is still in its infancy but is generating considerable interest, partly due to recent advances in genomics providing high-resolution genotype datasets. Some flagship studies have already been completed, including estimates of population demographics for white sharks in Australia and New Zealand.

We are interested in applying the method to the New Zealand southern right whale population, which underwent a dramatic decline after an estimated 35,000 whales were slaughtered during 19th century whaling, and is now recovering. We investigate the accuracy and precision of close-kin genetics for estimating population size for this species, and present a Shiny interface for investigating the performance of the method by simulation under realistic population trajectories.

We also present new ideas for extending close-kin genetics to a wider methodology for estimating population abundance and demographics. Instead of requiring the analyst to predetermine kinship between each pair of animals, and delete any pairs over which there is doubt, the new method is based on a pseudo-likelihood which incorporates multiple levels of kinship together with kinship uncertainty. We present preliminary results and compare the new approach with the standard close-kin genetics approach.

Keywords: Close-kin genetics

Toby A. Patterson (CSIRO) with Richard Hillary, Mark Bravington, Pierre Feutry, Peter Kyne and Richard Pillans.

Simultaneous estimates of abundance and generational connectivity using close kin mark recapture

06/25/2020 8:30:00 AM-8:45:00 AM

Session: Genetics and broad-scale assessment *(Chair: Ben Stevenson)*

Location: #acacia

We applied close-kin mark-recapture (CKMR) methods to estimate the abundance of mature speartooth sharks (Glyphis glyphis), a species where mature individuals are rarely encountered. Abundance was estimated in the genetically connected Adelaide and Alligator River populations of the Northern Territory, Australia, using samples from N=226 juveniles. We discuss extensions on previous CKMR modelling to include sex-specific spatial structure within a population dynamics model. We detail the likelihood components of the model which use both matches between half- and full-sibling pairs from single nucleotide polymorphism data and mitochondrial DNA to inform on whether sibling pairs were paternal or maternal. The model estimated the abundance of sharks across both rivers and spatial allocation of reproductive effort by sex. High river fidelity was estimated for females and males in the Adelaide River. However, male sharks in the Alligator River were estimated to have a high chance of allocating reproductive output to the Adelaide River. This study demonstrates the utility of CKMR methods for producing estimates of population size and also how adults allocate their reproductive output within a meta-population. Unlike typical population genetics studies, which consider population connectivity on evolutionary timescales, the CKMR approach detailed here, can establish patterns of connectivity in long-lived populations with low reproductive output over generational time scales. As genetic samples were collected from within the last 5 years from a highly cryptic and little studied species, this case study also demonstrates the utility of the CKMR in producing abundance and connectivity estimates within a relatively rapid time frame.

Keywords: Abundance/richness/diversity estimation, Capture-mark-recapture, Close kin mark recapture, Population dynamics, Population genetics

Manuel Ramos Martins (Universidade do Algarve) with David Abecasis and Jorge Assis

Changes in fish species suitable habitat as a response to climate change

06/25/2020 8:45:00 AM-9:00:00 AM

Session: Genetics and broad-scale assessment *(Chair: Ben Stevenson)*

Location: #acacia

In order to understand how climate change induced range shifts may impact fisheries in the future we projected the distributions of EU's main fishing targets under different scenarios of greenhouse gas emissions and analysed the difference in current fishing effort acting upon species' present and future distributions. Future climatic conditions were separately predicted under scenarios RCP2.6 (an optimistic scenario that projects future climatic conditions under reduced emissions of greenhouse gases) and RCP8.5 (a pessimistic scenario that projects future climate if no changes to current greenhouse gas emissions are made).

To predict species' distributions, we employed state of the art ecological niche modelling. We combined the results of two predictive machine learning algorithms in a final ensemble that reflected species distributions. For benthic species, predictions were made considering only benthic variables and constricted to each species depth range. For pelagic and bentho-pelagic species the final distribution projection was a combination of predictions made with superficial and benthic variables. This allowed us to get a more reliable projection for species that inhabit any environment between their maximum depth range and superficial waters. We were therefore able to model species distributions across their latitudinal, longitudinal and depth ranges.

By highlighting variation in fishing effort inside species' future distributions we aim to provide information so management authorities are able to (i) better allocate fish stocks per country and (ii) restructure the distribution of fishing effort in a way that fishers are not as affected by climate change and target species are protected from overfishing.

Keywords: Fisheries management, Machine learning, Species distribution modelling

Christopher C.M. Baker (Kunming Institute of Zoology) with Douglas W. Yu, Yinqiu Ji, Viorel Popescu, Wang Lin, Qinzhong Wen and Naomi E. Pierce

Use of leech-derived iDNA to parameterise an occupancy model of vertebrate biodiversity in Ailaoshan Nature Reserve

06/25/2020 10:00:00 AM-10:15:00 AM

Session: High Throughput Community Data *(Chair: Doug Yu)*

Location: #acacia

Environmental DNA has great potential to complement or substitute for camera traps, while circumventing some of the logistical issues with equipment deployment and reducing taxonomic bias. We report here the first attempt to use leech-derived environmental DNA to estimate vertebrate occupancy at the scale of an entire protected area, the 677 sq. km Ailaoshan national-level nature reserve in Yunnan province, SW China. We contracted 163 park rangers to collect leeches in 172 patrol areas, resulting in 30,468 total leeches, divided over 893 replicate samples. Replicate samples were achieved by providing small, preservative-filled tubes, forcing each ranger to place their leeches into multiple tubes. We find that leech-derived DNA data can generate plausible and useful occupancy patterns for a wide range of vertebrates in a reasonable time frame. For instance, domestic species (cows, sheep, goats) have higher occupancy in park-edge patrol areas, while large mammal wildlife (e.g. sambar, black bear, serow, macaque) have higher occupancy in the reserve’s core. We tentatively conclude that iDNA can contribute to a protected-area effectiveness metric for vertebrate-biodiversity outcomes and also provide information on the spatial distributions and environmental and human-related correlates of vertebrate species, helping us to optimize the deployment of management resources within the reserve.

Keywords: Abundance/richness/diversity estimation, Community ecology, Distance sampling, Metagenomics, Occupancy analysis

Florian Hartig (University of Regensburg) with Maximilian Pichler

Scalability, accuracy and assumptions of joint species distribution models - a synthesis

06/25/2020 10:15:00 AM-10:30:00 AM

Session: High Throughput Community Data *(Chair: Doug Yu)*

Location: #acacia

In recent years, interest in ecology has shifted from analyzing the association of single species with their environment (as in standard species distribution / niche models) to the analysis of entire communities. Community data allows, at least in principle, to simultaneously infer the importance of biotic and abiotic factors for species distributions, which promises many new avenues for testing ecological theories and making predictions.

Most current statistical methods approach this task through a multivariate probit model, with a covariance matrix that is often further regularized through a latent variable structure. An issue for many current methods is that they often scale poorly on large datasets, which limits their use for emerging novel data sources, such as acoustic or eDNA data. A second question is the accuracy of the inference - to reduce the degrees of freedom in the covariance matrix, latent-variable models introduce an auxiliary latent-variable structure into the model, and it is somewhat unclear to which extent this structure creates bias or limitations on the fitted species interactions.

In this contribution, we will first summarize the statistical theory of estimating multivariate probit models. We will then compare how current software solutions scale for large datasets, and examine if latent-variable approaches create constraints on the species-species covariance matrix that limits their accuracy for inferring species associations. Finally, we will present an alternative and more flexible method for fast and scalable estimation of multivariate probit models.

Keywords: Community ecology, EDNA, Machine learning, Multivariate analysis/joint species distribution models

Emily McColl-Gausden (University of Melbourne) with Andrew Weeks, Josh Griffiths and Reid Tingley

The power of one (or many): A comparison between single and multi-species eDNA detection methods using site occupancy-detection models

06/25/2020 10:30:00 AM-10:45:00 AM

Session: High Throughput Community Data *(Chair: Doug Yu)*

Location: #acacia *Student*

Environmental DNA sampling (detection of extra-organismal DNA from environmental samples) can be used as a single-species or multi-species detection method. The relative sensitivity of these two methods may present a trade-off between target species' sensitivity, and the number of species detected. I compared the sensitivity of qPCR (single-species detection method) and metabarcoding (multi-species detection method) for detecting platypuses (target species) at 262 stream sites across the greater Melbourne region. I used two thresholds to declare a water sample positive for platypus using the single-species method 1) "high" requiring 2/3 positive replicate qPCRs, 2) "low" requiring 1/3 positive replicate qPCRs. I used hierarchical, site occupancy-detection models in a Bayesian framework to investigate how the method used impacted detection probability. Platypuses were detected at 127 (48%) or 73 sites (28%) using the single species method with the low or high threshold respectively, and 46 sites (18%) using metabarcoding. The results of this analysis suggest there is a trade-off between a single and multi-species detection method and that this result is sensitive to the threshold used. When using the low threshold, platypuses were more likely to be detected using the single-species method compared to metabarcoding. The direction of this relationship was certain. However, using the high threshold, the direction of the relationship became uncertain. My results show that eDNA is a promising new tool but is sensitive to thresholds and the detection method used. These data can help inform managers and researchers which eDNA sampling method is more appropriate for a study.

Keywords: Hierarchical modelling, Occupancy analysis

Otso Ovaskainen (University of Helsinki) with Tomas Roslin and David Dunson

LIFEPLAN: A planetary inventory of life - a new synthesis built on Big Data combined with novel statistical methods

06/25/2020 10:45:00 AM-11:00:00 AM

Session: High Throughput Community Data *(Chair: Doug Yu)*

Location: #acacia

I describe the ERC-synergy project LIFEPLAN (2020-2026) that has its main focus in statistical ecology: LIFEPLAN will develop new statistical methods for complex and big ecological data, it will use recently emerged methods to sample global biodiversity, and in particular it will apply the newly developed statistical methods to make sense of the global biodiversity data. I discuss the state of the art and future development needs for the following three areas that are in the core of LIFEPLAN: (1) sampling biodiversity with cost-effective and highly repeatable methods based on DNA, audio and image; (2) Automated species identification from DNA, audio and image, including robust uncertainty quantification; (3) Joint-species distribution modelling of very high-dimensional spatio-temporally structured ecological data. I discuss the state-of-the-art of these methods in the context of their application to global data on insects and fungi (DNA), and local case study data on birds (audio) and mammals (image).

Keywords: Camera trap data, Citizen science, Community ecology, Hierarchical modelling, Machine learning, Metagenomics, Multivariate analysis/joint species distribution models

Abouabdallah Mohamed Anwar (Pleiade, INRAE-INRIA-Miat INRAE) with Olivier Coulaud, Alain Franc and Nathalie Peyrard

Statistical learning for OTUs identification

06/25/2020 11:00:00 AM-11:15:00 AM

Session: High Throughput Community Data *(Chair: Doug Yu)*

Location: #acacia

Molecular based inventories are currently made rountinely with metabarcoding. However, comparisons with optical based inventories are scarce in micro-organisms. Here, we study whether a morphological based taxonomy and unsupervized clustering of amplicons on a same dataset provide the same picture of diversity. For OTU building, we implement both HAC and a novel approach based on the Stochastic Block Models (SBM).

Plants are among the best known organisms (both botanically and with molecular phylogenies). Therefore, we use a dataset of amplicons (trnH-psbA) of 1502 trees from an experimental plot in French Guiana, over a large spectrum of botanical diversity, identified by field botanists. We study whether the convergence/divergence of the 3 classifications depends on the taxonomic level addressed (order, family, genus). We deploy the HAC and test several aggregation methods. We deploy SBM with Poisson probability distribution to model the pattern of distances between sequences. Finally, we compare the 3 classifications we obtained by building contingency tables.

Preliminary result show that the convergence of the three methods depends on the distribution of intra and inter-class distances. For instance, in Magnoliales they are well differentiated and convergence is very good, whereas for the Gentianales convergence is poor and distances are not well differentiated.

Moreover, the SBM provides a matrix of parameters which quantify the connection between the classes. It is an excellent candidate for being a multivariate index of diversity, richer than a scalar one. Finally, we will discuss the issue of scaling of this approach to metabarcoding.

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Keywords: Abundance/richness/diversity estimation, Machine learning, Metagenomics

Sarah P. Saunders (National Audubon Society) with Walter Piper, Matthew T. Farr, Brooke L. Bateman, Nicole L. Michel, Henrik Westerkam, and Chad Wilsey

Synergistic impacts of anthropogenic-induced change on a climate-vulnerable waterbird

06/25/2020 12:15:00 AM-12:30:00 AM

Session: Landscapes and ecosystems *(Chair: Kiona Ogle)*

Location: #banksia

Climate and land-use variability play a crucial role in determining species distribution and abundance, but quantifying the relative impacts of these processes on current and future population trajectories remains elusive due to time lags, interactive effects, and data limitations. We developed a coupled integrated population model-Bayesian population viability analysis to project survival and reproductive success for common loons (Gavia immer) 10 years into the future (2020 - 2029) by linking vital rates to changes in climate and land use. Our model synthesizes long-term population survey, nest monitoring, and mark-resight data collected on nearly 200 lakes in northern Wisconsin. Cumulative summer rainfall was negatively related to fecundity, albeit this relationship was mediated by a lagged interaction with the winter North Atlantic Oscillation index. However, fecundity did not play a significant role in explaining annual variation in population growth. Adult survival was the largest contributor to population change, followed by juvenile survival, a latent parameter representing a mixture of survival from fledging to 3 y old and transition to the adult stage. The NAO during the winter preceding the breeding season, and annual changes in land use within breeding areas, had strongly negative influences on adult survival. We compared population viability under 12 future scenarios, and found that the smallest population sizes were predicted under positive NAO trend simulations, a pattern which is anticipated to occur with climate change. Our findings demonstrate how concurrent analysis of multiple data types collected over long time periods can provide a mechanistic understanding of the ecological implications of anthropogenic-induced change occurring at multiple spatial scales.

Keywords: Integrated population models

Christophe Botella (CNRS) with Maximilien Servajean, Benjamin Deneu, Pierre Bonnet, and Alexis Joly

GeoLifeCLEF, a cooperative evaluation campaign for species distribution methods

06/25/2020 8:00:00 AM-8:15:00 AM

Session: Citizen science and species distributions *(Chair: Janine Illian)*

Location: #banksia *Student*

Available geolocated species occurrences have drastically grown through citizen sciences projects, along with high resolution environmental data thanks to remote sensing technologies. We could thus refine the spatial grain of plant species distribution models (SDM) predictions down to a few meters, but occurrences fill a negligible part of space at this scale. In this context, deep learning SDM showed a significant improvement in performances but have a prohibitive development cost. To tackle this problem, we opened a cooperative annual campaign, called GeoLifeCLEF, to evaluate SDM prediction algorithms. GeoLifeCLEF was organized in 2018, 2019 and 2020. We compiled massive citizen sciences occurrences of many species and environmental data over large territories enabling participants to focus on developing algorithms. We evaluated of participants algorithms to predict the most likely plant species across space through a hidden test set of high quality geolocated occurrences. The participants wrote working notes describing their own methodology, while we analysed and summarized the results globally. GeoLifeCLEF confirmed the superiority of deep learning SDM, based on convolutional neural networks and environmental landscapes, compared to state-of-the-art SDM. It emphasized the relevance of multi-species models, capturing more robust environmental patterns, especially when they include non-plant species. However, it highlighted the difficulty of designing an unbiased evaluation procedure based solely on opportunistic occurrences, and also to handle the detection abilities, heterogeneous across species detections and datasets, in the model training. To our knowledge, this is the first example of totally reproducible, cooperative and open international evaluation campaign for SDM.

Keywords: Citizen science, GPS data, Interdisciplinary ecology, Machine learning, Multivariate analysis/joint species distribution models, Species distribution modelling

Ehsan Moqanaki (Norwegian University of Life Sciences)

Modelling site use of a large mammal community across a global biodiversity hotspot using landscape-scale citizen-science data

06/25/2020 8:15:00 AM-8:30:00 AM

Session: Citizen science and species distributions *(Chair: Janine Illian)*

Location: #banksia *Student*

Public surveys that include opportunistic sightings by local informants are increasingly used to map biodiversity across large geographic extents, especially for spatial conservation prioritization. We explored how analyzing these data with occupancy models can strengthen inferences by integrating data with different levels of reliability. We showcase an empirical assessment of site use for a threatened, large mammal community within a global biodiversity hotspot in the Southern Caucasus. We tested how the addition of less reliable (i.e. ambiguous) data can improve the identification of priority areas for species conservation. We found out when corrected for false positives, the addition of ambiguous detections will improve precision of parameter estimates for rare species (low occupancy) in our study system. This approach provided reliable estimates of probability of occurrence for multiple species simultaneously, irrespective of differences in rarity, detection probability, or home range size. Our approach is applicable to wide-ranging, rare or elusive species in human-dominated landscapes, where costly, large-scale non-invasive survey methods, such as camera trapping and DNA sampling, might be impractical.

Keywords: Citizen science, Community ecology, Hierarchical modelling, Occupancy analysis

Erik Kusch (Aarhus University) with Richard Davy

KrigR - An R Package providing an integrated workflow for downloading state-of-the-art climate data and statistically downscaling it to suit user demands

06/25/2020 8:30:00 AM-8:45:00 AM

Session: Citizen science and species distributions *(Chair: Janine Illian)*

Location: #banksia *Student*

Here we present a new R-package (KrigR) for acquiring and statistically downscaling climate data for ecological applications. The package is principally designed to make use of two of the most recent global reanalysis climate products from the European Centre for Medium Range Weather Forecasting: ERA5 and ERA5-land. These reanalysis products include numerous climate variables relevant for ecological applications including air temperature, precipitation, and soil moisture at hourly resolution and spatial resolutions of 30 by 30km and 9 by 9 km respectively.

Reanalysis products resolve issues of biases, discontinuities and inconsistencies within individual observational products (e.g. WorldClim, CRU), and represent the state-of-the-art knowledge on historical climate. While the hourly temporal resolution of the ERA5 data family marks a great improvement over many other climate data sets, this can be further improved using statistical downscaling to match the spatial resolution of such legacy datasets. Our package uses kriging to downscale the reanalysis output to a user-specified resolution, reliably up to one order of magnitude finer than the reanalysis product. Our approach in designing KrigR was to give the user as much freedom as possible while making the existing downloading and kriging methodology more streamlined. KrigR allows one to download any ERA5-family variable, at any given temporal resolution, in any chosen region (rectangular or as a shape) across the globe. Furthermore, while we supply the user with a downloading function for the covariates used for kriging, our kriging method does allow for user-input not generated by our download functions.

Keywords: Climate data, Climate reanalysis, Interdisciplinary ecology, Macroecology, R, R Package, Statistical downscaling

Saras Windecker (University of Melbourne) with Nick Golding

Integrating citizen science records, abundance estimates, and scat survey data in a species distribution model

06/25/2020 8:45:00 AM-9:00:00 AM

Session: Citizen science and species distributions *(Chair: Janine Illian)*

Location: #banksia *Student*

To make the most accurate prediction of a species' distribution it is important to make use of all relevant data, but heterogenous data types are each subject to their own bias from reporting rates or imperfect detection that must be accounted for. In this study we investigate statistical methods for data integration in a species distribution model, using the ringtail possum, Pseudocheirus peregrinus, in Victoria as a case study. We integrate broad spatial-scale presence-only data from citizen science records in the Atlas of Living Australia, dense but spatially restricted scat survey data, and abundance data from spotlighting surveys. Abundance estimates were collected across an intermediate spatial scale compared to the citizen science and scat survey data, allowing calibration between the tight structured and unstructured data types. We use a hierarchical Poisson point process GLM with separate bias models for each occurrence data type. This model-based data integration explicitly describes the differences in how each dataset was assembled, and propagates information contained in each while accounting for appropriate biases. This project advances the statistical methods currently in use for data integration in species distribution models.

Keywords: Abundance/richness/diversity estimation, Data integration, Hierarchical modelling, Spatio-temporal statistics, Species distribution modelling

Roozbeh Valavi (University of Melbourne) with Jane Elith, JosÃ© J. Lahoz-Monfort and Gurutzeta Guillera-Arroita

Block cross-validation for species distribution modelling: introducing the blockCV package

06/25/2020 10:00:00 AM-10:15:00 AM

Session: Presence-only data *(Chair: Yan Wang)*

Location: #banksia *Student*

Modelling species distributions involves relating species occurrences to relevant environmental variables. An important step in this process is assessing how well the model predicts the distribution of a target species. We generally do this by evaluating the predictions made for a set of locations that are not included in the model fitting process -i.e. independent data.

Since fully independent data are rarely available, a common approach involves sub-sampling the data available for modelling. In ecology, this usually involves splitting data into a training set (for model fitting) and a testing set (for model validation), and this can be repeated (e.g. for cross-validation).

Cross-validation is typically done randomly. So, testing points are sometimes located close to training points. As ecological data are often autocorrelated i.e. observations close to each other (in space or time) are more similar than distant ones, random splits can lead to an over-estimation of the model’s predictive power. Spatially-separated training and testing datasets can help determine whether the model performs as well in nearby locations as it does in more distant places.

Here we introduce a recently developed tool, written in the R programming language that generates spatially or environmentally separated cross-validation folds and includes functionalities that helps modellers make informed decisions about the choice of block cross-validation techniques. The package blockCV enables ecologists to more easily implement a range of evaluation approaches that will contribute to robust estimation of the predictive performance of species distribution models.

Keywords: Block cross-validation, Model evaluation, Spatial autocorrelation, Species distribution modelling

Ian Renner (University of Newcastle) with Olivier Gimenez and Julie Louvrier

Extending the combined likelihood toolkit for species distribution models fitted to multi-source data

06/25/2020 10:15:00 AM-10:30:00 AM

Session: Presence-only data *(Chair: Yan Wang)*

Location: #banksia

As the availability of species data grows, there is an increasing need to build species distribution models that account for multiple data types. Some recent developments in this area involve a combined likelihood framework in which the log-likelihood expressions for the individual data sources are added together. Often, these developments make use of presence-only data and consequently incorporate the log-likelihood expression of a Poisson point process model for such data.

However, what if a Poisson point process model is not appropriate for the given data and covariates? Furthermore, how can we address potential overfitting through the inclusion of uninformative covariates? In this talk, I will present a new combined penalised likelihood framework we have developed to address these questions through the incorporation of a broader class of point process model likelihood expressions and lasso-type penalties. I will demonstrate via simulation the benefits of this approach over standard combined likelihood in the presence of spatial dependence and overfitting, and apply the new method to model the distribution of the Eurasian lynx in the Jura Mountains of France.

Keywords: Citizen science, Data integration, Penalised likelihood, Point process models, Species distribution modelling

Guido A. Moreira (Federal University of Rio de Janeiro) with Dani Gamerman

Logistic modelling of point process: a Bayesian approach for presence-only data

06/25/2020 10:30:00 AM-10:45:00 AM

Session: Presence-only data *(Chair: Yan Wang)*

Location: #banksia *Student*

Species distribution models (SDMs) are extremely useful for determining preferences and habitats for different species. Appropriate estimation of species distribution depends on the adequate random sampling scheme which isn’t always available. Instead, data is frequently composed of georeferenced locations where the species has been observed, which is commonly referred to as presence-only (PO) data.

In 2018, a model was presented in the ISEC conference intended to be used on such data. It uses an Inhomogeneous Poisson Process without the need to approximate the intractable integral in its likelihood function.

The model has had improvements that result in faster MCMC convergence. Results are shown on real data sets from Brazil and Australia, comparing it with the already established MaxEnt, MaxLike and traditional log-linear IPP models. AUC metric is calculated with full posterior uncertainty taken into account.

The proposal still keeps the properties of the model previously presented, such as calculating the likelihood function without approximating it and dealing with the unidentifiability issue that usually accompanies such model when it comes to the intensity observer bias covariates.

The work is presented with as few technical terms as necessary in order for the innovation to be understood by ecologists and Statisticians alike.

Keywords: Population ecology, Species distribution modelling

Stephanie Elizabeth Hogg (RMIT University) with Yan Wang and Lewi Stone

Modelling Dependencies between Species for Presence-Background Data

06/25/2020 10:45:00 AM-11:00:00 AM

Session: Presence-only data *(Chair: Yan Wang)*

Location: #banksia *Student*

For species distribution models, presence background (PB) data is more commonly available than survey data. PB data can be modelled as a spatially distributed point process, and Inhomogeneous Poisson Point process (IPP) models have been used mostly in species distribution modelling with success. However most such models have assumed species independence when applied to multiple species studies. Examination of actual multi-species presence-background data also reveals that there are strong spatial and interspecies interaction existing after controlling for environmental impact. In this paper, we proposed a new Multivariate Gaussian Process (MGP) model to predict the multiple species' niche by incorporating both inter-species interaction and spatial correlations into consideration. The model performance has been explored and validated by simulation studies. We also applied the MGP model to a multiple forest species data in south-east Australia. The MGP model was shown to outperform the existing models assuming independences (IPP models), or models that assume either species independence or no spatial correlation.

Keywords: Model assessment/validation, Multivariate analysis/joint species distribution models, Species distribution modelling

Elliot Dovers (UNSW Sydney) with David Warton, Gordana Popovic and Wesley Brooks

Fast approximations for fitting log-Gaussian Cox Processes to presence-only data

06/25/2020 11:00:00 AM-11:15:00 AM

Session: Presence-only data *(Chair: Yan Wang)*

Location: #banksia

Presence-only data are a potential source of important information about species' distributions, although difficult to model because of uncontrolled sources of variation and biased sampling due to opportunistic collection. Log-Gaussian Cox processes (LGCP) offer a framework to handle such records. The latent Gaussian random field has the capacity to deal with unmodelled sources of clustering, and account for correlation across different species (in a multi-species model) or across different data sources (when combining data across species). Such a hierarchical structure lends itself to inference via Monte Carlo sampling methods where lengthy computation times abound. We have developed a fast approximation method that considers the LGCP as a type of extension of generalised linear mixed models (GLMM). Three aspects comprise our novel approach. First, variational approximation permits a closed-form approximation to the marginalised log-likelihood. Second, a rank reduced approximation to the large, spatial variance-covariance matrices enables computation where these would be otherwise restrictive. Finally, automatic differentiation is used to quickly obtain gradient information for efficient optimisation and inference. This talk will further describe the methodology, illustrated and assessed via application to both simulated and real data.

Sina Mews (Bielefeld University) with Roland Langrock, Ruth King and Nicola Quick

Multi-state capture-recapture in continuous time

06/25/2020 8:00:00 AM-8:15:00 AM

Session: Continuous times models *(Chair: Charlotte Jones-Todd)*

Location: #corymbia *Student*

Our modelling approach is motivated by individual sighting histories of bottlenose dolphins off the east coast of Scotland. Due to ongoing offshore development, conservation managers seek to better understand the temporal movement patterns of the dolphin population between different sites. The Arnason-Schwarz (AS) model is often used to analyse such transitions between different states, which here correspond to the location (site) of a given individual. Within the AS model, transitions between states are modelled using a discrete-time Markov chain. In our case, however, the capture occasions do not follow a regular sampling protocol, which is why we develop a continuous-time analogue of the AS model. In contrast to the AS model, the new modelling framework does not require capture occasions to be regularly spaced in time.

Statistical inference is carried out by regarding the capture-recapture data as realisations from a (continuous-time) hidden Markov model (HMM). Embedding the capture-recapture setting in the HMM framework allows the associated efficient algorithms to be used in particular for (numerical) maximum likelihood estimation and state decoding. For scenarios with time-varying covariates affecting the state-switching rates, we develop an approximate maximum likelihood approach.

In our present analysis, we are particularly interested in seasonal effects on the migration rates of bottlenose dolphins along the Scottish east coast. The results reveal seasonal migration patterns between two main areas, information that can help to inform conservation management. While motivated by a particular data set, our modelling framework is generally applicable to irregularly sampled capture-recapture data where individuals traverse through different states.

Keywords: Capture-mark-recapture

Paul G. Blackwell (University of Sheffield)

Continuous-time Hidden Markov Models for Animal Movement

06/25/2020 8:15:00 AM-8:30:00 AM

Session: Continuous times models *(Chair: Charlotte Jones-Todd)*

Location: #corymbia

The modelling of animal movement in continuous time is increasingly recognised as important in principle, but is often neglected due to issues of computational cost as well as lack of familiarity.

I will show how, with the right perspective, a continuous-time movement model with switching between behaviours can be written as a Hidden Markov Model (HMM). This enables the use of HMM-type algorithms to evaluate the likelihood, leading to statistical analysis that is much faster than existing methods and that scales much better with the number of observations, addressing key limitations of Blackwell et al (2016). In addition, the HMM formulation means that models can be written in a way that is much more familiar to practitioners. This approach helps to broaden the applicability of the benefits of recent advances in standard discrete-time HMMs as well as shedding light on some of their potential pitfalls.

I will illustrate these ideas with applications to real data-sets, both `homogeneous', extending the dynamic Brownian bridge approach of Kranstauber et al (2012), and `heterogeneous', where behaviour is dependent on a spatial covariate.

References

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Keywords: Hidden Markov models, Movement modelling

Richard Glennie (University of St Andrews)

Continuous-time behaviour-switching animal movement modelling by maximum likelihood

06/25/2020 8:30:00 AM-8:45:00 AM

Session: Continuous times models *(Chair: Charlotte Jones-Todd)*

Location: #corymbia

Animal movement analyses often contend with three concurrent issues: locations are recorded irregularly in time, locations are recorded with measurement error, and animals exhibit different behaviours over time. Two current approaches that account for these components are fully Bayesian MCMC (Michelot et al. 2019) and two-stage models with multiple imputation (McClintock 2017). The MCMC approach can be slow, due to reconstruction of the behaviour state process, but is exact, while the two-stage approach is easier to implement using hidden Markov models, but the two stages do not form a single, coherent model. Here, we propose a one-stage continuous-time behaviour-switching animal movement model that can account for measurement error and can be fit by maximum likelihood. A system of Fokker-Planck partial differential equations describe how the probability density function (PDF) of an animal's location and behaviour change over time (Pedersen 2011). This PDF is approximated in space by a finite element method which reduces the system of equations to a single matrix differential equation which can solved exactly with Krylov sparse matrix exponential methods, requiring no time discretization or reconstruction of the behaviour process. The sparse matrices and finite-dimensional approximation allow this method to efficiently estimate behaviours and animal movement parameters jointly within the standard maximum likelihood framework. The method is compared to the two current approaches by simulation study and within real data analyses. This new method provides a compromise between the exact, coherent MCMC implementation and the more efficient, two-stage multiple imputation approach.

Keywords: Movement modelling

Katie T Bickerton (Institute of Zoology, ZSL/ University of Kent)

Mark-recapture modelling to inform conservation management in Mauritius

06/25/2020 10:00:00 AM-10:15:00 AM

Session: Contributed talks *(Chair: Birgit Erni)*

Location: #corymbia *Student*

Conservation translocations involve the deliberate movement of organisms to improve the conservation status of a population, species or ecosystem, and are being increasingly used by conservation ecologists and managers. Management decisions informing translocations are complex and rarely make use of ecological modelling prior to movement, even when the data are available. Mauritius once contained a rich and diverse reptile assemblage; however, many species are now either extinct or threatened due to habitat destruction and introduced mammalian predators. One species under threat is the lesser night gecko (Nactus coindemirensis), which is now restricted to four outlying islands, of which three are smaller than 0.025km2. The population on Ile Marianne, one of the three smaller islands (0.022km2), is present due to a translocation undertaken in 2011. Released individuals were either (1) wild caught from a nearby island, or (2) captive bred from Jersey Zoo and are uniquely identifiable by their dorsal markings. We have undertaken 8 years of post-release monitoring using mark-recapture techniques to estimate survival and abundance. The results from this study suggest that certain biotic factors, such as size, make individuals better suited to translocation, and abiotic factors, such as moonlight and temperature, can alter capture success during surveys. These results will be used to inform future translocations and post release monitoring schemes of lesser night gecko in more complex ecosystems, such as one proposed for Round Island in 2020.

Keywords: Capture-mark-recapture, Conservation ecology, Conservation Management

Jennifer Pohle (Bielefeld University) with Timo Adam, Roland Langrock and Larissa T. Beumer

Flexible estimation of the state dwell-time distribution in hidden semi-Markov models

06/25/2020 10:15:00 AM-10:30:00 AM

Session: Contributed talks *(Chair: Birgit Erni)*

Location: #corymbia *Student*

In a basic hidden Markov model (HMM), the state dwell time, i.e. the number of consecutive time points spent in a given state, follows a geometric distribution with modal dwell-time being one. This can be unrealistic in ecological applications, for example when a ruminant's movement is subject to specific behavioural rhythms. Hidden semi-Markov models (HSMMs) generalise HMMs by explicitly modelling the time spent in a state, the so-called dwell-time distribution, using some distribution on the positive integers. Typical choices for the state dwell-time distribution in applications are parametric distributions such as Poisson or negative binomial, but this again a priori restricts the overall shape. To avoid such restrictive assumptions, we developped a fully data-driven penalised maximum likelihood approach for fitting HSMMs without the need to specify a distributional assumption for the state dwell times. The proposed method can either be used for direct modelling purposes, or as a basis for subsequent modelling choices, for example in order to decide whether an HMM would be appropriate for the data at hand, or what distributional assumption may be adequate within a conventional HSMM. The approach is illustrated using animal movement data from muskoxen (Ovibos moschatus) tracked in Greenland.

Keywords: Dynamic state models

Michael G. Walsh (University of Sydney) with Siobhan M. Mor, Hindol Maity, Shah Hossain

A preliminary ecological profile of Kyasanur Forest disease virus hosts among the mammalian wildlife of the Western Ghats, India

06/25/2020 10:30:00 AM-10:45:00 AM

Session: Contributed talks *(Chair: Birgit Erni)*

Location: #corymbia

Kyasanur Forest disease (KFD) is one of India’s most severe arboviruses and has been expanding beyond its historical endemic locus at an alarming rate over the last two decades. The natural nidus of this zoonosis is located in the monsoon rainforest of the Western Ghats of Karnataka, India, which is one of the world’s most important biodiversity hotspots. Definitive reservoir hosts for KFD virus (KFDV) have yet to be delineated, and thus much of the infection ecology of this virus, and its consequent transmission dynamics, remains uncertain. This uncertainty has been exacerbated by diminished research efforts in wildlife surveillance over the last two decades, coinciding with the expansion of the range of KFD across the region. The current investigation sought to define a preliminary ecological profile of KFDV hosts based on their life history and feeding traits to aid in re-establishing targeted wildlife surveillance and to discern those ecological traits of wildlife hosts that may improve our understanding of KFD epidemiology. We compared mammalian traits between host and non-host species using general additive models. This study found that both body mass and forest forage were strongly associated with mammalian host infection status, but that reproductive life history traits were not. These findings will help in structuring ecologically based wildlife surveillance and field investigations, while also helping to parameterise novel epidemiological models of zoonotic infection risk that incorporate species functional traits in a region where biogeography, landscape ecology, and community ecology manifest extraordinary complexity.

Keywords: Disease ecology, Interdisciplinary ecology, Trait based ecology

Magdalena M. Mair (University of Regensburg) with Florian Hartig

How to test for the absence of an effect - an overview of methods and approaches

06/25/2020 10:45:00 AM-11:00:00 AM

Session: Contributed talks *(Chair: Birgit Erni)*

Location: #corymbia

Most scientific projects are designed to show the presence of effects. Standard hypothesis tests with a point null hypothesis at zero are designed exactly for this goal. For some research questions, however, for example drug or pesticide approval, the goal is the opposite: to decide whether there is no effect. Standard hypothesis tests are ill-suited for this purpose, because they are asymmetric: a non-significant result is inconclusive, and does not indicate that the null hypothesis is correct. Parameter estimates and confidence intervals could be interpreted instead, but if the goal is to make a decision about the absence of an effect, they have to be converted into a dichotomous value. Here, we review and compare different methods that have been suggested in the literature for deciding whether the absence of an effect has been sufficiently demonstrated. We discuss their advantages and weaknesses using theory and simulation, and argue that the inclusion of these methods in our own statistical toolbox opens up valuable opportunities to broaden the type of questions we can address in our research.

Keywords: Study design

Jasper A. Slingsby (South African Environmental Observation Network (SAEON)) with Glenn R. Moncrieff and Adam M. Wilson

A core model for forecasting the dynamics of a fire-prone ecosystem

06/25/2020 11:00:00 AM-11:15:00 AM

Session: Contributed talks *(Chair: Birgit Erni)*

Location: #corymbia

Longitudinal ecological studies are commonly limited in their spatial grain and extent, relying on regular, continuous global measurements of vegetation properties from satellites to extrapolate to a broader context. This is readily feasible for ecosystems with easily interpretable changes in the temporal vegetation signal, but is far more complex for ecosystems subject to stochastic natural disturbance events and post-disturbance recovery trajectories. We have developed a time-series model to monitor and predict natural land surface processes and evaluate near real-time changes in the state of a crown fire-dependent and seasonally fluctuating ecosystem, the Fynbos of South Africa. The model allows near-real time estimation of above ground biomass, impacts on streamflow, and detection of anomalous vegetation signals such as high mortality, vegetation clearing, or invasion by alien trees. The modelling framework is particularly novel in that it also allows estimation of the factors that drive variation in post-fire recovery, such as climatic, edaphic, or vegetative properties such as plant traits. Our core model is highly flexible and ideal for exploring the drivers of multiple ecosystem functions within one framework. It also tests our understanding of the ecosystem, guiding further sampling and research, and iteritive updating of the model, data and forecasts.

Keywords: Ecological stability and resilience, Ecosystem ecology, Hierarchical modelling

Aline Magdalena Lee (Norwegian University of Science and Technology) with Eva Fuglei, John-AndrÃ© Henden and Ä¹shild Pedersen

Using stochastic modeling to overcome data limitations - a case study on Svalbard rock ptarmigan

06/25/2020 8:00:00 AM-8:15:00 AM

Session: Design and estimation *(Chair: Louise McMillan)*

Location: #darwinia

One of the major challenges for our ability to understand and predict population dynamics in species of management concern is limited data. Recently, concern was raised about the population dynamics of the Svalbard rock ptarmigan (Lagopus muta hyperborea) when a study indicated that the total population size might be declining, despite the number of territorial males, which is regularly monitored, having stayed constant. The suggestions that an unknown nonbreeding segment of the population could be buffering the breeding population and masking an ongoing decline raised an urgent need to better understand the demography of the population. However, because monitoring has been based on censuses of territorial males and hunting data, it has previously proven difficult to study their demography in greater detail. Here, we show how we used stochastic modeling to improve our understanding of the demography of this species, despite extremely scarce data, as well as to pinpoint what type of data should be collected in the future. We used a Bayesian framework to combine the available data with parameter distributions from the literature and local knowledge of population processes. In this way different scenarios that could cause observed patterns in monitoring data and hunting output were identified. Simulations were used to quantify expected population trajectories in the most likely scenarios. Importantly, we also combined our model with simulations of data to compare different data collection schemes and identify ones with the most potential to improve our understanding of Svalbard rock ptarmigan population dynamics in the future.

Keywords: Hierarchical modelling, Population dynamics, Population ecology

Nilanjan Chatterjee (Wildlife Institute of India) with Bilal Habib

Estimating population density of uniquely unidentifiable species from camera traps

06/25/2020 8:15:00 AM-8:30:00 AM

Session: Design and estimation *(Chair: Louise McMillan)*

Location: #darwinia *Student*

Camera trap surveys are increasingly becoming popular in collecting data cost-effectively for multiple species. Density estimation is challenging for elusive and cryptic species occurring in low densities. For species that lack phenotypic traits that aid in individual identification, photo recaptures do not come handy. Advances in statistical techniques have facilitated the analysis of camera trap data allowing concurrent density estimation of multiple species. We used data from camera trap field surveys conducted across multiple years in deciduous forests of Maharashtra, India, to estimate the densities of small carnivore species through an extension of spatial count models. These models are an extension of spatial capture-recapture models that enable the density estimation of species lacking characters allowing individual identification using a latent variable approach. We used both informative and non-informative priors to evaluate effectiveness of the model. The density estimates were not significantly different across informative and non-informative priors. Although there are no prior density estimates available for study species, we compared the density estimates with individually identifiable species of similar body size. The density estimates from our studies and past published studies had overlapping confidence intervals. We also recommend the modification of the sampling grid size based on the target species aiming to minimize spatial auto-correlation. Camera traps can be used for economical and effective long-term monitoring projects enabling the simultaneous estimation of multiple species' densities with carefully designed sampling designs. As this approach does not require species to be individually identifiable, it has wide applicability and replicability for other species.

Keywords: Camera trap data, Population ecology, Spatial capture-recapture

Ian Durbach (University of St Andrews) with Chris Sutherland, Koustubh Sharma and David Borchers

Approximately optimal survey design for spatial capture-recapture

06/25/2020 8:30:00 AM-8:45:00 AM

Session: Design and estimation *(Chair: Louise McMillan)*

Location: #darwinia

Spatial capture-recapture methods use the location of detectors and the locations at which animals were detected to estimate animal density. Despite the often large expense and effort involved in placing detectors in a landscape, there has been relatively little work on how detectors should be located. A natural criterion is to place traps so as to maximize the precision of density estimates, but the lack of a closed-form expression for precision has made optimizing this criterion computationally intractable. Recent results by Efford and Boulanger (2019) show that precision can be well approximated by a function of the expected number of detected individuals and expected number of recapture events, both of which can be evaluated at low computational cost. We use these results to develop a method for obtaining survey designs that optimize this approximate precision, and are thus approximately optimal survey designs for studies using count or binary proximity detectors, or multi-catch traps. We show how the basic design protocol can be extended to incorporate non-uniform distributions of activity centers and heterogeneous space use by animals, and illustrate our approach by simulating from a camera trap study of snow leopards in Mongolia. Improvements in the precision of density and abundance estimates is scenario-dependent but in our experiments varied from <1% to 26%. The designs remove the need for subjective decisions about detector placement, or at least provide guidance to inform such decisions.

Keywords: Camera trap data, Spatial capture-recapture

Kathryn Knights (University of Melbourne) with Mick McCarthy, James Camac and Gurutzeta Guillera-Arroita

Efficient effort allocation in line-transect distance sampling of high-density species: when to walk further, measure less-often and gain precision

06/25/2020 8:45:00 AM-9:00:00 AM

Session: Design and estimation *(Chair: Louise McMillan)*

Location: #darwinia *Student*

We present a method that improves the efficiency of line-transect distance sampling when the target species is high-density. A proportion of distances to detected targets are measured to model the detection function, and the time saved on the survey is used to cover a longer total length of transect and accrue a larger "count only" sample. This approach can improve the precision of the population density estimate relative to conventional distance sampling when the cost of measuring the distance to a detected target is high relative to the cost of walking to the next target. We derive an expression for the optimal proportion of distances to measure (to minimise the variance of the density estimate) using the delta method approximation of variance and relating this mathematically to the overall budget and costs. We use a further expression to predict the benefit in precision of using the optimised approach compared with conventional distance sampling. Our simulated distance sampling data indicates that the optimised method delivers benefits in precision, and we find that, in all three of our case studies on Australian plants, the optimised approach could improve the precision gained from a distance sampling survey, with the degree of benefit being ~20-50%. This new approach could broaden the ecological contexts in which distance sampling is applied, for instance, to include estimation of densities of highly abundant taxa where plots are conventionally used, multispecies surveys or those using cues or signs that occur at high-density.

Keywords: Abundance/richness/diversity estimation, Distance sampling

Riki Herliansyah (University of Edinburgh/ Kalimantan Institute of Technology) with Ruth King, Stuart King and Bruce Worton

Fast-Automatic Differentiation for Estimating Capture-Recapture Models in the presence of the Individual Heterogeneity

06/25/2020 10:00:00 AM-10:15:00 AM

Session: Capture-recapture *(Chair: David Borchers)*

Location: #darwinia *Student*

Capture-recapture studies are common for obtaining data on wildlife population. Associated individual heterogeneity capture-recapture models are popular to incorporate unobserved heterogeneity. Incorporating these unobserved random effects is challenging as one has to integrate the corresponding random effect terms out within the observed data likelihood which does not have a closed form. Thus, previous approaches include numerical integration schemes as well as Bayesian data augmentation technique. As the number of individuals observed and/or capture occasions increases, however, the methods can suffer from the computational expense required to fit the models to the data. We consider the promising approach of approximating the analytically intractable integral in the likelihood via Laplace approximation which has the accuracy of order 1/n where n is the number of observations implying the accuracy increases with the increasing sample size. We conduct a simulation study to assess the performance of the Laplace approximation for both closed and open capture-recapture models, extending the traditional Laplace approximation to higher order, for improved accuracy. In order to evaluate the higher order derivatives required in the approximation, we use automatic differentiation, and the package Template Model Builder (TMB). Finally we compare different numerical integration schemes for a real data study, both in terms of accuracy and computational resources.

Keywords: Capture-mark-recapture

Res Altwegg (University of Cape Town) with Chris Barichievy

Estimating poaching mortality of rhinos

06/25/2020 10:15:00 AM-10:30:00 AM

Session: Capture-recapture *(Chair: David Borchers)*

Location: #darwinia

Conservation interventions on black rhino (Diceros bicornis) are often directed towards those that limit poaching, but are they successful? We developed a Jolly-Seber-type model to estimate survival, recruitment and poaching mortality from capture-mark-resighting data of marked individuals. Important derived estimates were population size and the number of rhinos killed by poachers. Our model accounted for differences between age classes, sex and management section, and for the fact that individuals are often translocated between conservation areas. We implemented the model as a multi-state model in a Bayesian framework and tested it on 25 years of monitoring data from two sections with contrasting rhino densities in Tsavo West National Park, Kenya. We estimated annual survival probabilities to be 0.98 for females and 0.97 for males. The estimated population growth rate was positive. Poaching mortality was slightly higher than natural mortality and its reduction could increase the population growth rate. Even though the carcass detection probability was low, comparing the number of unidentified carcasses against the number of individuals estimated to have a low probability of being alive suggested that the model was able to account for almost all animals and their cause of death. The model further suggested that previous management interventions aimed at reducing densities (e.g. translocation) were successful at increasing the population growth rate. We now plan to use this model to guide a type of investment in rhino conservation that is based on payments for results.

Keywords: Capture-mark-recapture, Hierarchical modelling, Population dynamics, Population ecology

Wei Zhang (University of California, Berkeley) with Simon J. Bonner and Rachel S. McCrea

Latent multinomial models for extended batch mark data

06/25/2020 10:30:00 AM-10:45:00 AM

Session: Capture-recapture *(Chair: David Borchers)*

Location: #darwinia

The latent multinomial model (LMM) provides a general framework for modelling data from mark-recapture experiments in which individuals' true capture histories may not be observed. In essence, the model considers the true histories as latent variables that are mapped to the observed data through a known linear transformation. The likelihood for these models is generally intractable because it can only be evaluated by summing over all possible configurations of the true histories consistent with the observed counts. However, Zhang et al. (2019, Biometrics 75, 723-733) proposed a general and fast maximum likelihood method based on the saddlepoint approximation, making it much easier to fit these models.

We show how models from batch marking experiments can be cast as a LMM and then be fitted easily by the saddlepoint method. Batch marks are commonly used when it is costly or impractical to apply individual marks. However, the data obtained from batch mark studies is harder to model because the exact capture histories cannot be known. Only the counts of initially marked, recaptured (previously marked), and unmarked individuals on each sampling occasion can be observed. The model structure we develop is flexible and easily extended to incorporate data collected from more complex studies (e.g., the robust design) and to combine data from both marked and unmarked individuals into the same analysis. We apply our methods to study survival rates and trends in abundance of the golden mantella (Mantella aurantiaca), a small terrestrial frog endemic central Madagascar that is critically endangered.

Keywords: Capture-mark-recapture

Ruth King (University of Edinburgh) with Blanca Sarzo

Capture-recapture: dealing with the challenges of quantity

06/25/2020 10:45:00 AM-11:00:00 AM

Session: Capture-recapture *(Chair: David Borchers)*

Location: #darwinia

Capture-recapture data and associated models have a long history which has seen significant development in the last 50 years. However, a new challenge is emerging with large (long-term) studies in that it can be that fitting the many now standard models is becoming computationally challenging. This is because many statistical techniques do not scale in a computationally feasible manner. To motivate the problem we will consider a capture-recapture study relating to common guillemots where we wish to fit a standardindividual random effect model in relation to the associated survival and/or recapture probabilities to reflect individual heterogeneity. Such models can be easily fitted with BUGS/JAGS using a Bayesian data augmentation technique. However for the given dataset there are nearly 30,000 ringed individuals, which is continuing to increase annually. Due to the size of the dataset (and associated model) even simple Cormack-Jolly-Seber models with individual (continuous) heterogeneity become computationally expensive to fit (on the scale of days), so that fitting multiple competing models and checking convergence or other associated diagnostics starts to become infeasible. We will describe a subsampling scheme for obtaining a smaller data sample which can be fitted within BUGS/JAGS within a significantly shorter timescale and the associated sampled parameter values corrected to obtain an approximate sample from the full dataset.

Keywords: Capture-mark-recapture, Individual-based models

Kiona Ogle (Northern Arizona University) with Drew Peltier, Jessica Guo, and Jarrett Barber

A Bayesian approach to quantifying time-scales of influence and ecological memory

06/25/2020 9:00:00 PM-9:50:00 PM

Location: #acacia *Plenary (Chair: Peter Vesk)*

Many time-varying ecological processes are influenced by both concurrent and antecedent (past) conditions; in some cases, antecedent conditions may outweigh concurrent influences. The time-scales over which environmental conditions influence processes of interest (e.g., photosynthesis, carbon and water fluxes, tree growth, ecosystem productivity) are not well understood, motivating our development and application of the stochastic antecedent modeling (SAM) approach. The SAM approach is applied to ecological time-series data within a Bayesian statistical framework to quantify ecological memory. We use "memory" to broadly describe time-scales of influence, including the importance of antecedent conditions experienced at different times into the past, potentially revealing lagged responses. The coupled Bayesian-SAM approach, however, can lead to computational inefficiencies, and we describe reparameterization "solutions" to address such issues. To illustrate, we apply the approach to responses operating at distinctly different time-scales: annual tree growth (e.g., tree-rings widths) and sub-daily plant physiological responses (e.g., indices of stomatal behavior). Our Bayesian-SAM applications to tree growth in arid and semi-arid regions has identified particular seasons or individual months during which climatic conditions (e.g., precipitation inputs or temperature) are most influential to subsequent tree growth; in many cases, conditions experienced 2-4 years ago continue to influence growth. The analysis has also revealed novel, multi-day lagged responses of plant stomatal behavior and water stress status to soil and atmospheric moisture conditions. In general, the Bayesian-SAM approach has demonstrated that ecological memory is an important process governing plant and ecosystem responses to environmental perturbations.

Hideyasu Shimadzu (Loughborough University)

Modelling temporal species interactions in an ecological community

06/25/2020 10:30:00 PM-10:45:00 PM

Session: Interactions and study design *(Chair: Morgan Tingley)*

Location: #acacia

Understanding the temporal interaction amongst species within an ecological community has been a critical challenge in ecological research. Often the species interaction possesses a feedback mechanism, in which the outputs of the past can be the inputs to the current state of the processes. Given the observations of multi-species time series, we developed a time series model for a multivariate feedback system, assuming linear interactions between the species as a tractable approximation. The feedback model is then analysed in the spectrum domain to examine the extent to which the abundance of a given species is driven by other species at different frequency ranges, in other words, longer or shorter time lag effects as interactions. The results show that the modelling approach delineates new insights into species interaction. We demonstrate how it enables further analysis into ecologically relevant groups of species that underpin the dynamics of the system.

Keywords: Abundance/richness/diversity estimation, Community ecology

Elizabeth W. Eisenhauer (Pennsylvania State University) with Ephraim Hanks

A lattice and random intermediate point sampling design for animal movement

06/25/2020 10:45:00 PM-11:00:00 PM

Session: Interactions and study design *(Chair: Morgan Tingley)*

Location: #acacia *Student*

Animal movement studies have become ubiquitous in animal ecology for the estimation of space use and the analysis of movement behavior. In these studies, animal movement data are primarily collected at regular time intervals. We propose an irregular sampling design that could lead to greater efficiency and information gain in animal movement studies. Our novel sampling design, called lattice and random intermediate point (LARI), combines samples at regular and random time intervals. We compare the LARI sampling design to regular sampling designs in an example with common black carpenter ant location data, an example with guppy location data, and a simulation study of movement with a point of attraction. We modify a general stochastic differential equation model to allow for irregular time intervals and use this framework to compare sampling designs. When parameters are estimated reasonably well, regular sampling results in greater precision and accuracy in prediction of missing data. However, in each of the data and simulation examples explored, LARI sampling results in more accurate and precise parameter estimation and, thus, better prediction of missing data as well. This result suggests that researchers might gain greater insight into underlying animal movement processes by choosing LARI sampling over regular sampling.

Keywords: Movement modelling, Sampling design

Loic Chalmandrier (University of Canterbury/ University of Regensburg) with Florian Hartig, Loic Pellissier, Daniel Stouffer

Calibrating community models through functional traits

06/25/2020 11:00:00 PM-11:15:00 PM

Session: Interactions and study design *(Chair: Morgan Tingley)*

Location: #acacia

Community models, e.g. Lotka-Volterra models, have been recently advocated as a response to the limitations of correlative biodiversity modelling approaches. In particular, the inclusion of calibrated biotic interactions is a challenge that has yet to be solved to provide reliable predictions at small spatial scale. Ecological theory has produced multiple models that can act as a basis for that purpose; they have been extensively used to demonstrate theoretical properties of communities and provide insights into the causes of biodiversity structure. However because they often require the estimation of a large number of parameters, their direct fit to empirical data has often been limited to simplified experimental settings, thus strongly limiting their use for ambitious modelling projects. Here we propose a way forward by presenting a modelling framework that relates functional trait data to the parameters of a community model. Our approach specifically uses a transfer function between the empirical functional traits and the phenomenological demographic rates from the model (e.g. growth rate, interaction coefficients). The transfer function is then calibrated to maximize the fit of the model to species abundance data while making limited assumptions about the relationship between demographic rates and functional traits. We demonstrate the value of this approach on several datasets of herbaceous communities. We then discuss the perspectives and limits of the approach. Our approach outlines a flexible methodology to more easily fit and compare community models on species-rich systems by drastically decreasing the number of parameters to estimate while making strategic use of increasingly available trait data.

Keywords: Abundance/richness/diversity estimation, Community ecology, Mechanistic models, Theoretical ecology, Trait based ecology

Hao Ran Lai (University of Canterbury) with Daniel B. Stouffer

The role of higher-order biotic interactions on tropical tree growth

06/25/2020 11:15:00 PM-11:30:00 PM

Session: Interactions and study design *(Chair: Morgan Tingley)*

Location: #acacia

Growth in individuals' size or biomass is a key demographic component in population models, with wide-ranging applications from quantifying species performance across abiotic or biotic conditions to assessing landscape-level dynamics under global change. In plant systems, a branch of ecology focuses on how individual tree growth responds to biotic interactions. To date, most studies only examine the direct competitive or facilitative interactions between species pairs, despite the increasing evidence for demography to be driven by indirect interactions when additional species interfere with the direct, pairwise interaction through intrasitive loops or non-additivity. Indirect interactions may prevent a species from extirpation by countering strong direct competitive interactions, thereby maintaining diversity especially in species-rich systems. Using a tropical tree community dataset, we built a size-dependent diameter-growth model for individuals across ten woody-plant species, and then allowed both direct and indirect interactions within communities to influence the species-specific growth parameter in a generalized Lotka--Volterra fashion. Specifically, indirect interactions enter the model as higher-order quadratic terms, i.e. non-additive effects of conspecific and heterospecific neighbour size on the focal individual's growth. The model that includes higher-order interactions is more supported (as judged but WAIC) than the model that includes only direct interactions, despite the former containing a far greater number of parameters. In general, higher-order interactions have comparable magnitudes but opposite directions than direct interactions. In other words, higher-order interactions tend to counteract strong effects of direct interaction, such that the total neighbourhood effect on the focal species' diameter growth is closer to zero. Our study highlights the potential of higher-order interactions in stabilising ecological communities.

Keywords: Biotic interaction, Community ecology, Diameter growth, Fitness models, Hierarchical modelling, Population dynamics, Tropical forest

Jake Ferguson (University of Hawai`i) with John Fieberg

Sampling fast and slow: applying lessons from optimal foraging theory to population surveys

06/25/2020 11:30:00 PM-11:45:00 PM

Session: Interactions and study design *(Chair: Morgan Tingley)*

Location: #acacia

I will discuss trade-offs in double-observer designs that emerged during a study to estimate densities of invasive zebra mussels in Minnesota lakes. We examined how the compromise between surveyor speed and detectability affects the precision of density estimates under a fixed survey time. This trade-off leads to a connection between time-limited surveys and optimal foraging theory, a body of ecological work that predicts how animals should behave when searching for food. We discuss the optimal design strategies predicted from this framework as well as similarities and differences between predictions from optimal foraging theory.

Keywords: Abundance/richness/diversity estimation, Distance sampling

Peter A. Vesk (University of Melbourne) with Will Morris, Will Neal, Karel Mokany and Laura Pollock

Evaluating predictive transfer of trait-environment models

06/25/2020 11:45:00 PM-12:00:00 AM

Session: Interactions and study design *(Chair: Morgan Tingley)*

Location: #acacia

Testing for associations between functional traits and environment is common. Applying the knowledge from those associations is less common. Predicting where species occur, rather than just explaining their distributions is a challenging problem. Trait-based species distribution models offer a way to incorporate functional information into correlative models. This might provide a middle ground between detailed species-specific mechanistic models and climate envelope models. But needs evaluation.

Here we fit models to presence absence data on 20 eucalypt tree species distributions along 4 environmental gradients using 3 traits, in a small region Gariwerd (Grampian Mountains) of Victoria and predict to ~85 eucalypt species in 18 other bioregions in southeast Australia. Well-calibrated models should show higher performance on relevant performance metrics based on presences and absence. We evaluate predictive performance and test whether predictive performance declines with geographic distance and with environmental distance and with compositional dissimilarity. We found reasonable transferability considering we are doing this without knowledge of the species identity and only a limited set of traits compared to other studies testing within taxon transfer. Yet the measure of performance matters. This suggests trait-based SDM can provide good first-order models for species responses along environmental gradients.

Keywords: Hierarchical modelling, Model assessment/validation, Species distribution modelling, Trait based ecology

Nicole L. Michel (National Audubon Society) with Sarah P. Saunders, Timothy D. Meehan and Chad B. Wilsey

Evaluating Conservation Effectiveness Through Trend Analysis of Community Science Data

06/25/2020 12:00:00 AM-12:15:00 AM

Session: Landscapes and ecosystems *(Chair: Kiona Ogle)*

Location: #banksia

Evaluation of protected area effectiveness is critical for conservation of biodiversity. Protected areas that prioritize biodiversity conservation are, optimally, located and managed in ways that support relatively large and stable or increasing wildlife populations. Yet evaluating conservation effectiveness remains a challenging endeavor. Here, we utilize an extensive community science dataset, eBird, to evaluate effectiveness of protected areas for birds across the Gulf of Mexico and Atlantic coasts of the United States. National Audubon Society identified 13 priority birds that use these coastal areas during one or more stages of the annual cycle. We extracted eBird checklists collected in breeding and wintering periods during 2007-2018. We filtered data following recommended protocols, subsampled data to produce spatiotemporally balanced samples, and used INLA to estimate population trends across the study area, repeating each subsample and analysis 100 times. We separately modelled population trends at two types of protected areas: sites where National Audubon Society conducts stewardship and/or management efforts, and protected areas managed for biodiversity or conservation, and evaluated differences in relative abundance and trend between protected areas and the Gulf and Atlantic coasts as a whole. We found that all 13 priority species showed a positive response (i.e., either higher relative abundance or more positive trend) at sites where Audubon works, versus 7 species at protected areas overall. The sites where Audubon works, combined with the stewardship and management efforts conducted there, provide effective conservation for priority coastal bird species that helps ensure conservation of priority coastal bird species.

Keywords: Citizen science

Joern Pagel (University of Hohenheim)

Integrating statistical models of plant species co-occurrence with demography and community dynamics

06/25/2020 10:30:00 PM-10:45:00 PM

Session: Joint species distribution models *(Chair: Laura Pollock)*

Location: #banksia

Spatial patterns of biodiversity depend on the ability of species to coexist at different scales and across environmental gradients. Explaining the geographic distributions of species does thus not only require the quantification of species' ecological niches, but also an understanding of the context-dependent capability of species to grow in the presence of each other (coviability). Commonly applied static joint species distribution models (jSDMs) aim at disentangling ecological niches and biotic interactions by estimating environment-occurrence relationships simultaneously for multiple species and including a covariance structure that describes residual patterns of co-occurrence. However, covariance in species' occurrence can result from a range of different factors and estimated model parameters cannot be interpreted as interaction coefficients of joint population dynamics. Here, we instead analyse species co-occurrence data with an integrated statistical model of community dynamics. The model combines species-specific demographic responses to environmental variation (pre-interactive Hutchinsonian niches) with Lotka-Volterra-type population dynamics to predict stochastic equilibria of species abundances and population growth rates in different abiotic and biotic environments. We apply our approach to multi-scale biodiversity data for Proteacea shrubs in the South African Fynbos that comprise (i) ordinal abundance data for 55,000 Proteaceae communities, (ii) proxies of population growth for 1,500 species-community combinations and (iii) individual-level measurements of demographic rates in comprehensively mapped plant communities. This data integration enables us to test whether effects of biotic interactions on local population growth can explain range-wide co-occurrence patterns, thereby enhancing our predictive understanding of large-scale biodiversity dynamics.

Keywords: Community ecology, Hierarchical modelling, Occupancy analysis, Population dynamics

Trevor James Hefley (Kansas State University) with Haoyu Zhang, Brian R. Gray, and Kristen L. Bouska

Model selection for ecological community data using tree shrinkage priors

06/25/2020 10:45:00 PM-11:00:00 PM

Session: Joint species distribution models *(Chair: Laura Pollock)*

Location: #banksia

Model development and selection for ecological community data is difficult because a high level of complexity is desired and achieved by including numerous parameters, which can degrade predictive accuracy and be challenging to interpret and communicate. Like other statistical models, multi-species distribution models can be overparameterized. Regularization is a model selection technique that optimizes predictive accuracy by shrinking or eliminating model parameters. For Bayesian models, the prior distribution automatically regularizes parameters. We propose a tree shrinkage prior for Bayesian multi-species distributions models that performs regularization and reduces the number of regression coefficients associated with predictor variables. Using this prior, the number of regression coefficients in multi-species distributions models is reduced by estimation of unique regression coefficients for a smaller number of guilds rather than a larger number of species. We demonstrated our tree shrinkage prior using examples of presence-absence data for six species of aquatic vegetation and relative abundance data for 15 species of fish. Our results show that the tree shrinkage prior can increase the predictive accuracy of multi-species distribution models and enable researchers to infer the number and species composition of guilds from ecological community data. The desire to incorporate more detail and parameters into models must be tempered by the limitations of the data and objectives of a study, which may include developing models that have good predictive accuracy and output that is easier to share with policymakers. Our tree shrinkage prior reduces model complexity while incorporating ecological theory, expanding inference, and can increase the predictive accuracy and interpretability of Bayesian multi-species distribution models.

Keywords: Hierarchical modelling, Multivariate analysis/joint species distribution models

David Wilkinson (University of Melbourne) with Nick Golding, Gurutzeta Guillera-Arroita, Reid Tingley and Michael McCarthy

Defining and evaluating the predictions of joint species distribution models

06/25/2020 11:00:00 PM-11:15:00 PM

Session: Joint species distribution models *(Chair: Laura Pollock)*

Location: #banksia *Student*

Joint species distribution models (JSDMs) extend the standard single species distribution model (SDM) approach by allowing multiple species to be modelled simultaneously. This approach accounts for species correlations not explained by available environmental predictors. Despite increasing adoption of JSDMs in the literature, it remains unclear how JSDM predictions differ from those of standard SDMs. By stacking multiple SDMs together we can predict community assemblage or species richness, but this does not account for species correlations. JSDMs, however, allow us to perform predictions in a variety of different ways: species-level environment-only predictions akin to the stacked SDM approach, community assemblage predictions accounting for species correlations, and species- or community-level predictions conditional on known occurrence states of one or more species in the community. Predictions need to be evaluated and there is a wide array of potential metrics for JSDMs and their different prediction types. These include common SDM metrics evaluated at the species level, like AUC, and metrics that operate at the community level like community dissimilarity metrics or species richness. We performed a comparison of predictive performance of six JSDMs and two stacked SDMs using these new prediction methods for 22 real or simulated datasets. We found that while likelihood-based metrics indicate that the JSDMs are better fit to the data than the SSDMs, all other metric classes generally found the SSDM predictions to outperform the JSDMs by a small margin for predictions performed at both the species- and community-level.

Keywords: Abundance/richness/diversity estimation, Community ecology, Model assessment/validation, Multivariate analysis/joint species distribution models

Max Joseph (University of Colorado Boulder)

Neural hierarchical models of ecological populations

06/25/2020 11:15:00 PM-11:30:00 PM

Session: Joint species distribution models *(Chair: Laura Pollock)*

Location: #banksia

Neural networks are increasingly being used in science to infer hidden dynamics of natural systems from noisy observations, a task typically handled by hierarchical models in ecology. This talk describes an emergent class of hierarchical models parameterized by neural networks: neural hierarchical models. The derivation of such models analogizes the relationship between regression and neural networks. A case study is developed for a neural dynamic occupancy model of North American bird populations, trained on millions of detection/non-detection time series for hundreds of species, providing insights into colonization and extinction at a continental scale. Flexible models are increasingly needed that scale to large data and represent ecological processes. Neural hierarchical models satisfy this need, providing a bridge between deep learning and ecological modeling that combines the function representation power of neural networks with the inferential capacity of hierarchical models.

Keywords: Capture-mark-recapture, Hierarchical modelling, Machine learning, Movement modelling, Multivariate analysis/joint species distribution models, Occupancy analysis, Population ecology, Species distribution modelling

Ben J. Maslen (UNSW Sydney) with David Warton and Gordana Popovic

ecopower: An R package for sample size estimates of multivariate community data

06/25/2020 11:30:00 PM-11:45:00 PM

Session: Joint species distribution models *(Chair: Laura Pollock)*

Location: #banksia

Sample size estimation through power analysis is a fundamental tool in planning an ecological study, yet there are currently no well established procedures for power analysis of multivariate community data. Such a procedure would need to address three main challenges: designing a parsimonious simulation model that captures key data properties of community data; measuring effect size in a realistic but readily interpretable fashion; ensuring computational feasibility of a procedure that necessitates both significance and power estimation through simulation or resampling of analyses conducted on many response variables simultaneously. In this talk we propose such a power analysis procedure. Our simulation model uses a recently developed Gaussian copula model, with factor analysis used to characterise correlation across predictors in a parsimonious way. Effect size is measured by using expert opinion to classify taxa as ``increasers", ``decreasers" or ``no effect" taxa, and then applying some common effect size to each ``effect" taxon. Thus, allowing users to study the size of effects that can be detected from a given design, or decide what sample size is required to detect a given effect size. Computational issues are addressed by using a critical value approach where significance is tested globally through only one set of simulated datasets (under the null hypothesis) to find a critical value to be used in ensuing power simulations. This approach reduced standard computation time by a factor of 500, such that the time taken for a power analysis of a moderately sized dataset could be reduced from a day to several minutes. The procedure is illustrated using the Crayweed Restoration Project, to study the sample size required to detect changes in fish abundances of a given effect size, due to restoration efforts. The methods have also been implemented as a general purpose R package; ecopower.

Keywords: Community ecology, Multivariate analysis/joint species distribution models, Sample size estimation, Software development

Michelle Lim (UNSW Sydney) with David Warton

A Multivariate Equivalence Testing Approach for Ecological Restoration

06/25/2020 11:45:00 PM-12:00:00 AM

Session: Joint species distribution models *(Chair: Laura Pollock)*

Location: #banksia

Ecological restoration aims to initiate, accelerate or recreate the recovery of an ecosystem that has been disturbed. Assessment of restoration efforts generally involves comparing the restored site with a reference site, usually represented by nearby undisturbed sites, to find evidence of similarity. Multivariate abundance data are often collected by simultaneously recording abundances of different taxa in an assemblage and used as the basis for comparing sites. A classical hypothesis testing approach is not well suited to this problem, as the technique looks for evidence that the restored and reference sites are different rather than similar. We propose using equivalence testing instead, an idea commonly used in manufacturing and pharmaceutical development, but challenging to extend to a multivariate context. Equivalence testing requires a well-defined notion of effect size, for which we propose an original approach suited to multivariate abundances in ecology, combined with simulation from a Gaussian copula model. We use simulation to verify the performance of the technique and illustrate how it can be used to assess the effects of crayweed restoration on the fish assemblages along the coastline of Sydney, Australia. Software to implement this is currently available in the ecopower package on GitHub.

Keywords: Ecological restoration

Jorge Sicacha Parada (Norwegian University of Science and Technology) with Ingelin Steinsland, Benjamin Cretois and Jan Borgelt

Accounting for spatial varying sampling effort in Citizen Science data: A case study in Norway

06/25/2020 12:00:00 AM-12:15:00 AM

Session: Citizen science and opportunistic data *(Chair: Skipton Woolley)*

Location: #corymbia

Citizen Scientists together with an increasing access to technology provide large datasets that can be used to study e.g. ecology and biodiversity. Unknown and varying sampling effort are major issues when making inference based on citizen science data. We propose a modeling approach for accounting for variation in sampling effort due to accessibility. Then, we present an illustrative case study using citizen science data of moose occurrence in Hedmark, Norway. The aim is to make inference about the importance of geographical properties known to influence moose occurrence. Explanatory analysis show that moose occurrences are overrepresented close to roads, and we use distance to roads as a proxy for accessibility. We propose a model based on a Bayesian Log-Gaussian Cox Process specification for occurrence. The model accounts for accessibility through a distance sampling approach. This approach can be seen as a thinning process where probability of thinning, i.e. not observing, increases with increasing distances. For the moose case study distance to roads are used. The proposed model as well as the consequences of not accounting for varying sampling effort due to accessibility are studied through a simulation study based on the case study. Considerable biases are found in estimates for the effect of radiation on moose occurrence when accessibility is not considered in the model. Finally, we consider the fusion with presence-absence data in order to improve the understanding of the distribution of a given species. A case study with species in Norway as well as a simulation study are developed.

Keywords: Citizen science, Hierarchical modelling, Species distribution modelling

Philippe Marchand (UniversitÃ© du QuÃ©bec en Abitibi-TÃ©miscamingue) with Miguel Montoro Girona, Mathieu Bouchard and Hubert Morin

Fusing multiple data sources for better forecasting models of forest insect outbreaks

06/25/2020 10:30:00 PM-10:45:00 PM

Session: Population modelling *(Chair: Perry de Valpine)*

Location: #corymbia

Insect outbreaks are among the main disturbances shaping the structure of North American boreal forests. Precise estimates of past defoliation across different host species, forest compositions and climatic conditions are essential for the design of models that can successfully forecast the spread and impact of future outbreaks. In this study, we produce quantitative maps of defoliation intensity for the 1967-1992 spruce budworm outbreak in QuÃ©bec, Canada by combining two complementary data sources: aerial surveys, which partition the study region into discrete defoliation classes, and tree-ring data from forest inventory plots, which provide a quantitative record of cumulative defoliation via its impact on tree growth. We use a hierarchical Bayesian model that relates the underlying outbreak intensity (latent variable) to both the defoliation classes in aerial surveys (ordinal logistic regression) and the standardized tree-ring widths (autoregressive model with cumulative defoliation effects on growth). Consistent with previous studies, our model shows that a year of defoliation affects the growth of spruce budworm hosts for at least the five following years. Due to the limited spatial coverage of inventory plots and unmeasured factors affecting tree growth at the local scale, spatial smoothing constraints were required to stabilize defoliation estimates across the study area. This model will serve as an observation sub-model to be coupled with process sub-models as part of a larger project to forecast the spread of spruce budworm outbreaks at the landscape scale.

Keywords: Hierarchical modelling, Spatio-temporal statistics

Alison C. Ketz (University of Wisconsin - Madison) with Daniel P. Storm and Daniel J. Walsh

A spatiotemporal integrated population model to forecast population impacts of heterogeneous disease dynamics

06/25/2020 10:45:00 PM-11:00:00 PM

Session: Population modelling *(Chair: Perry de Valpine)*

Location: #corymbia

Transmission dynamics, geographic spread, infection patterns, genetics and movements of hosts, and pathogen variation are processes that determine the impact of diseases on host populations. These processes operate on multiple scales across space and time, further complicating population effects. This complexity necessitates a flexible modeling approach that can structurally incorporate these ecological and biological processes. We have developed a spatio-temporal integrated population model (IPM) that assimilates disease dynamics within a host population model. We use our approach to examine impacts of chronic wasting disease (CWD), a contagious prion disease that affects cervids and exhibits intricate epizootic patterns. Our model incorporates data from numerous sources, including age-at-harvest, cross-sectional surveillance, GPS-collar locations of adults, VHF telemetry locations of juveniles, aerial surveys, pregnancy rates, and camera trap data, to assess the population impacts of CWD on white-tailed deer (Odocoileus virginianus) in the CWD-endemic region of south-central Wisconsin, USA. Previous studies indicate precipitous declines of CWD-affected cervid populations in the Rocky Mountains, but due to strikingly different environmental, behavioral, demographic, and density patterns, assessment for the mid-western USA is needed. IPMs frequently use mark-recapture data to obtain survival and disease rates, however, we use a time-to-event, age-period survival sub-model that includes infection status of marked individuals that can vary over time and across ages of individuals in the host population. We use the IPM to forecast population trends under a variety of management actions, that are likely to influence population trajectories over time.

Keywords: Disease ecology, Dynamic state models, Hierarchical modelling, Integrated population models, Population dynamics, Population ecology, Spatio-temporal statistics

Oscar Rodriguez de Rivera Ortega (Statistical Ecology at Kent (University of Kent)) with A. Lopez-Quilez, Rachel McCrea, N. Cole

Assessing the Spatio-Temporal distribution of invasive species

06/25/2020 11:00:00 PM-11:15:00 PM

Session: Population modelling *(Chair: Perry de Valpine)*

Location: #corymbia

The control of invasive alien species (IAS) and protection of vulnerable native species require species-specific conservation actions, such as IAS control and eradication. Estimates of abundance and distribution before and after IAS removal activities can be a useful metric to evaluate control/eradication plans. However, several methods of estimating population size are too labour intensive and expensive to implement. Statistical models offer a crucial tool that can be used to test, develop and optimise plans to control.

The aim of this study is to build a spatio-temporal model to predict the distribution of Chromolaena odorata, an invasive species present in Round Island (Mauritius).

Keywords: Hierarchical Bayesian models, Integrated nested Laplace approximation, Invasive species, Spatio-temporal model, Stochastic partial differential equations

Rebecca J. Groenewegen (University of Melbourne) with Graeme R. Finlayson, Kate Taylor and Brendan Wintle

An application of spatial count models to assess invasive predator management

06/25/2020 11:15:00 PM-11:30:00 PM

Session: Population modelling *(Chair: Perry de Valpine)*

Location: #corymbia *Student*

Effective invasive predator management requires an understanding of the impacts of control on target populations, yet inference has long relied upon abundance indices. To adequately assess control regime effectiveness for native fauna outcomes, reliable measures of predator population dynamics are crucial. Confidence in estimating population size relies upon our ability to quantify rates of detection. Spatial capture-recapture explicitly accounts for two major sources of heterogeneity in detection (the location of individuals relative to detectors, and their movement range) allowing density estimation of cryptic, wide-ranging species.

Spatial count (SC) models can be applied to unmarked species, or where high uncertainty in individual identification occurs. We used multisession SC models with an informative prior on the movement scale to track feral cat (Felis catus) and red fox (Vulpes vulpes) densities in central South Australia. Two 48 camera grids were operated year-round inside and outside an intensive predator management area. We shared detection parameters across grids and within seasons, to obtain monthly density estimates of both species where detection was low and improve precision. The Bayesian framework allowed us to estimate population size in months where no detections occurred. SC models revealed different predator population fluctuations over time than detection rates alone. This research provides a robust framework on which to develop predator population models and predict impacts of management on predator populations and native fauna.

Keywords: Population ecology, Spatial capture-recapture

Barbara B. Vuillaume (UniversitÃ© Laval) with Thomas Cornulier, Xavier Lambin, JoÃ«lle Taillon, Vincent Brodeur, Marco Festa-Bianchet and Steeve D. CÃ´tÃ©

Integrated population models to rebuild and predict population dynamics of migratory caribou herds

06/25/2020 11:30:00 PM-11:45:00 PM

Session: Population modelling *(Chair: Perry de Valpine)*

Location: #corymbia *Student*

Migratory caribou in northern Quebec and Labrador (Canada) are in sharp decline. In 2017, the Committee on the Status of Endangered Wildlife in Canada assessed these populations as Endangered. To improve their management and conservation, we must understand the environmental drivers of demographic change in these populations. We combined the strengths of advanced Bayesian statistics and extensive ecological data to improve our knowledge of demographic changes in migratory caribou. We used integrated population models to rebuild the population dynamics of the RiviÄ re-aux-Feuilles and the RiviÄ re-George herds over the past 30 years and predict future changes in population size. To overcome the lack of frequent and accurate censuses of the populations, we used multiple data types: seasonal and annual adult survival estimates, autumn recruitment rates, aerial surveys, and hunting harvest rates. Models also included past and forecasted weather and resource variables known to affect survival, leading to predictions of population dynamics. Integrated population models of the population dynamics narrowed the confidence intervals of previously available estimates of survival and population size for both herds, and clarified past demographic changes. Environmental factors showed stronger effects on individual survival than on population dynamics which were driven more by changes in survival parameters than by a direct effect of the environment. Our analyses provide useful knowledge to manage these threatened herds. We encourage the use of integrated population models to monitor the dynamics of wildlife populations.

Keywords: Capture-mark-recapture, Integrated population models, Migratory caribou, Population dynamics

Marie Etienne (Agrocampus Ouest) with ThÃ©o Michelot, Paul Blackwell and Pierre Gloaguen

A continuous time movement model to understand habitat selection

06/25/2020 11:45:00 PM-12:00:00 AM

Session: Population modelling *(Chair: Perry de Valpine)*

Location: #corymbia

Measuring habitat suitability for a given species is a key step in any wildlife management plan. In recent decades, improvements in tracking technologies have produced large amounts of animal location data, and statistical methods have been developed to estimate the utilisation distribution of animals from telemetry observations, and to link their movements to habitat preferences and space use (Hooten et al., 2017). The most popular approaches to estimate utilisation ignore the sequential structure of the data and habitat preference in the movement itself, or use unrealistic movement assumptions.

In recent work, integrated movement models have been proposed to account for environmental covariates (Hanks et al., 2015,, Avgar et al., 2016; WIlson et al., 2018). In those approaches, time and/or space are discretized, and the comparison between different data sets involving different discretizations is difficult. Moreover, due to the discretization, the estimation of such models is often CPU and/or memory intensive.

We propose the Langevin diffusion model as a new continuous-time and continuous-space model to link short-term movement to long-term space use. The analysis of the steady-state distribution of this model allows to quantify habitat preferences.

Using standard approximation techniques, the model can be written as a linear model, and parameter inference is straightforward. Standard tools such as residuals can be used for model checking.

The performance and the limits of this this integrated movement model are examined using the Rhabit package through different examples (French deer, Capreolus capreolus L.; Stellar sea lions, Eumetopias jubatus).

Keywords: Habitat selection, Movement modelling, Stochastic processes

Casey Visintin (University of Melbourne) with Natalie Briscoe, Skipton Woolley, Pia Lentini, Reid Tingley, Brendan Wintle and Nick Golding

steps: open-source software for spatially- and temporally-explicit population simulations

06/25/2020 12:00:00 AM-12:15:00 AM

Session: Populations in time and space *(Chair: Rahel Sollmann)*

Location: #darwinia

Spatial simulation of species populations for ecological applications is an area of research and management with broad interest, yet currently-available tools are limited by license fees, a lack of transparency and inflexibility. Presently, no single software offering allows users to develop models that incorporate common spatial and temporal factors of interest, such as climate and weather, fire, landscape dynamics, species' physiological requirements, and evolution, in a open-source, customisable and multi-platform environment.

We believe that steps addresses this need, and demonstrate its utility using a motivating case study of greater glider populations in south-eastern Australia under realistic scenarios of habitat loss and the impacts of fires. This is but one example of how it can be used; because of its simple interface, accessible code, and flexibility to accommodate multiple data inputs and custom functions, our software actually enables researchers or environmental managers to simulate population changes for an unlimited variety of scenarios.

Keywords: Abundance/richness/diversity estimation, Population dynamics, Software development, Species distribution modelling

Adam C. Smith (Canadian Wildlife Service) with Brandon P.M. Edwards

Improved status and trend estimates from the North American Breeding Bird Survey using a hierarchical Bayesian generalized additive model

06/25/2020 12:15:00 AM-12:30:00 AM

Session: Populations in time and space *(Chair: Rahel Sollmann)*

Location: #darwinia

The status and trend estimates derived from the North American Breeding Bird Survey (BBS), are critical sources of information for bird conservation. However, many of the varied uses of these estimates are poorly supported by the current standard model. We will describe hierarchical Bayesian generalized additive mixed-models (GAM) that generate status and trend estimates particularly well suited for many common types of conservation assessments. We will demonstrate the models and their benefits using data for a selection of species. We will show results from a full cross-validation analysis of the Bayesian models. The GAMs have better predictive fit than the standard model and better or comparable predictive fit compared to an alternative first difference model.

One version of our model estimates a population trajectory that can be decomposed into a smooth component and the annual fluctuations around that smooth. This decomposition also allows trend estimates based only on the smooth component, which are more stable between years and are therefore more useful for trend-based status assessments, such as those by the IUCN. This model also allows for the easy customization of a BBS analysis to incorporate covariates that influence the smooth component separately from those that influence annual fluctuations (e.g., climate cycles vs annual precipitation). Overall, this model is broadly useful for the BBS and other long-term surveys, because of its flexibility, its decomposition, and the hierarchical structure that shares information among regions.

Keywords: Bayesian methods, Breeding Bird Survey, GAM, Hierarchical modelling, Population monitoring

Rachel M. Fewster (University of Auckland) with Paul van Dam-Bates, Ben Stevenson and David Borchers

Cluster capture-recapture for acoustic monitoring

06/25/2020 10:30:00 PM-10:45:00 PM

Session: Acoustics and movement *(Chair: Theo Michelot)*

Location: #darwinia

Cluster capture-recapture (CCR) is a new framework for capture-recapture-type studies where individuals cannot be identified with certainty. Instead of capture histories, we make observations that are informative, but not definitive, about identity. CCR is based on the idea that repeat detections of the same individual will have similar, albeit not identical, observations. Instead of attempting to match detections to individual identities, CCR treats observations from all individuals together as a clustered point process. The challenge is to ensure that the parameters of interest, such as abundance or cue-production rate, are identified by a process-level analysis of the clustered data.

Using CCR could represent a transformative saving in effort for practitioners, who would normally have to undergo a time-consuming process of sample-matching. It is therefore a promising new approach for analysing the "big data" that will result when new wildlife surveying technologies are deployed on a massive scale.

Here, we present a CCR model for acoustic monitoring data. We show how we can estimate call-rate and detection parameters from a simple two-microphone design, without making any attempts to identify or localise calling animals. By using two microphones a known distance apart, we can establish a contrast between the intensity of sounds received within and between microphones, to gain information on the decay of detection with distance. This blends ideas of distance sampling and spatial capture-recapture, but without measuring distances to animals and without constructing capture histories. We discuss preliminary results and applications.

Keywords: Abundance/richness/diversity estimation, Capture-mark-recapture, Spatial capture-recapture

Charlotte M. Jones-Todd (University of Auckland) with Enrico Pirotta and Len Thomas

A Continuous-time, discrete-space model of marine mammal exposure to Navy sonar

06/25/2020 10:45:00 PM-11:00:00 PM

Session: Acoustics and movement *(Chair: Theo Michelot)*

Location: #darwinia

Many wildlife species are increasingly being exposed to disturbances resulting from human activity. Such exposures may cause individuals to change their natural behaviour. Disturbance caused by these activities has the potential to have an adverse effect on how individuals use that area. To infer the consequences of anthropogenic disturbance on animal populations a framework is required that considers where individuals travel in an area, when individuals are exposed, and how they may respond. Using telemetry data, collected with uncertainty, this talk will discuss a discrete-space, continuous-time model that estimates individual transition rates across boundaries of an area of interest. Whilst also inferring the effect of stressors on the transition rates, and estimating the gradual decay of the stressor effect to baseline behaviour, this framework allows the differences amongst individuals to be quantified. The modelling framework is illustrated using Blainville's beaked whale (Mesoplodon densirostris) telemetry data from the Atlantic Undersea Test and Evaluation Center (AUTEC), Bahamas---a region used by the US Navy for military training exercises.

Keywords: Behavioural ecology, GPS data, Movement modelling, Population dynamics

RocÃo Joo (University of Florida) with Matthew E. Boone, Thomas A. Clay, Samantha C. Patrick, Susana Clusella-Trullas, and Mathieu Basille

R packages for movement: lessons for the statistical ecology community

06/25/2020 11:00:00 PM-11:15:00 PM

Session: Acoustics and movement *(Chair: Theo Michelot)*

Location: #darwinia

The advent of miniaturized biologging devices has provided ecologists with unprecedented opportunities to record animal movement across scales, and has led to the collection of ever-increasing quantities of tracking data. In parallel, sophisticated tools have been developed to process, visualize and analyze tracking data, particularly in the R software environment. In a recent study, within R alone, we listed 58 packages created to deal with tracking data, greatly benefiting the statistical ecology community; and the number keeps growing. However, with package proliferation comes with redundancy, disconnection and a lack of documentation.

This presentation is meant for our entire research community, including users and developers. We describe packages for tracking data in a workflow broken down into three stages: pre-processing, post-processing and analysis (e.g. data visualization, path reconstruction, behavioral pattern identification, space use characterization). We suggest that both users and developers pay careful attention to the documentation of the package regarding not only its use but also the methods behind it, to improve packages and facilitate statistically sound research. We will also discuss the usefulness of peer review processes for packages (e.g. rOpenSci, JOSS). This set of good practices, together with fundamental tools and resources, is not only relevant for movement ecologists, but for all statistical ecologists (and ecological statisticians) to grow together as a stronger community.

Keywords: Biologging, Data processing and analysis, GPS data, Interdisciplinary ecology, Movement ecology, Software development, Spatio-temporal statistics, Tracking data

Fanny Empacher (University of St Andrews) with Len Thomas and Ken Newman

Using the Kalman Filter to approximate the likelihood in complex state-space models - a seal example

06/25/2020 11:15:00 PM-11:30:00 PM

Session: Acoustics and movement *(Chair: Theo Michelot)*

Location: #darwinia

State-space models have many uses in ecological inference, including modelling animal movement and population dynamics. Most realistic models are non-linear and non-Gaussian, but in this case, it is often impossible or intractable to calculate the likelihood given a parameter vector, making inference difficult. While Monte Carlo methods like Sequential Monte Carlo deliver an unbiased estimate of the likelihood, these estimates can suffer from high variance unless the computation time is relatively high. As the likelihood is often required for further steps, for example as part of an MCMC algorithm in a Bayesian context or as the objective function in an optimisation algorithm in a frequentist context, high computation time quickly becomes prohibitive. A deterministic alternative to calculate the likelihood is the computationally much faster Kalman filter, which in its most simple form is an algorithm for linear and Gaussian SSMs. We applied the Kalman filter to a population dynamics model of UK Grey Seal. This model is non-linear and non-Gaussian but we replaced the transition and observation densities with linear and Gaussian approximations. Through a simulation study, we show how close the true likelihood is to the likelihood calculated by the Kalman filter and discuss the usefulness of this approximation in various settings. We also discuss further improvements that build on the Kalman filter and its extensions.

Keywords: Dynamic state models, Population dynamics

Amanda J. Warlick (University of Washington) with Nathan J. Hostetter and Sarah J. Converse

Estimating reproductive output using a Bayesian nest survival model with uncertain nest age and nest state for pigeon guillemots in Puget Sound, Washington, USA

06/25/2020 11:30:00 PM-11:45:00 PM

Session: Acoustics and movement *(Chair: Theo Michelot)*

Location: #darwinia *Student*

Reproductive output is a key component driving population dynamics, and understanding this demographic rate is fundamental to the conservation and management of wild populations. However, estimating fecundity or reproductive success can be challenging for bird species whose nests are not directly observable, where nest state and age are therefore unknown. We present a novel approach for estimating reproductive output that accounts for uncertainty in both nest state and nest age that is useful when either the study design or location of nests precludes observing precisely when nests are initiated, eggs hatch, or chicks fledge, but where repeated observations of parental behavior can provide information about the likely true state of the nest (e.g., when an egg or hatchling is present). We demonstrate a Bayesian implementation of our model to estimate egg survival, chick survival, and total reproductive output of a study population. We use this model to evaluate environmental indices such as sea surface temperature and upwelling as potential factors affecting annual reproductive success for the pigeon guillemot (Cepphus columba) in Puget Sound, Washington, USA. We discuss the feasibility of using this framework within an integrated population model to derive much-needed abundance estimates and demographic rates for a species that has been identified as an important ecological indicator for the region. Our model framework is applicable to other populations with fully or partially unobservable nests and provides important information on the status of this indicator species, which is particularly relevant given ongoing environmental change in the Puget Sound region.

Keywords: Capture-mark-recapture, Integrated population models, Population dynamics

Paul J. van Dam-Bates (University of St Andrews) with David L. Borchers, Michail Papathomas, Rachel M. Fewster and Ben C. Stevenson

Latent ID Acoustic Spatial Capture-Recapture

06/25/2020 11:45:00 PM-12:00:00 AM

Session: Acoustics and movement *(Chair: Theo Michelot)*

Location: #darwinia *Student*

Spatial capture-recapture (SCR) can be applied to acoustic monitoring using a grid of microphones where the call is recaptured across the grid. Currently, without additional information about individual ID between calls, acoustic SCR is only able to estimate call and not animal density. For species that stay relatively close to the same location throughout the study, we observe clusters of calls around their activity centre. We also observe the times the calls arrive on the microphones. Using this spatial and temporal information can help differentiate the unique individuals in the population. We parameterize the traditional acoustic spatial SCR model as a mixture of individual animal locations. We are then able to fit this as a Dirichlet Process Mixture Model to assign animals to calls based on spatial and temporal clustering. The results from a simulation study will demonstrate how the method can be applied in practice.

Keywords: Spatial capture-recapture

Thomas Neyens (Catholic University of Leuven/Hasselt University) with Peter J. Diggle, Christel Faes, Natalie Beenaerts, Tom Artois and Emanuele Giorgi

Mapping species richness using opportunistic samples: a case study on ground-floor bryophyte species richness in the Belgian province of Limburg

06/26/2020 8:00:00 AM-8:15:00 AM

Session: Species distributions and data challenges *(Chair: Eve Slavich)*

Location: #acacia

In species richness studies, citizen-science surveys where participants make individual decisions regarding sampling strategies provide a cost-effective approach to collect a large amount of data. However, it is unclear to what extent the bias inherent to opportunistically collected samples may invalidate our inferences. Here, we compare spatial predictions of forest ground-floor bryophyte species richness in Limburg (Belgium), based on crowd- and expert-sourced data, where the latter are collected by adhering to a rigorous geographical randomisation and data collection protocol. We develop a log-Gaussian Cox process model to analyse the opportunistic sampling process of the crowd-sourced data and assess its sampling bias. We then fit two geostatistical Poisson models to both data-sets and compare the parameter estimates and species richness predictions. We find that the citizens had a higher propensity for locations that were close to their homes and environmentally more valuable. The estimated effects of ecological predictors and spatial species richness predictions differ strongly between the two geostatistical models. Unknown inconsistencies in the sampling process, such as unreported observer's effort, and the lack of a hypothesis-driven study protocol can lead to the occurrence of multiple sources of sampling bias, making it difficult, if not impossible, to provide reliable inferences.

Keywords: Abundance/richness/diversity estimation, Citizen science, Spatio-temporal statistics

Philipp H. Boersch-Supan (British Trust for Ornithology)

Integrating citizen science data sets to improve a national bird monitoring scheme

06/26/2020 8:15:00 AM-8:30:00 AM

Session: Species distributions and data challenges *(Chair: Eve Slavich)*

Location: #acacia

Citizen scientists are collecting opportunistic biodiversity records on unprecedented temporal and spatial scales, vastly outnumbering the records achievable from structured surveys. Opportunistic records may exhibit spatio-temporal biases and/or large heterogeneity in observer effort and skill. Data integration has the potential to leverage information from both types of data to improve inferences about the population status of data poor species and/or regions - and thus fill gaps in biodiversity monitoring schemes.

We combined count data from a structured survey, the UK Breeding Bird Survey, and detection-nondetection data from an opportunistic citizen science programme, BirdTrack, to make inferences about the population dynamics of UK birds at different spatial scales. Observations were jointly modelled using state-space models with a survival and a dispersal component and dedicated observation models for each data source. Jointly modelled population trends had much better precision than trends based on individual data sources, and - where available - showed good agreement with independent data on population trends.

Parameter estimation did not scale well to large (i.e. national scale) data sets and further model development is required to overcome such computational challenges. However, joint models offered promising results for deriving local and regional avian population trends thereby improving inferences on spatial scales highly relevant to conservation management and public engagement.

Keywords: Citizen science, Integrated population models, Occupancy analysis

Lionel Hertzog (ThÃ¼nen Institute for Biodiversity) with Claudia Frank, Sebastian Klimek and Johannes Kamp

Does model-based integration of different Citizen-Science datasets provide improved estimates of bird population temporal trends?

06/26/2020 8:30:00 AM-8:45:00 AM

Session: Species distributions and data challenges *(Chair: Eve Slavich)*

Location: #acacia

Assessing trends in biodiversity over space and time through monitoring is a prerequisite for informed decision-making and timely reporting on progress towards biodiversity conservation targets. Currently, monitoring data of biodiversity over large spatial and temporal scales are mostly arising from citizen science programs. The diversity of these programs leads to datasets with varying structure and uncertainties, from standardized random sampling to completely opportunistic observations. Model-based integration of different data sources and their respective strengths is believed to improve the estimation of species' spatio-temporal trends while optimizing the use of available data. However, there are still few real-life examples that evaluate the power of data integration approaches. Most previous studies used simulated data or small-scale datasets to showcase the potential of this approach. Therefore, the usefulness of data integration methods for biodiversity monitoring programs remains to be demonstrated especially in comparison with current simple, but widely used approaches. Here, we aim at integrating various monitoring dataset along a gradient of field methods standardization. We evaluated for 26 common farmland bird species in Germany, if and how data integration improved the estimation of temporal trends over the last 15 years. We integrated five different data sources that varied with respect to the degree of standardization in field methods and sampling design, the level of observer skills, and inherent spatial bias. Comparing the estimated temporal trends from various levels of data integration enabled us to identify the benefits and limitations of this approach in regard to commonly used trend monitoring analysis, and for official reporting purposes.

Keywords: Citizen science

Michael P. Scroggie (Arthur Rylah Institute for Environmental Research) with Garry N.L. Peterson, Detlef H. Rohr, Evelyn Nicholson and Geoffrey W. Heard.

Using multispecies dynamic occupancy models to understand the responses of grassland fauna to habitat fragmentation and disturbance

06/26/2020 8:45:00 AM-9:00:00 AM

Session: Species distributions and data challenges *(Chair: Eve Slavich)*

Location: #acacia

For effective decision-making, wildlife managers must understand the interacting effects of landscape configuration, habitat quality and management actions on populations. When species of interest are rare, cryptic or both, then estimating population trends and responses to management can be especially challenging.

We monitored responses of a suite of small vertebrates to grassland fragmentation and disturbance in south-eastern Australia. Using artificial cover object arrays, we conducted over 4000 surveys at 291 sites over 9 years. Sites had varying degrees of fragmentation, and diverse disturbance regimes in the form of fuel-reduction burning and livestock grazing. The resulting detection data were analysed using a multispecies dynamic occupancy model to quantify the effects of fragmentation, fire and grazing on patch-level probabilities of extinction and colonisation.

We specified hierarchical hyperpriors on parameters related to detection, occupancy, extinction and colonisation in order to improve estimation of parameters for rare and cryptic species. Species exhibited contrasting responses to fragmentation and disturbance, meaning that uniform approaches to management may not serve the needs of all species. Latent occupancy-state parameters of the model were used to assess changes in the number of occupied sites over time. Furthermore, by simulating occupancy dynamics under a range of fire and grazing regimes, we were able to assess the likely overall conservation outcomes of different management regimes. Our hierarchical, multispecies approach allowed us to address questions of direct relevance to managers in a single cohesive model, and to explore the conservation implications of alternative management regimes.

Keywords: Dynamic state models, Hierarchical modelling, Occupancy analysis

David Borchers (University of St Andrews)

Its about time: modelling detection processes continuously in time

06/26/2020 9:45:00 AM-10:35:00 AM

Location: #acacia *Plenary (Chair: Rachel McCrea)*

"If all you have is a hammer, everything looks like a nail" (Maslow, 1966). And if all you have is a discrete-time model, then time looks discrete. But it is not.

Because statistical models for ecological surveys were developed in an era in which gathering continuous time-stamped data was infeasible, statistical models for detection processes from this era treat surveys as instantaneous. But they are not.

We now live in a world in which gathering continuous time-stamped data is commonplace. Camera traps survey continuously and record exact times of detection events, so do airborne video cameras, so do microphone and hydrophone arrays, and we carry around phones that know our locations continuously. But we still use models from an era before the advent of continuously recording detection devices.

In this talk I will use examples of from my, and my colleagues' research to illustrate the utility of developing and using temporal, and spatio-temporal, stochastic process models to model detection events continuously in time. I will consider examples from line transect surveys, from camera trap surveys and from acoustic surveys, and will illustrate the added value that you get from using continuous-time models in each case. And I am sure that the added value contained in continuous-time data is not restricted to the few examples that I consider.

Shane M Baylis (CSIRO) with Rohan Clarke and Paul Sunnucks

Can we do better than Maximum Recorded Longevities for evolutionary comparative analyses of survival?

06/26/2020 8:00:00 AM-8:15:00 AM

Session: Demography and visualisation *(Chair: Nick Golding)*

Location: #banksia

Evolutionary comparative analyses of survival explore patterns of population survival parameters in an attempt to explain survival in terms of life history theory, behavioural ecology, evolutionary optimality models, and so on. In order to explore these models in detail, researchers require survival data for large numbers of species. Sourcing the data to fit these models is a monumental task - most species have never been subject to explicit survival analyses, and of those that have, Variability in data sources, survival models used, and parameters estimated can complicate downstream analyses.

In response to these challenges, Maximum Recorded Longevities (MRLs) have become a popular data type for evolutionary comparisons. MRLs are conceptually simple, and many species have an oldest known individual from zoo records or marking records of free-living species. However, they are subject to biases that severely limit their usefulness. In particular, differences in MRL are a function of sample size, recovery or monitoring type, and the functional form of the species' true mortality curve. The differences in MRL arising from interspecies differences in sample size and recovery or monitoring type can easily swamp the relatively small effects expected in evolutionary comparative analyses.

Here, I present a set of model-based population mortality curves based on open-access Australian Bird and Bat Banding Scheme data using a consistent modelling framework, accompanied by simulation-based tests of their reliability. Despite some remaining imperfections, I present the case for abandoning MRLs in favour of model-based population survival parameters wherever possible.

Keywords: Capture-mark-recapture, Spatial capture-recapture

Victor Nyaliki Mose (African Conservation Centre) with David Western

Using Spatial Data Visualization for Ecological Hypothesis Generation and Modelling in Rural Africa

06/26/2020 8:15:00 AM-8:30:00 AM

Session: Demography and visualisation *(Chair: Nick Golding)*

Location: #banksia

Using spatial exploratory data analysis to visualize and generate hypothesis is fast becoming a method of choice for many researchers working across disciplines. The visualization allows scientist and local community teams to work together in building ideas about how local ecological systems work. We used dynamic and static spatial exploratory analysis to visualize more than forty years of data on large mammal species and environmental variables collected from aerial surveys in the Amboseli ecosystem, southern Kenya. Massive amounts of data were transformed into meaningful information enabling the understanding of spatio-temporal ecological data. We show how spatial exploratory data analysis can reduce complex ecological hypothesis on Human Wildlife Interactions and perceptions, to simple visual presentations with cross-cutting research applications. The approach requires no prior knowledge about the data and can be rapidly applied to formulate and test hypothesis in visual form with wide applications.

Keywords: Citizen science, Ecosystem ecology, Interdisciplinary ecology, Spatio-temporal statistics

Achaz von Hardenberg (University of Chester,) with Alejandro Gonzalez-Voyer

An easy implementation of Bayesian Phylogenetic Path Analysis for causal inference in evolutionary ecology

06/26/2020 8:30:00 AM-8:45:00 AM

Session: Demography and visualisation *(Chair: Nick Golding)*

Location: #banksia

One of the main limitations of phylogenetic comparative analyses is that associations between life history, ecological and behavioural traits can only be interpreted as correlations. We recently proposed Phylogenetic Path Analysis (PPA, doi.org/10.1111/ j.1558-5646.2012.01790.x) as a powerful tool for causal inference in macroecology and evolution, allowing to disentangle direct from indirect relationships among traits which are not independent because of common ancestry. Here we show how PPA can be easily implemented in a Bayesian framework using the probabilistic programming language Stan through the R package ‘brms’ (doi.org/10.32614/RJ-2018-017). Compared to the frequentist PPA approach, the proposed Bayesian method is much more flexible allowing the use of data with different kinds of distributions (e.g. binomial and Poisson), provides a straightforward solution to the problem of missing values as well as the possibility to take into account uncertainty in traits values. Best fitting models can be selected using standard Bayesian model selection criteria (such as WAIC and LOO) among those fulfilling all conditional independencies implied by the hypothesised causal models. We exemplify the method both with simulated and real data and discuss its benefits and possible future developments and applications.

Keywords: Macro-ecology, Macro-evolution, Phylogenetic Comparative Methods

Glenn R. Moncrieff (South African Environmental Observation Network)

Rapid, automated detection of shrubland land cover change in satellite image time series using convolutional neural networks

06/26/2020 8:00:00 AM-8:15:00 AM

Session: Contributed talks *(Chair: Florian Hartig)*

Location: #corymbia

Improvements in the temporal and spatial resolution of remote sensing have facilitated the development of methods that allow for the rapid detection of land cover change in satellite image time-series (SITS). Existing efforts to detect land cover change in SITS have mostly focussed on forested ecosystems in the tropics and northern hemisphere. Less progress has been made in detecting change in low productivity, disturbance prone vegetation such as grasslands and shrublands. Renosterveld is a critically endangered shrubland ecosystem in South Africa with less than 10% of its original extent remaining in small, highly fragmented patches. Despite legislation prohibiting the transformation of remaining patches, habitat loss continues unabated, with the complete loss of renosterveld projected to occur before the end of the current century. I demonstrate an approach that can accurately detect the transformation of renosterveld within a few days of its occurrence. A training dataset of precisely dated vegetation change events between 2016 and 2020 was obtained from daily, high resolution Planet satellite data. This dataset was then used to train 1D convolutional neural networks to accurately detect anomalies in multivariate time-series of vegetation activity from the Sentinel 2 satellites. Updated anomaly detections are processed automatically every 5 days when new imagery becomes available. There is great potential for such a system to slow the ongoing loss of renosterveld - and other shrubland ecosystems - through aiding investigation of ongoing offences and deterring future infringements.

Keywords: Machine learning

Louise McMillan (Victoria University of Wellington) with Rachel Fewster

Directional measures of population differentiation

06/26/2020 8:15:00 AM-8:30:00 AM

Session: Contributed talks *(Chair: Florian Hartig)*

Location: #corymbia

McMillan & Fewster (2017) proposed GenePlots, a visualization method for genetic assignment of individuals. We have also proposed new methods for quantifying population genetic structure, which are are derived using the saddlepoint method to approximate the genetic distribution of a population, based on the posterior allele frequencies.

One measure is the incumbent selection probability: for two random genotypes arising from populations A and B, the probability that the `incumbent', i.e. the one from A, has the better fit to A. Another measure is the home assignment probability: the probability that a random genotype arising from A would be correctly assigned to its home population, A, rather than to population B. We originally designed these measures for pairs of populations, but have since extended them to compare multiple populations. These measures have been used to compare southern right whales (_Eubalaena australis_) from various breeding grounds in the Southern Oceans.

Using permutation tests, we can also test for significant population separation. These permutation tests are sensitive to subtle population structure, and are particularly useful for eliciting directional features of the population structure, e.g. where one population has undergone extensive genetic drift but the other population has remained large enough to retain greater genetic diversity.

These methods have been implemented in an R package. We illustrate the methods using microsatellite and large-scale SNP data.

Keywords: Population genetics, Software development

Koustubh Sharma (Snow Leopard Trust) with Gantulga Bayandonoi, Ian Durbach, Purevjav Lkhagvajav, Justine Shanti Alexander and David Borchers

Estimating snow leopard populations across half a million square kilometers

06/26/2020 8:30:00 AM-8:45:00 AM

Session: Contributed talks *(Chair: Florian Hartig)*

Location: #corymbia

Snow leopards are distributed across the mountains of 12 countries spread across 2 million km^2 in Central and South Asia. Despite more than 3 decades of research and conservation effort, the best estimates of its population size are guestimates. Largely due to inaccessibility and local priorities, only a tiny a fraction of the species' distribution range has ever been selected for sampling, with a strong bias towards high density areas. The PAWS (population assessment of the world's snow leopards) program, spearheaded by a multi-country, multi-organizational alliance GSLEP (Global Snow Leopard and Ecosystem Protection Program) was initiated in 2018 to estimate snow leopard abundance across their range using stratified random sampling. In Mongolia, a consortium led by WWF and SLCF/SLT, supported by various other NGOs and Government agencies, conducted surveys based on signs of snow leopard presence across half a million km^2 of potential snow leopard habitat. The survey, in line with protocols set by PAWS, provides the first comprehensive estimated distribution maps of snow leopard occupancy from Mongolia. Ruggedness, vegetation index, altitude and area under forest cover were considered as site specific occupancy covariates in this analysis. The consortium has also jointly conducted 26 camera trapping surveys in the past 2 years, spanning an area of roughly 115,000 km^2 (with a substantially smaller effective area). We show how spatial capture-recapture analyses of completed surveys can be used to inform decisions about where and how much sampling is required to achieve density (and abundance) estimates within a desired level of precision for an entire country.

Keywords: Abundance/richness/diversity estimation, Camera trap data, Occupancy analysis, Snow leopard, Spatial capture-recapture, Species distribution modelling

John Alroy (Macquarie University)

Three methods of estimating richness and evenness

06/26/2020 8:45:00 AM-9:00:00 AM

Session: Contributed talks *(Chair: Florian Hartig)*

Location: #corymbia

Standard diversity metrics such as Chao 1, Shannon's H, and Pielou's J are handicapped by sampling biases and precision problems. I present simulations and empirical analyses to explore methods of quantifying evenness and of extrapolating and interpolating richness. The Chao 1 extrapolator can be interpreted as assuming Poisson sampling from a uniform distribution. It is imprecise because it relies on the often small count of doubletons. Chao's approach can be generalised, and the better equations in the resulting family ignore doubletons. One in particular unifies Poisson sampling theory with the first-order jackknife. A common method of interpolation called quorum subsampling or coverage-based rarefaction estimates richness given a selected value of Good's u. The resulting values correlate with both richness and evenness. This by itself is unproblematic, but the evenness signal can be strong. I discuss a simple method that brings together rarefaction, Simpson's D, and Good's u to produce diversity estimates with stronger richness signals. The values correlate with Shannon's H but are insensitive to the size of the raw data set, unlike H. Meanwhile, the evenness metric called Pielou's J is biased by raw richness. A simple formula called the ratio of means, which involves first log transforming species counts, removes the bias while presenting a strong evenness signal. The values have a lower bound of zero but no upper bound, and they correlate with standard deviations of underlying logged frequencies when distributions are log normal. All diversity metrics are imperfect, but these three are worth considering.

Keywords: Abundance/richness/diversity estimation, Community ecology, Theoretical ecology

Birgit Erni (University of Cape Town)

Modelling Lagged Response in Time Series Data

06/26/2020 8:00:00 AM-8:15:00 AM

Session: Spatio-temporal data *(Chair: Theoni Photopoulou)*

Location: #darwinia

Environmental variables often have a cumulative and / or a lagged effect on response variables. For example, daily pollen counts may depend on cumulative and lagged temperature, wind and rainfall values. Similarly, start of pollen season (phenology) may depend on a range of cumulative conditions many weeks earlier. Lagged environmental variables are often autocorrelated and can be problematic for regression models. Traditionally, this is solved by taking averages over arbitrary intervals, or incorporating arbitrary lagged variables.

To better understand which preceding conditions are important, I compare three approaches that can deal with lagged response: penalized signal regression, distributed lag models, and stochastic antecedent models (Ogle et al., 2015). The three approaches differ in terms of number of parameters required, ease in which interactions can be modelled, and ease of model formulation and fitting. I give a brief overview of these three approaches and illustrate them on an example of daily pollen count predictions.

Keywords: Phenology, Time series

Ben Stevenson (University of Auckland) with Jessie Colbert, Melissa Bowen, and Rochelle Constantine

Spatiotemporal models to estimate cetacean distribution in the Hauraki Gulf, Auckland, New Zealand

06/26/2020 8:15:00 AM-8:30:00 AM

Session: Spatio-temporal data *(Chair: Theoni Photopoulou)*

Location: #darwinia

Environmental variables like sea surface temperature (SST) are critical drivers of ocean processes, and key determinants of the abundance and distribution of marine species. In this talk, I describe spatiotemporal models fitted to cetacean sighting data collected from 2000--2019 in the Hauraki Gulf, Auckland, New Zealand, by the crew of a commercial whale watching vessel. We incorporate sea surface temperature measurements taken daily at the nearby Leigh Marine Laboratory.

Using latent spatiotemporal Gaussian processes, our models estimate animal distribution and how it varies from one month to the next, revealing hot spots in animal density that have some temporal persistence. We also identify a spatial resdistribution of animals related to changes in SST.

The majority of existing species distribution models fitted to cetacean sighting data have relied solely on fixed effects of environmental covariates. Our work highlights the importance of taking a flexible approach that can unveil spatial and temporal patterns unrelated to observed variables. With recent rapid advancements in computational methods and software, such TMB and INLA, fitting complex spatiotemporal models is possible even for large data sets like ours, which included 8601 cetacan sightings on 981 whale watching trips across a 20-year period.

Keywords: Citizen science, Hierarchical modelling, Spatio-temporal statistics, Species distribution modelling

Nathalie Peyrard (INRAE) with RÃ©gis Sabbadin, Marie-JosÃ©e Cros, Ronan TrÃ©pos and Sam Nicol

A hidden semi-Markov model for inferring the structure of migratory bird flyway networks

06/26/2020 8:30:00 AM-8:45:00 AM

Session: Spatio-temporal data *(Chair: Theoni Photopoulou)*

Location: #darwinia

Every year, >50 million shorebirds migrate from breeding grounds in Siberia to overwintering habitat in Australasia. This migration is threatened by development pressures at stopover sites along the migratory route. Prioritising critical bird habitat requires knowledge of the routes followed by birds, but our knowledge on the relative numbers of birds moving between stopover sites is limited. It currently relies on few observations and expert judgement.

We propose to use a network model and observed count data to determine the most likely migration routes using statistical modelling and efficient inference tools. Available count data is collected at irregular intervals and is noisy due to detection errors. We model the discrete network, noisy data and duration of stopover time at sites as a set of interacting Hidden Semi Markov Models (HSMM). In our model, individual birds sojourn in stopover nodes for a period of time before moving to other nodes with an unknown probability that we aim to estimate. For this kind of HSMM, exact estimation of model parameters using existing approaches is not possible for even a small number of nodes due to the dimension of the hidden state. We designed three dedicated estimation algorithms for our model: Monte Carlo EM, ABC, and Variational Bayes EM. We will present and compare the efficiency and quality of estimation of these three approaches on synthetic data.

The proposed approach is general and can model the spread dynamics of any population of individuals on a network of sites.

Keywords: Movement modelling, Population dynamics, Spatio-temporal statistics

James Clarke (University of Kent) with Rachel S. McCrea, Emily Dennis and Byron Morgan

Modelling butterfly lifespans using citizen-science count data

06/26/2020 8:45:00 AM-9:00:00 AM

Session: Spatio-temporal data *(Chair: Theoni Photopoulou)*

Location: #darwinia

Over the past four decades, three-quarters of UK butterfly species have declined in abundance, distribution or both. Butterflies respond quickly to habitat and climatic change, hence their population status is a valuable biodiversity indicator. Analysis of long-term butterfly monitoring datasets has provided some of the world’s best evidence of the biological impacts of climate change, including major phenological and distribution shifts, evolutionary responses and the impacts of extreme events.

Butterfly lifespans have the potential to be a useful conservation status indicator for butterfly species, with those with shorter lifespans more susceptible to temporal fragmentation, and, therefore, are of greater extinction risk. In this study we are aiming to validate the use of the Generalized Abundance Index, developed by Dennis et al. 2016, to provide lifespan estimates using long-term citizen science count data. The use of this dataset should also allow us to determine the influence of lifespan on butterfly population trends and, therefore, which species require increased conservation effort.

Population trends are primarily assessed at national scales. Within this talk I will present a new statistical model which allows detailed analysis of count data across varying spatial scales, for example across regions, specific habitats or individual sites, in particular by considering for spatial variation in species’ phenology. The new approach also accounts for the influence of external factors such as weather conditions and time of day on the transect counts.

Keywords: Abundance/richness/diversity estimation, Citizen science

Sarah Bauduin (CEFE/ONCFS) with Laetitia Blanc, Aïs Charbonnel, Christophe Duchamp, Nolwenn Drouet-Hoguet, Estelle Germain, Stephanie Kramer-Schadt, Alain Morand, Fridolin Zimmermann, and Olivier Gimenez

Integrating statistical and individual-based models to mitigate lynx-vehicle collisions

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Large carnivores are wide-ranging species, highly mobile, that live in human-dominated landscapes where habitat destruction and fragmentation are important threats. In parallel, the terrestrial transportation network is getting denser and acts as a barrier for the movement of these animals as well as it increases the risk of collisions. The Eurasian lynx (Lynx lynx) is no exception and its populations are at risk, with vehicle collision being the main source of mortality.

Transportation planners and land managers need models to assess the current situation and the consequences of potential future management actions. We built a tool to estimate lynx population viability by combining i) a spatially explicit individual-based model that accounts for lynx movement and demography and ii) two statistical models to quantify lynx favorable habitat and the risk of collision with cars and trains. We built the habitat layer with a dynamic occupancy model using landscape data and opportunistic data on lynx presence. We estimated the risk of collision with a generalized linear model accounting for rare events using road characteristics and data on lynx collisions. The whole model is integrated in a Shiny interface therefore allowing users to easily interact with the model.

We demonstrate how the users can consider various management scenarios simulating actions on the road network, the landscape cover and the lynx populations, and how population viability responds to these perturbations.

Keywords: Dynamic state models, Individual-based models, Mechanistic models, Movement modelling, Occupancy analysis, Population dynamics

Yi-Hsiu Chen (Academia Sinica) with Kyle W. Shertzer and Shay Viehman

Spatio-temporal dynamics of Threatened elkhorn corals Acropora palmata: Implications for conservation under climate change

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Species distribution models (SDM) can be useful for predicting future spatial dynamics. For species vulnerable to climate change, much attention has focused on predicting the future range of occurrence. However, predicted range changes provide little information about the potential impacts on population structure. Here, we develop the application of an SDM approach that incorporates population demography of a Threatened coral species (U.S. Endangered Species Act). We applied process-based dynamic range models to jointly model the spatio-temporal population dynamics and spatial habitat suitability for the Threatened elkhorn coral Acropora palmata in the U.S. Virgin Islands. The approach integrates information from multiple data sources under a hierarchical Bayesian framework. The models connect two components: (1) a niche model that correlates environmental predictors with demographic rates and (2) a size-structured population model that describes local population dynamics and dispersal. Results from models incorporating current climate conditions and future climate scenarios predicted that 1) A. palmata will occur at only a small proportion of the potential habitat of the species, and 2) colony size structure will shift from larger toward smaller colony sizes. Model predictions of a limited geographic range and smaller colony sizes indicate a limitation to future population success. We show that inclusion of population structure into a population range model provides critical information for conservation efforts in the context of climate change.

Keywords: Acropora palmata, Bayesian modelling, Elkhorn coral, Hierarchical modelling, Population dynamics, Process-based model, Species distribution modelling

Diana J. Cole (University of Kent)

Inference with parameter redundant models: reparameterisation, constraints, robust design and integrated models

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

In a parameter redundant or non-identifiable model it is not possible to estimate all the parameters regardless of the amount of data collected (see for example Cole et al, 2010, Mathematical Biosciences). One model that is obviously parameter redundant is the time dependent Cormack-Jolly-Seber capture-recapture model. This is because the last survival parameter and the last recovery parameter only ever appear as a product.

However what if this, or another more complex parameter redundant model, is the model we want to fit to the data? In this talk we discuss the different methods that can be used to adapt a model so that it is no longer parameter redundant.

We could reparameterise the model, for example we could estimate the product of the last survival and recovery parameter. We could use a constraint, for example set the last recapture probability to be 1. Alternatively we could collect more data of a different type and use a robust design or integrated population model. This talk discusses the practicalities of these different methods.

Keywords: Capture-recapture, Identifiability, Inference

Marta Cousido-Rocha (Instituto Español de Oceanografía) with Santiago Cerviño and Maria Grazia Pennino

Rfishpop: A new R-package for the analyses of the fisheries population under uncertainty.

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

The analysis of the dynamic of a population has become a fundamental tool in ecology, conservation biology, and particularly in fisheries science to assess the status of exploited resources. Uncertainty is an inherent component in fishery systems that makes difficult taking management decisions. Here, we present Rfishpop (available on https://github.com/IMPRESSPROJECT/Rfishpop) a package dealing with uncertainty for analyzing exploited populations in R. In its current state, the package includes tools to simulate the real dynamics of a fishery system using a generic age-structured operating model (OM). OM includes a biological system with recruitment, growth, maturity and mortality and a fishery system were fishing intensity and selection are modeled. This system allows to implement structural uncertainty having different options for each process and natural stochasticity playing with variability in these processes. Once the exploited population has been generated through the OM, the package also contains a set of methods to estimate Maximum Sustainable Yield (MSY) reference points. These allow to identify management targets in terms of fishing intensity, population status and yield. The package also contains statistical methods to simulate sampling error, which is another source of uncertainty in fishery management, providing different data types which can suit different assessment methods, from simple data-limited methods to more complex age or length-structured methods. Concluding, the described functions of Rfishpop package allow to verify the performance of management strategies or procedures in different settings generated from the OM. We illustrate some of the capabilities of the package by doing a demonstration with simulated data.

Keywords: Fisheries management, MSE, Population dynamics

Dushyant R. Dudhagara (Bhakta Kavi Narsinh Mehta University)

PAHs distribution and ecological risk assessment using multivariate analysis to decode the impact on ecosystem and microcosm-based bioremediation using identified bacteria

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

The carcinogenic polycyclic aromatic hydrocarbons (PAHs) are widespread environmental contaminants resulting from incomplete combustion of organic materials. The concentration, distribution and ecological risk of PAHs have been investigated in surface sediments western coastline of the Gulf of Cambay, India. Sum of all the PAHs detected in sediment samples represent as a total PAHs (?PAH). The concentration of PAHs detected was ranged from 5.02 to 981.18 mg g-1 dry weight, indicating heavy pollution. The source of PAHs in polluted sediment samples can be diagnosed by calculating various ratios. The various PAHs ratios were used to identify the possible PAHs source. These data of samples were analysed using multivariate statistics such as principal component analysis (PCA), which is gives an idea about the distribution pattern of PAHs, their correlation and their toxicity which are crucial for ecological risk assessment and risk management. Furthermore, the hierarchical cluster analysis (HCA) was performed to grouping the individual PAHs concentrations. Ecological risk assessment can be useful tool for characterization of PAHs risk to organisms and ecosystem proposed the risk measurement of organic substances using risk quotient (RQ) and toxic equivalency factors (TEFs). Based on the assessment of the ecological risk of elevated levels of ?PAHs, I have isolated the bacteria for effective bioremediation strategies and tested for biodegradation of LMW and HMW PAHs under simulated soil conditions. Mycobacterium litorale, was found to degrade a wide range of LMW and HMW PAHs. Degradation of individual PAHs in various stimulated soil matrices was measured at every week up to 5 weeks. Biodegradation kinetics determines biodegradation rate constant (K) and half-life (t1/2) of pollutants in 5 different microcosm soil. Highest degradation of ?PAHs was in soil Compost soil (93.21%) after 35 day. Statistical models have demonstrated, routes of PAHs exposure leading to high risk on marine biota and harmful to food chain and food web. the Study also suggest the novel approach to isolate the bacteria based on the ecological distribution and assessment and development of the bioremediation strategies to remove the PAHs from the polluted site.

Keywords: Ecological risk categorization, Multivariate analysis/joint species distribution models, Risk quotient

Olivier Gimenez (CNRS) with Chistophe Duchamp

Flexible spatio-temporal modelling of occupancy using penalized splines: A case study with the distribution of large carnivores in France.

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

The occupancy state variable may be used as an ecological indicator to inform policy decisions for biodiversity conservation. In this context, occupancy models are increasingly used to investigate the occurrence of animal species while accounting for imperfect detection. Temporal and spatial variation in occupancy may be captured by incorporating relevant covariates. Here, we propose nonparametric and semiparametric regression methods for estimating occupancy. Using the Nimble R package, we employ a fully Bayesian approach using Markov chain Monte Carlo simulations to estimate the model parameters. We illustrate our work by a study of gray wolves (Canis lupus) and Eurasian lynx (Lynx lynx) in France, in which occupancy probabilities are expressed as nonlinear functions of time and geographical coordinates, possibly in interaction, using data from a semi-structured citizen science program.

Keywords: Citizen science, Generalized additive models, Nimble, Occupancy analysis, Species distribution modelling

Clara Grazian (UNSW Sydney) with Pasquale Valentini and Paolo Giordani

Bayesian spatial model for lichen abundance data

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Lichen functional traits are widely used as ecological indicators of environmental quality and, especially, of air pollution. However, due to the high variability of lichen flora across geographic, climatic and ecological gradients, it is often difficult to differentiate the effects of atmospheric pollutants and those of other environmental variables. In order to evaluate this complex relationship, a Bayesian generalised common spatial factor model has been applied to a real dataset concerning lichen biodiversity in Liguria region (Italy). Through a fully Bayesian approach, we contribute to the recent empirical literature by melding together factor models, spatial regression models and geostatistical techniques, in order to explain the multifactorial nature of environmental variables and lichen flora.

Keywords: Abundance/richness/diversity estimation, Dynamic state models, Ecosystem ecology, Hierarchical modelling, Spatio-temporal statistics, Species distribution modelling

Gopal Khanal (Department of National Parks and Wildlife Conservation, Nepal) with Charudutt Mishra and Kulbhushansingh Suryawanshi

Using spatial capture-recapture methods to establish baseline abundance and density estimates of snow leopard in western Himalaya Nepal

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Reliable estimates of animal abundance and density are central to species conservation. For snow leopard Panthera uncia, a large mammalian carnivore of Asian high mountains, lack of reliable estimates of its population status has been a key limiting factor for effective conservation planning. In fact, merely 2 % of its distribution range has been surveyed adequately for its population state variables, which highlights both uncertainty over its estimated global population status and the need for more rigorous field-based assessments. We obtained first ever baseline estimate of abundance and density of snow leopard in Shey Phoksundo National Park, Nepal. We deployed a total of 65 camera traps (Model HC550; Reonyx Inc, and Cuddeback IR) at 62 stations in the two study sites-Upper Dolpa and Lower Dolpa over an area of approximately 1000 km2 from November 2017 through April 2018. Spatial capture recapture history of 23 unique snow leopard were prepared for the first 90 sampling occasions and included for analysis to adhere the closure assumption. Spatially explicit capture recapture analysis of camera trapping data showed snow leopard density of 1.24 (95% CI 0.58–2.54) and 2.51 (95% CI 1.36–4.60) adults per 100 square kilometers in Lower and Upper Dolpa, respectively. Overall, this study established the reliable estimates of snow leopard abundance and density for Nepal’s Shey Phoksundo National Park, which in addition to serving as useful baseline measure for future monitoring has immediate implications for park level conservation planning.

Keywords: Abundance/richness/diversity estimation, Spatial capture-recapture

Stefan Kunz (University Landau) with Chuck Hawkins, LeRoy Poff, Laura Twardochleb, Philippe Usseglio-Polatera, Ben Kefford, Astrid Schmidt-Kloiber, Wolfram Graf, Christoph Matthaei,and Ralf B. Schäfer

Do the trait profiles of macroinvertebrates converge across different biogeographic regions?

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

Over the last decades, comprehensive databases on macroinvertebrate traits have been compiled by aquatic ecologists. Traits can be linked to environmental drivers to establish mechanistic explanations of species distributions and assemblage compositions. Trait–environment relationships could potentially be transferred across regions, as studies showed a largely similar trait distribution over North America and Europe. However, inconsistent and spurious trait-environment relationships may arise when trait interactions are ignored, given that the entire organism, not an individual trait, responds to its environment. In fact, evolutionary processes such as natural selection have likely selected multiple traits simultaneously, so-called trait profiles, that together provide adaptation to changing environmental conditions. For example, the combination of rapid growth and obligate diapause allows adapting to habitats with predictable intervals of short favorable conditions and long adverse conditions.

We collated and harmonized the available freshwater invertebrate trait information from different biogeographic regions (Europe, North America, Australia, and New Zealand) to establish a unified trait database that allows for large-scale trait analyses. Using hierarchical cluster analysis, we defined groups of organisms with similar trait profiles, i.e. trait profile groups (TPG). For these TPGs, we identified the most important traits for TPG selection using Random Forests. By comparing the TPGs across regions and across climatic zones we reveal large scale patterns of TPGs and evaluate convergent evolutionary adaption. We discuss our results with regard to the applicability of trait-environment relationships across regions and point out future perspectives on the usage of trait profiles in assessing trait-environment relationships.

Keywords: Trait based ecology

Erik Kusch (Universitetet i Bergen) with Alistair Seddon and Richard Davy

Understanding Ecosystem Resilience - Intrinsic vegetation memory as a proxy of engineering resilience may be an oversimplification.

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

Vegetation memory describes the effect of antecedent environmental and ecosystem states on ecosystem state in the present and has been used as an important proxy for ecosystem recovery rates potentially a key component of vegetation resilience, at a global scale. We tested the components and drivers of vegetation memory in dryland regions using state-of-the-art climate reanalysis data and geo-statistical downscaling methods which have hitherto been used sparsely in ecology and certainly not at global scales. Furthermore, we refined statistical models and model selection to identify vegetation-memory characteristics across global dryland regions. We showed that (1) dryland regions are characterised by strong vegetation memory (intrinsic and extrinsic), (2) it is possible to distinguish intrinsic and extrinsic vegetation memory to a hitherto unachieved degree using novel, downscaled climate reanalysis data sets, (3) the link between intrinsic vegetation memory and resilience may be an oversimplification, and (4) dryland vegetation does not react to bioclimatic forcing in the same way across the Earth. Our findings demonstrate novel observations of vegetation memory patterns across dryland regions such as regional differences of processes forming vegetation memory capabilities. Consequently, this study provides a helpful stepping stone for refining and combining already existing methodology which could, in turn, generate important knowledge of ecosystem functioning and resilience particularly of interest for policy makers and land-use managers. Currently, we are working to establish the link between vegetation memory and plant function to bolster usability of this framework by non-biologists.

Keywords: Ecosystem ecology, GPS data, Interdisciplinary ecology, Population dynamics, Population ecology, Remote Sensing, Resilience, Spatio-temporal statistics, Theoretical ecology, Trait based ecology

Kevin D Newman (University of Melbourne)

Optimal Surveillance Methods

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

Often referred to as a nuisance parameter, in some contexts detection is a priority in occupancy modelling to locate individuals or colonies for protection. Technological developments have improved the ability to detect rare or critically endangered species and detection of these species are important for their conservation. The available budget and various costs should be considered when aiming to maximize detection probability, where the budget and costs are either monetary or available effort. Direct surveying methods, such as spotlighting, line counts, and thermal imaging,require large amounts of time spent out in the field and relevant expertise and equipment to ensure accuracy. Indirect methods, such as remote sensing cameras and acoustic monitoring, require initial set up followed by a period of maintenance, and the bulk of time might be spent post fieldwork to go through large amounts of data. I define a budget of effort and split into two considerations,establishment of a site and then ongoing maintenance or processing of the site.Here I examine occupancy models in which a target species occupies a fraction of the possible survey sites (?), establishing a new site has a fixed cost (c), each survey of a site entails a cost (t), there is imperfect detection of the species during each survey (q), and there is a total budget that can be allocated across establishing sites and surveying them (B). I show that the expected number of detections is maximized by surveying each site with a particular number of visits (v). This can be utilised by researchers to optimise their detection prior to field work and provide opportunities for optimal allocation of budget

Keywords: Occupancy analysis

David A. Nipperess (Macquarie University)

Generalised Complementarity Analysis: a framework for measuring and modelling the contribution of places to regional, national or global biodiversity

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Efficient spatial conservation planning requires the determination of the contribution of each site to regional, national or global biodiversity. That is, we must measure, for each site, Complementarity (the gain in diversity achieved when adding that site to a set of other sites) and Irreplaceability (the overall complementarity of that site when compared to a range of possible combinations of other sites). Generalised Complementarity Analysis (GCA) provides an exact analytical solution for the expected complementarity of a focal site, when added to a set of any other sites of a given size (??). Diversity is defined very generally to allow for complementarity to be calculated for species richness, Functional Diversity or Phylogenetic Diversity. The expected irreplaceability of a focal site is then defined as the area under the curve of expected complementarity for all possible values of ??. GCA is much more computationally efficient than existing algorithmic approaches and is scalable to very large numbers of sites. Further, complementarity can be modelled for unknown sites from environmental predictors, under the robust assumption that environmentally distinctive sites are more likely to make unique contributions to overall diversity. By modelling both the alpha-diversity of each site and the compositional dissimilarity of all pairs of sites (from Generalised Dissimilarity Modelling), the complementarity and irreplaceability of each site can be determined.

Keywords: Abundance/richness/diversity estimation, Community ecology, Multivariate analysis/joint species distribution models

Maria Grazia Pennino (Instituto Español de Oceanografia) with Francisco Izquierdo, Marta Cousido, Santiago Cerviño, Francisco Velasco, Jaime Otero, Rafael Bañón and Alex Alonso-Fernández

Improving abundance indexes for fish stock assessment model calibration

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Time series of abundance indices are the main source of information to calibrate stock assessment models. Accurate and precise abundance indices are essential for successful conservation and management of fish stocks. Commonly, scientific standardized surveys are used for this aim and ensure that estimates are unbiased. However, the statistical efficiency of a design-based estimator may be low under certain circumstances. In particular the sole (Solea solea) is a species with a biological bathymetric range between 0 and 200 meters in the Iberian Atlantic waters. The annual scientific survey that collects data for demersal species in this area only cover partially this bathymetric range and the resultant abundance indexes are consequently underestimated. In addition, habitat variables, (i.e., bathymetry), can influence these estimates as well as the spatio-temporal variability. Alternatively, standardized CPUEs (catch per unit effort) derived fishery-dependent data can be used as a proxy of the species abundance. Within this context, in this study will be produced two different abundances indexes and contrast them with a classical design-based index, evaluating the impacts on the sole assessment using as stock assessment model the SPiCT (stochastic surplus production model in continuous time). In particular fishery independent data were analyzed using a Bayesian hurdle hierarchical spatial-temporal models, considering bathymetry as an environmental variable. Fishery-depended data were also analyzed using a Bayesian Generalized Mixed Model and spatio-temporal effects. We argue that using explicitly spatio-temporal abundance indexes can improve the assessment of stocks and in particular for the ones that are in a data-limited situation.

Keywords: Abundance/richness/diversity estimation, Bayesian analysis, Fishery management, Spatial ecology, Stock assessment model

Enrico Pirotta (Washington State University) with Vincent Hin, Marc Mangel, Leslie New, Daniel P. Costa, André M. de Roos and John Harwood

Applying state-dependent life-history theory to a dynamic energy budget model to investigate reproductive strategy and susceptibility to disturbance

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Animals initiate, interrupt or invest resources in reproduction in light of their physiology and the state of the environment. The energetic risks entailed in an individual’s reproductive strategy can have a strong influence on the ability to cope with additional stressors, such as anthropogenic climate change and disturbance. To explore the trade-offs between internal state, external environment and reproduction, we applied state-dependent life-history theory (SDLHT, implemented via stochastic dynamic programming) to a dynamic energy budget (DEB) model for a medium-sized cetacean (long-finned pilot whales Globicephala melas). We investigated how different reproductive strategies emerge from the interplay between fitness maximisation and the propensity to take energetic risks, and how these strategies then affect susceptibility of individual vital rates to disturbance. In the absence of disturbance, facultative, optimised behaviour from SDLHT and fixed behavioural rules in the corresponding DEB model led to comparable individual fitness. However, when animals were exposed to disturbance, the reproductive strategies emerging from SDLHT increased vulnerability to energetic risks, resulting in a lower fitness than fixed rules. Heterogeneous environmental conditions favoured more cautious, and thus more robust, strategies, particularly when environmental oscillations were more predictable. Age at first reproduction and the amount of milk delivered to calves emerged as critical components of an individual’s strategy. Our results demonstrate that the assumptions of bioenergetic models around the dynamic trade-offs underlying an individual’s decision-making can have important consequences for predicting the effects of anthropogenic stressors on wildlife populations and the resulting management implications.

Keywords: Behavioural ecology, Dynamic state models, Fitness models, Individual-based models, Mechanistic models

Jenicca Poongavanan (University of Cape Town/ University of Florida) with Res Altwegg, Ian Durbach and John Measey

Modelling the range-wide density patterns of the Arthroleptella Lightfooti using acoustic monitoring data

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

Species distributions are often limited by environmental factors and according to the abundant-centre hypothesis, abundance should be highest where the environment is most favourable for the species. So, do the same environmental factors determine occurrence and abundance patterns inside the range? I examined this question using Arthroleptella lightfooti, a species of frog from the family of Pyxicephalidae, endemic to the mountains of the Cape peninsula, South Africa.

I used density estimates obtained from acoustic Spatially Explicit Capture Recapture (aSCR) methods and data from an acoustic survey to construct the first peninsula wide population-density surface for this visually cryptic but acoustically active species. Two data sets were created from the original: one shows whether the species is present or not and the other indicates the density when the species is present. A Hurdle Model was then fitted to the two sets of data. The two resulting best models were then combined to estimate the expected density of the species.

I found that covariates explaining variation in occurrence were not the same as those explaining variation in density, suggesting that processes determining occurrence were not always those determining density. Presence of the Lightfoot's moss frog was largely explained by topographic features and availability of water. Moreover, this study produces the first Peninsula wide population density surface of A. lightfooti. At the same time, I assess the ability of opportunistically collected presence-only records to improve the estimation of the expected population-density surface. The presence-only records were constructed into a habitat suitability map using an ensemble of species distribution models and was then integrated in the modelling framework as a covariate.

Keywords: Abundance/richness/diversity estimation, Acoustic survey, Machine learning, Spatially explicit capture recapture, Species abundance modelling, Species distribution modelling

Edgar Santos-Fernandez (Queensland University of Technology) with Erin Peterson and Kerrie Mengersen

Bayesian item response models for citizen science ecological data

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

So-called citizen science data elicited from crowds has become increasingly popular in ecology. However, the quality of this information is being fiercely debated by many within the scientific community. Therefore, modern citizen science implementations require measures of the users' proficiency that account for the difficulty of the tasks. We introduce a new methodological framework of item response and linear logistic test models with application to citizen science data used in ecology research. A specific feature of this approach is that spatial autocorrelation is accommodated within the item difficulties. The models produce relevant ecological measures of species and site-related difficulties, discriminatory power and guessing behaviour. These, along with estimates of the subject abilities allow better management of these programs. We found that the suggested methods outperform the traditional item response models in terms of RMSE, accuracy, and WAIC based on leave-one-out cross-validation on simulated and using empirical data. The fit of item response models to big data via divide-and-conquer is also discussed. We illustrate the implementation using a case study of species identification in the Serengeti, Tanzania.

Keywords: Ability estimation, Big data, Item response model, Latent variable regression, Spatial model

Meryl Theng (University of Adelaide) with Phill Cassey and Steven S. Delean

Capturing the complexity of animal movement in model estimation from camera-trap data

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

In the past decade, the advent of remotely-triggered cameras has greatly improved our understanding of ecological relationships and population dynamics of terrestrial mammal species. However, limitations in the ability to make quantitative inferences from the data continue to impede the field of applied conservation at great financial and logistic cost. This is a particular issue with species without unique markings, which constitute the majority of the mammal fauna. Despite this, camera assessments continue to rely on existing occupancy and abundance models to quantify spatial and temporal differences in species or communities, often without full consideration of the underlying limitations and assumptions that are usually violated in the field. Numerous confounders such as space use, movement speed, and body size obscure parameters of interest on the species-, population- and even individual- level. We discuss how to address some of these ecological complexities of community studies in Bayesian hierarchical multispecies occupancy and abundance models by incorporating prior species-level information and evaluating its performance within spatially-explicit movement simulations.

Keywords: Abundance/richness/diversity estimation, Camera trap data, Community ecology, Hierarchical modelling, Model assessment/validation

Udani Abhisheka Wijewardhana (Swinburne University of Technology) with Denny Meyer and Madawa Jayawarda

Statistical models for the persistence of birds developed using citizen science data

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

In the past fox predation was the greatest land-based threat to the long-term viability of the shorebird colonies on Phillip Island, Victoria, Australia. Regular fox control for 20 years up to 2006 had reduced the fox population, but shorebirds continued to be decimated. Therefore, an eradication program was put in place in 2006. This program targeted the entire semi-isolated fox population taking mainland migrants into account. There were three phases to this program called knock-down, clean-up and post-eradication. Each campaign was arranged to avoid the summer season with a strong emphasis on the winter season. An effective knock-down was declared in 2011. In the clean-up phase, in addition to the island-wide baiting effort, more intensive baiting with a range of bait types is being conducted for sites with any sign of foxes. However, the impact of these measures for local shorebirds has never been thoroughly assessed. This study aims to track the effects of the fox eradication program on abundance measures for the eight local shorebird species found on Philip Island. These include the locally threatened Hooded Plover and Sooty Oystercatcher. For this purpose, we have used monthly citizen science data for 2002 to 2017, adjusted for possible confounding variables such as mean temperature, rainfall and resident human population in an attempt to control for some of the biases inherent in our citizen science data. Changepoint analysis techniques have been used in this context to assess the impact of the fox eradication program and other interventions such as dog controls. The findings will inform policy making for future pest eradication programs affecting shorebird populations.

Keywords: Abundance/richness/diversity estimation, Changepoint analysis, Citizen science, Occupancy analysis, Probability of persistence, Spatio-temporal models, Spatio-temporal statistics, Species distribution modelling

Nan Zheng (Memorial University of Newfoundland) with Noel Cadigan

Spatiotemporal modelling approach for combined estimation of fish growth and maturity when data are collected through length stratified sampling

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Fish growth is biphasic due to the reallocation of energy for reproduction upon maturity. Therefore, it is usually necessary to estimate age patterns in growth and maturity together, especially when data are collected through length selective sampling. We investigate many published models and extend them as spatiotemporal mixed effects models suitable for large spatial scale and long term fisheries survey programs. The models and the methodology are applied to data for an American plaice fish stock in the Northwest Atlantic (NAFO Divisions 3LNO) to find the optimal approach for estimating spatiotemporal variation in size- and age-at-maturity. For more precise inferences, issues such as the research survey gear selectivity, the sampling scheme, and between-individual variation in growth and maturation all need to be effectively accounted for. We develop the theory and methodology to deal with these issues with feasible calculation costs for fine spatiotemporal resolution and big survey data. The estimates of the distribution of size-at-age and age/length-at-maturation are important inputs to a spatial stock assessment model being developed for 3LNO American plaice.

Keywords: Hierarchical modelling, Model assessment/validation, Spatio-temporal statistics

Lekshmi Ashok (National Institute of Technology Calicut) with George K.Varghese and Santosh G.Thampi

Payoff calculations when Game Theory is applied to biodiversity conservation

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

A major challenge in applying game theory to resolve environmental conflicts is the difficulty in arriving at the payoffs of stakeholders corresponding to the strategies they adopt. This study demonstrates payoff calculation for a game formulated to conserve the biodiversity of the Western Ghats mountain ranges in India. As per the recommendation of a panel of experts, a two-layered buffer-zone around the protected areas, with varying restrictions in activities, was accepted as one of the measures to protect the biodiversity of the Western Ghats. But, the implementation of the proposal in the densely populated areas that fall under the buffer layer leads to the nature-man conflict. The game was formulated to find ways of implementing the proposal with least resistance from stakeholders. The players of the game were identified as the Government, the residents of the Western Ghats, and the non-residents. Each player was identified with two strategies and the corresponding payoffs were calculated. The payoff of the residents depends on the restrictions for their activities in the buffer layer, concerned. Around 184 villages in the Kerala state will be affected by the proposal. The population of the affected village was selected as the criteria for conducting a questionnaire survey among the different groups of residents for payoff calculation. A Chi-Square test was performed to check whether the sample correctly represented the population. Conjoint analysis was conducted among the non-residents to find out their willingness to pay for the indirect benefits from the protected environment. The payoffs, so calculated, was used in a non-cooperative game theory formulated with 3 players and the solution of game, i.e., the Nash Equilibrium was identified based on the principle of dominance.

Keywords: Applied Ecology, Biodiversity conservation, Game Theory, Pay-off Calculation, Theoretical ecology

Francisco Cervantes (University of Cape Town) with Theoni Photopoulou, Rob E. Simmons and Birgit Erni

A flexible kernel density estimator for animal activity distribution based on movement trajectories

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

It is not always possible to deploy tracking devices to study animal movement, necessitating the use of other, more opportunistic methods for data collection. For example, vantage point surveys, from which observers map bird movements, are standard practice in the study of raptor activity around wind farms to identify areas that accumulate flight activity. Although fragmented and potentially short, treating observed flights as isolated points may result in the loss of important spatial information. We propose a kernel-based procedure to estimate the distribution of raptor activity intensity using flight trajectories mapped by human observers. Following traditional kernel density estimation, a kernel function is centred at each observation and the total density is given by the average of the kernels of all observations. However, in this case, each trajectory is considered to be a single observation. Thus, the shape of the kernel function depends both on the shape of the flight and on a smoothing parameter, which is selected using a blocking likelihood cross-validation procedure. This involves leaving out one full trajectory at a time and selecting the smoothing parameter that produces kernel estimates with the highest likelihood for the unobserved (left out) trajectories. In this poster, we present the method used to build the kernel function for each trajectory, as well as the procedure to select an appropriate bandwidth. We finish by showing how this kernel density procedure outperforms a selection of methods designed for independent and identically distributed data.

Keywords: Kernel density, Movement modelling

Louisa C Mamalis (Universidade Federal do Rio Grande do Sul) with G. Ferraz and V. Zulian

Using citizen science to map geographic range: a case study of the Greater Rhea, Rhea americana in Rio Grande do Sul, Brazil

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Determining the distribution of species and examining the species-habitat interactions are key themes that need to be understood for successful conservation management planning. This is especially important under the landscape scale changes being seen due to increasing human activities. This large scale data can be labour intensive to collect therefore citizen science is a tool that is being increasingly employed. It can be used to generate data on species distribution on a large spatial and temporal scale in a less intensive way. The greater rhea is a large flightless bird endemic to South America where it's grassland habitat its threatened, mainly by, soyabean cultivation and cattle ranching. The aim of this study was to test two hypotheses 1) that there would be a positive relationship between the greater rhea and the presence of cattle ranching and 2) to determine the influence of soyabean cultivation on the estimated occupancy of the greater rhea. Presence-absence data was used to create an occupancy model within a Bayesian framework. This tested site occupancy of the greater rhea alongside the two covariates. The occupancy estimates showed a positive relationship between both the cattle ranching (0.06 ± 0.02) and soyabean cultivation (3.90 ± 1.68). These results show the greater rhea as an opportunistic and generalist species capable of living within human modified landscapes, especially cattle ranches due to the provision of food and safety. This has implications for the protection and conservation of the species and grassland such as increasing suitable food resources within cattle ranches.

Keywords: Citizen science

Jorge A. Navarro Alberto (Universidad Autónoma de Yucatán) with Bryan F. J. Manly

Null modeling approach resists to die: Faddy distributions in a probabilistic randomization protocol for presence-absence data

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Frequentist techniques have contributed to the development of null model analysis of (1-0) data in community ecology using randomization tests, assuming probability distributions under the null scenarios as in the work by Navarro and Manly (2009) (NM), a protocol that has been applied in the analysis of plant and microbial communities, and chemical hazards. We provide the theoretical formulation of the original NM protocol for null model analysis, and then expand the quasi-abundance distributions, based on extended Poisson processes (Faddy 1997), to allow general distributions of over-dispersed and under-dispersed discrete random variables. For the binomial case and Faddy distributions, nonlinear constrained optimization algorithms are needed in order to get maximum likelihood estimates thus, the null-model selection process faces challenging numerical problems (non-convergence to the global optimum). In addition, the process may end up suggesting that the best fitted probabilities for the generation of null matrices are those obtained from links different to the (canonical) logistic and the complementary log-log links. This property of the NM protocol should not be ignored, as an improper choice of the null matrix universe may impact the outcome of randomization tests.

Keywords: Community ecology, Model assessment/validation, Software development, Species distribution modelling

Grace J. Di Cecco (University of North Carolina - Chapel Hill) with Allen H. Hurlbert

Interaction of climate change and forest fragmentation effects on population trends in forest breeding birds

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

Climate change has driven large-scale population decline of many species and habitat fragmentation threatens decline in species abundance beyond those expected from total amount of habitat lost. While many studies have focused on studying the impacts of individual global change drivers on species, species are experiencing multiple changes to their environment simultaneously. We examine the interaction of these drivers at large geographic extents to provide insight into how global change drivers will affect biodiversity. We use bird abundance data from the Breeding Bird Survey along with land cover and climate data between 1990 and 2016 to model how forest fragmentation and climate change predict changes in population trends of 67 forest breeding bird species throughout the United States and Canada. Secondly, we determine whether ecological traits such as migratory strategy, habitat specialization, and thermal niche width can predict the susceptibility of species to the impacts of forest fragmentation and climate change. About 23% of species show response in abundance trend to changes in both trends in breeding season temperature and changes in forest cover and forest edge density and the majority of those species showed support for interactions between land cover and climate change metrics. Forest specialist species respond more negatively to increases in forest edge density. Relevant anthropogenic drivers of change in population trend are highly variable across species, however many species show context dependence in population responses to climate and land use change. Researchers should consider multiple sources of anthropogenic change when studying how global change impacts biodiversity.

Keywords: Population dynamics

Rebecca Fisher (Australian Institute of Marine Science) with Glenn R. Shiell, Rohan J. Sadler, Kari Inostroza, George Shedrawi, Thomas H. Holmes and James M. McGree

‘epower’: an R package for power analysis of Before-After-Control-Impact (BACI) designs.

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Before-After-Control-Impact (BACI) designs are widespread in environmental science, however their implicitly hierarchical nature complicates the calculation of statistical power. Here we describe ‘epower’, an R package for assessing statistical power of BACI designs. The package uses Bayesian statistical methods via the package INLA to fit the appropriate hierarchical model to user supplied pilot survey data. A posterior sample is then used to build a Monte Carlo simulation to test statistical power specifically for the Before/After × Control/Impact interaction term in the BACI model. Power can be assessed for any number of user specified effect sizes for the existing design, or across a range of levels of replication for any part of the sampling design hierarchy. The package offers a user friendly robust approach for assessing statistical power of BACI designs whilst accounting for uncertainty in parameter values within a fully generalized framework.

Keywords: Abundance/richness/diversity estimation, Before-after-control-impact, Environmental impact detection, Hierarchical modelling, Power analysis, Sampling design assessment, Software development

Chloe M. Francis (University of Kent) with Diana J. Cole, Rachel S. McCrea and Simon Tollington

Statistical Modelling of Spatial and Temporal Patterns in Human-Elephant Conflict

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

Elephant sighting data have been collected from two spatially independent populations: ‘Goalpara’ on the southern side of the river Brahmaputra and ‘Sonitpur’ on the northern side in Assam, India. Sightings were collected on a regional basis and several monitors were employed to record sightings form their home area – either made by themselves or reported to them by other villages. The observations comprise of all sightings regardless of whether that sighting also included an incident of ‘conflict’, where damage was recorded to person, property or elephant.

The number of sightings has decreased over time, along with the number of elephants per sighting and the number of conflict incidents. However, this project has investigated whether these patterns are an artefact of recording bias. We have employed distance-sampling methods to estimate the ability of the monitors to detect elephants and have assessed whether detection functions have changed over time. Further, we will look at spatio-temporal patterns of elephant movement and will investigate whether we can obtain information on elephant population size, viability and reproduction from the available data.

Keywords: Distance sampling, Spatio-temporal statistics

Eric J. Gangloff (Ohio Wesleyan University) with Vianey Leos Barajas and Anne M. Bronikowski

Combining hidden Markov models and animal personality framework reveals personality axes in neonate garter snakes (Thamnophis elegans)

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Statistical methodologies to analyze and characterize the movements of animals across landscapes have advanced tremendously in recent years, for example the application of hidden Markov models to time-series data of animal location. At the same time, our understanding of the ecological and evolutionary consequences of within-individual consistency and correlation of behaviors has proved a fertile research area. Few studies, however, have combined these paradigms to explore how these different ecological questions – and their attendant statistical approaches – may be complementary. With this study, we repeated behavioral assays with captive-born western terrestrial garter snakes (Thamnophis elegans). We used video analysis to extract indicators of snake exploratory and risk aversion behavior (average movement speed, tongue-flick rate, latency to emerge, and area explored). Using mixed models in a Bayesian framework, we estimated within-individual consistency and correlations among these behaviors. We then applied a Bayesian hierarchical hidden Markov model to fine-scale movement data to assess whether discrete latent behavioral states explain movement data. Snakes exhibited high levels of among-individual variation for all traits, some of which could be explained by family effects. Bivariate mixed models revealed different patterns of within- and among-individual variation in behaviors that describe two distinct personality axes in snakes: exploratory-escape behaviour and boldness. In conjunction, our hidden Markov models revealed distinct behavioral states that predicted movement patterns and that these states were consistent across time. Together, our novel dataset and analyses provide direction to further explore the joint application of statistical methodologies often relegated to different fields.

Keywords: Behavioural ecology

Anjana Ghelani (Hemchandracharya North Gujarat University)

Microbial Composition and Functional Profiling of Coastal Soil of Arabian Sea by Metagenomics approach

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

Marine microorganisms constitute more than 90% of the biomass in the sea. They are crucial to nutrient recycling in ecosystems. Next-generation sequencing allows quick and inexpensive analysis of marine habitats and revolutionizing marine microbial ecology. In the present study, we are presenting the microbial composition and metabolic profiling of three sites of Gulf of Cambay, western India, i.e., Dandi (DA), Nargol (NA) and Umargam (UA) using whole shotgun sequencing by Illumina Miseq platform. Mg-RAST and STAMP were used to analyze the metagenomes. The total reads from DA were 3.7, 6.6 and 4.0 million for DA, NA and UA respectively. Total 18, 38 and 36 phyla were reported in DA, NA and UA metagenome. The most abundance community phyla Proteobacteria are 48.0%, 37.7% and 33.8% in DA, NA and UA respectively. Unidentified and unassigned sequences were also detected in all three samples, which indicate the possibilities to translate the hidden unculturable microbes. The detection of various key biological processes including response to biotic stimulus, stress response genes are the signs for adaptation against stresses exist in a marine ecosystem. Based on the detection of various molecular and cellular traits, nutritional versatility was also indicated in the marine microbial community of each site. Due to the detection of the diverse gene pool, cultivation approach has been used to trap the various traits and 8 potential species were isolated. Statistical and comparative analysis suggests the rich microbial diversity flourish in all three sites.

Keywords: Abundance/richness/diversity estimation, Ecosystem ecology, Marine metagenome, Metagenomics

Keshab Gogoi (Wildlife Institute of India) with Ujjwal Kumar, Kausik Banerjee and Yadvendradev V. Jhala

Counting the cats: A robust approach to estimate density and its determinants of Asiatic lions in the Gir Forests of India

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

Asiatic lions (Panthera leo persica) are an icon of conservation success, yet their status is inferred from total counts that cannot account for detection bias and double counts. Therefore, in this study we aimed to develop a robust yet easily applicable method to estimate lion density and underlying processes in western Gir Protected Area, India. We used spatially explicit capture recapture polygon search framework to estimate lion density in an area of 725 km2. Using vibrissae patterns and permanent body marks, we identified 67 lions from 368 lion sightings. We conducted distance sampling on 35 foot transects to estimate spatial prey density by using density surface modelling. Subsequently, we modeled lion spatial density with prey, habitat characteristics, anthropogenic factors and distance to baiting sites. Lion density (>1-year-old lions) was estimated at 8.53 (SE 1.05) /100 km2 with lionesses having smaller movement parameter (2.55 km; SE 0.12) than males (5.32 km; SE 0.33). Detection corrected sex ratio (female:male lions) was 1.14 (SE 0.02). Chital (Axis axis) was the most abundant ungulate with a density of 58.17 (SE 22.17)/km2, followed by sambar (Rusa unicolor) at 4.73 (SE 1.48)/km2. Spatial lion density was best explained by proximity to baiting sites and flat valley habitat but not as much by prey density. We demonstrate a scientifically robust approach to estimate lion abundance, that due to its spatial context, can be useful for management of habitat and human-lion interface. We recommend this method for lion population assessment across their range. Management practice of attracting lions for tourism can perturb natural lion densities, disrupt behavior, lion social dynamics and have detrimental effects on local prey densities.

Keywords: Abundance/richness/diversity estimation, Capture-mark-recapture, Distance sampling, GPS data, Multivariate analysis/joint species distribution models, Population ecology, Spatial capture-recapture, Species distribution modelling

Sony Lama (Red Panda Network) with Saroj Shrestha, Rayan P. Koju and Ang P. Sherpa

Assessment of the impacts of livestock grazing on red panda (Ailurus fulgens) habitat in Eastern Nepal.

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

The present study was carried out in Singhadevi and Chipchipe Community forest of Ilam district, Eastern Nepal mainly focusing on the evaluation of the impacts of livestock grazing on red panda and scrutinization of the habitat preferences of red panda. Questionnaire survey and Key Informant Interviews were carried out to evaluate the perception of local community on conservation menace and importance of red panda conservation. Besides, in the forests, 15 linear transects were delineated at an elevation gap of 100m. 10×10m plots were established both at the starting and end points of linear transects. Moreover, along each transect, additional plots were demarcated where any indication of red panda and livestock signs was observed. To explore the habitat preferences of red panda, vegetation abundance and coverage percentage of vegetation layers (canopy and shrub layer) were determined from each plot. Additionally, distance to the nearest water source was measured from the plot centre. Almost all delineated plots in Singhadevi Community forest, presented livestock presence. However, in Chipchipe Community forest, livestock disturbances were seen in 66% of the sampled areas. Litsea elongata, Lithocarpus pachyphylla and Rhododendron falconeri were found to be the most dominant plant species in both community forests. Water availability is recognized as an important aspect that determines the habitat of red panda. Livestock herding has induced detrimental impacts on the habitat of red panda inside the community forests.

Keywords: Abundance/richness/diversity estimation, Anthropogenic Impacts on habitat and persistence of endangered species, Behavioural ecology, Citizen science, Community Forest, Conservation threats, GPS data, Key Informant Interview, Livestock grazing, Multivaria

László Zoltán (Babes-Bolyai University,) with H. Beáta gy, Avar-L. Dénes, An Dénes, Orsolya Antal and Béla Tóthmérész

A combined measure of specialization and phylogenetic diversity with an Odonata case study

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Measuring the specialization of species, and beyond, the specialization of a whole community still remains a major challenge in ecology. Moreover, the relationship of specialization and diversity is even less explored. Here, we develop a combination of specialization indices for species and communities with the phylogenetic diversity index based on ecological and phylogenetic characteristic of dragonfly and damselfly species. Our proposal is based on the indices proposed by Fridley et al. (2007) and Cadotte et al. (2010). We used citizen science observation databases for calculating species specializations, and barcoding databases for calculating phylogenies. Then we applied these indices to assess the effects of local and landscape level factors for a set of Odonata communities of Szatmár Plain (Eastern Hungary and North-Western Romania). These methods for constructing and evaluating a combined specialization and phylogenetic index of dragonfly specialization could also be applied to other taxa and regions, particularly useful for global and/or biogeographic studies, as a contribution to comparative estimates of the degree of specialization of species. Thus, the combined index can be useful in ecological and evolutionary studies, and also in conservation planning.

Keywords: Abundance/richness/diversity estimation, Citizen science, Community ecology, Landscape genetics

Eleni Matechou (University of Kent) with Alex Dia, Fabian Ketwaroo and Jim E. Griffin

Efficient Bayesian variable selection in ecological models

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

We present newly developed R-Shiny apps for performing Bayesian variable selection for a range of ecological models, such as models for capture-recapture, occupancy and environmental DNA data. The models are fitted using Polya-gamma sampling for logistic regression models while the apps implement a sophisticated add-delete-swap MCMC algorithm that enables efficient Bayesian variable selection, even if the total number of possible models to be explored is large. The algorithm requires no tuning and hence can be used off-the-shelf for any data set. We demonstrate the new apps on real and simulated data, reporting on coverage and run times.

Keywords: Capture-mark-recapture, Environmental DNA, Occupancy analysis, Software development

Blanca Sarzo (University of Valencia) with Ruth King, David Conesa and Jos Hentati-Sundberg

To integrated models and beyond

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

In Ecology, due to the monitoring effort and the inaccessibility of breeding areas, it is often the case that a fraction of the population is monitored. These monitored areas are assumed to be a random sample of the whole population. However, this assumption is often violated. As a consequence, parameter estimates obtained from the monitored areas may be biased (Sanz et al. 2016). This problem is called partial monitoring.

We consider a particular case related to a large capture-recapture-recovery database obtained from the largest colony of Common guillemot (Uria aalge) of the Baltic Sea. We model annual survival and resighting probabilities in relation to the age of the individuals through integrated models (Besbeas et al. 2002). In particular, we establish four age categories: 1 (one year old individuals), 2 (two years old individuals), 3 (three years old individuals) and 4 (individuals from four to ten years old).

In this colony, the partial monitoring is present at breeding ledges, where mainly 3 and 4-10 individuals are resighted. As a result, survival probabilities for those age classes are underestimated while recapture probabilities are overestimated. In this study we compare the results obtained from the standard Cormack-Jolly-Seber model and the suitably parameterised integrated model that incorporates recoveries from all individuals in the colony (and not only those at the monitored sites). The results obtained show how the use of the integrated models solve this partial monitoring problem in this colony, although it can be easily extended to other populations.

Keywords: Capture-mark-recapture, Hierarchical modelling, Integrated population models, Partial monitoring, Population ecology

Bibek Raj Shrestha (University of East Anglia) with Simon Mahood, Sarah Brook, Som Sitha, Dr. Dia Bell and Dr. James Gilroy

Hatch of Hope? Survival Estimate and Habitat Association of Re-introduced Critically Endangered Royal Turtle of Cambodia

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Reintroduction of head started species is a widely applied management approach for conserving endangered species, especially for those having minimal or lack parental care. However, its conservation value is often challenged for its unknown success. Survival estimate is one of the vital demographic measures to inform the performance of released species, and in turn evaluation of project's efforts. Here, we estimated first ever survival rate of reintroduced individuals of Critically Endangered Southern river terrapin, Batagur affinis edwardmolli at Sre Ambel River, Cambodia. We used detection histories of 21 released individuals obtained from both active and passive acoustic telemetry for the year 2015-2016. We applied Cormack – Jolly - Seber model in Bayesian framework combining both data from both monitoring methods to estimate the annual apparent survival rate. We also modeled the possible habitat parameters influencing their occurrence in the river. We estimated an average apparent survival of 0.24 (CI: 0.10 - 0.44). This low survival estimate could be attributed to probable high emigration rates, which is not separated from mortality in the current model. Our assessment of the physio-chemical parameters of river water found that the turtles prefer slightly acidic water with moderate conuctivity during the months of April – June.

Keywords: GPS data, Population ecology, Spatial capture-recapture

Jessica Ward (Newcastle University) with Aileen Mill, Pete Robertson, and Steve Rushton

Modelling social foraging behaviours in carnivores using a metabolically scaled individual based models

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

Group foraging in carnivores is a social behaviour that is suggested to lead to individual fitness benefits through increasing hunt success or reducing predation risks. Whilst the benefits of group foraging have been recorded not all carnivore species exhibit the behaviour. To understand why differences in social behaviour occur within and between species, we need to consider the underlying drivers of foraging and predator avoidance. The processes driving social foraging behaviours are likely to operate over multiple temporal and spatial scales. Quantifying the relative contribution of different drivers requires integration of the different processes across the scales at which they operate.

There exists an intrinsic link between energetics and the foraging behaviours used to obtain prey and avoid predation. Differences in carnivore energy budgets scale with body size but little is known about how these adjustments vary with social hunting strategies, prey size, prey availability and predation pressures. Here we use individual Based Models of the drivers of metabolic scaling rules to explore the differences between social and solitary foragers to help understand the formation of social foraging groups. The model is used to investigate the fitness benefits of sociality as measured in terms of reproductive success.

Keywords: Behavioural ecology, Individual-based models

Ben Swallow (University of Glasgow) with Steve Buckland, Ruth King and Mike Toms

Towards efficient Bayesian computation and model selection for multi-species analyses in ecology

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

In ecological surveys, we are increasingly collecting data on not just one species, but simultaneously on a variety of different species. In general, most approaches to this problem would fit a single model independently to each of those species and compare results post-analysis. However, this risks ignoring the potential correlations between those species and potential interesting community-level interactions, as well as failing to take advantage of the added power that can appear when sharing parameters across multiple species. In this talk I will outline my work on Bayesian hierarchical multispecies models with a variety of approaches to model selection and apply the methods to a longitudinal dataset of garden birds in the UK over a 40-year period.

Keywords: Community ecology, Ecosystem ecology, Hierarchical modelling, Population ecology

Pravin Dudhagara (Veer Narmad South Gujarat University)

Community Microbiome Dynamics of Winogradsky Columns Established with Anthropogenic Samples to Evaluate the Community Response against Xenobiotics

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

The Winogradsky column is an important model microbial ecosystem to study the microbial and metabolic diversity and environmental influences on microbial community structure and dynamics. This complex community can be maintained under carefully controlled laboratory conditions. In the present study, four different Winogradsky columns were prepared by adding water and sediment of the polluted site– Amala khadi, India (Latitude:21°37'35 & Longitude 73°0'54) in a glass cylinders with additional supplements. The first column enriched with 2ml of quinalphos pesticide and second with 2ml of monocrotophos, third was supplemented with 2gm of low-density polyethylene (LDPE) and the fourth column was kept as control without addition of xenobiotic compounds. All columns were maintained under sunlight for eight weeks to develop environmental gradients within the column and creating diverse niches that allow enrichment of specific bacteria. After eight weeks of incubation columns were broken and upper- aerobic zone and lower- anaerobic zone were separated to extract the DNA from each zone of each column. The DNA was subjected to quality checking followed by 16s rRNA sequencing using Illumina Miseq Platform. The data were submitted to EBImetagenomics and analyzed by Kraken and One Codex database. Statistical and comparative analysis was performed by METAGENassist, Megan and STAMP. The result was also compared with the publically available WGS data of the Amalakhadi metagenome. The core-microbiome of aerobic and anaerobic zones of all columns was also analyzed to find the common persistent microbiota. The most dominated phyla were Proteobacteria and Chloroflexi. However, both phyla proportions were different in the aerobic and anaerobic zone of each column. The presence of phototropic bacteria with huge heterotrophic diversity indicates the site is rich with nutritionally versatile groups of microbes. The detection of xenobiotic-degrading photosynthetic groups of bacteria suggests the natural adaption of polluted environments. The community difference between control and xenobiotics enriched metagenome were analyzed by principal component analysis. Three clusters of eight metagenomes were found based using self-organizing maps and k-means. The further comparative analysis gives few outliner species responsible for the xenobiotics transformation. The detection of unculture species suggests the possible role of such organisms in the xenobiotics degradation. This is the first investigation to decode the stimulated microbial community of the polluted sites by metagenome analysis.

Keywords: Community ecology, Metagenomics, Population dynamics, Winogradsky column

Lungile H. Khuzwayo (University of Cape Town)

Detection and mapping of invasive alien plants in the Western Cape Water Supply System (WCWSS)

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

The subject of this is to test the repeatability of the model for the detection and mapping of the invasive alien plants (IAP) species in the Western Cape Water Supply System (WCWSS) using remote sensing. My project involves a pixel-based classification of the extent of invasion by alien plant species in selected mountain catchments of the Cape Floristic Region using high resolution satellite images. The multispectral satellite imagery will be sourced from the Sentinel-2 satellite database. Additionally, these classifications will be used for generating estimates of the rate of expansion of alien plant invasions over two consecutive years. Field data collected within a short time period of image acquisition will be used to train and validate classification algorithms. This project builds on initial attempts at mapping dense stands of invasive alien tree species within mountain catchment regions of the Fynbos using multispectral imagery through remote sensing. The availability of higher resolution multispectral imagery and advances in machine learning suggest that improvements are possible. The wider purpose of this project is to develop tools to make available rapidly updatable spatial data products that inform the management of invasive woody plants in threatened ecosystems and key water source areas. The focus is on Biodiversity Conservation (operating in endangered ecosystems with extremely high biodiversity), Water Security (monitoring invasive species in strategic water source regions) and Sustainable Forests and Woodlands (aiding to monitor natural vegetation clearing and implementation of environmental legislation where appropriate).

Keywords: Abundance/richness/diversity estimation, Distance sampling, Dynamic state models, Ecological stability and resilience, Ecosystem ecology, GPS data, Hierarchical modelling, Interdisciplinary ecology, Machine learning, Model assessment/validation, Network e

Felix T. Petersma (University of St Andrews) with Aaron M. Thode, Len Thomas, Tiago A. Marques, Gisela V. Cheoo and Katherine H. Kim

Conditioning spatial capture-recapture to exclude single detections: a case study using acoustic detections of bowhead whales.

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

Passive acoustic monitoring enables us to monitor continuously marine populations in vast areas. In some cases, estimates for absolute population density and abundance can be obtained. From 2007-2014, arrays of bottom-mounted direction-sensing acoustic recorders were deployed in late summer and early fall at five sites in the Beaufort Sea. The goal was to study changes in behaviour of migrating bowhead whales (Balaena mysticetus) in response to seismic explorations for oil and gas exploitation, but here we explore the potential for whale density estimation. Bowhead whale calls recorded at sensors within each array were identified and call detection histories created using an automated algorithm, which was trained using manually processed data from 2008 and 2009. We analysed detections from two sites in 2010. Detections made at only one recorder within an array ("single detections") were suspected to be mostly false positives (i.e., not whale calls). We therefore developed a novel extension of the acoustic spatial capture-recapture model that conditions on calls detected on more than one recorder, allowing us to exclude these single detections. We allowed density to vary spatially to account for the non-uniform spatial pattern of migrating whales. We also explored the benefits of extending the likelihood by adding detection bearings. When estimates for call rates become available, we will be able to convert call density to bowhead whale density.

Keywords: Abundance/richness/diversity estimation, Acoustics, Balaena mysticetus, Beaufort Sea, Bowhead whale, Spatial capture-recapture

Dorothea Hug Peter (Swiss Federal Insitute for Forest, Snow and Landscape Research WSL) with Florian Altermatt and Reinhard Furrer

Geostatistical models for stream ecologists - reconciling statistical requirements and end user needs

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Spatial autocorrelation is ubiquitous in ecological data as many ecological processes have a strong spatial component. Data from stream networks present a unique challenge in this context, because their spatial structure is inherently complex: relevant distances are typically hydrological distances and flow direction plays a major role in shaping spatial dependencies.

Peterson and Ver Hoef (2010) proposed a mixed-model moving-average approach for geostatistical modeling in stream networks.

While this approach has been successfully applied to predict chemical or physical stream characteristics, it has been less used for biodiversity data.

Using simulated data in Swiss river networks, we test the sensitivity of the model for different covariance functions and discuss practical aspects of the application of the model for stream ecologists.

Keywords: Freshwater Ecology, Spatial Ecology

Brandy S. Biggar (Memorial University of Newfoundland)

Empirical characterization of the multidimensional thermal niche of a globally distributed species, Carcinus meanas

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1 *Student*

Carcinus maenas is a formidable competitor that has invaded nearly every continent, making it a compelling model species to examine concepts of ecological theory. Using global time-series abundance data, I first describe the crab's thermal abundance relationship, examining the differences in the native and invasive distributions. Following this, I use a two-stage modelling approach to examine whether changes in population abundance are related to changes in temperature. The two-stage approach allows me to compare two variables that are changing through time, without actually including time in the global model. I predict that crab populations at the edges of their thermal tolerance zones will be most sensitive to extremes in environmental temperature, and that populations have been increasing globally through time. Understanding how this invasive species is responding to climate change can aid in local conservation and mitigation efforts.

Keywords: Invasive species, Macroecology, Spatio-temporal statistics

Nada Abdelatif (South African Medical Research Council) with Kesh S. Govinder, Chantel d. Beer, John W. Hargrove, Samuel O.M. Manda

Climatic Changes and Tsetse Fly Distributions in Kwazulu-Natal, South Africa: A Spatio-temporal Model

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Tsetse flies are the vectors of sleeping sickness in humans and nagana in cattle in Africa. African trypanosomiasis adversely affects rural development and poverty alleviation in Sub-Saharan Africa. This is due to a reduction in the supply of meat and milk and also animal draft power for crop production. Changing climate has and is resulting in increased adverse effects on health, such as changing patterns of infection. Tsetse flies are strongly affected by climatic conditions, where changes in climate alter the transmission seasons of the disease and geographic range of the tsetse fly itself. This study is aimed at modelling climatic changes and distribution of tsetse flies in KwaZulu-Natal, South Africa. A Bayesian spatiotemporal model will be used to assess environmental and climatic factors and to evaluate which of those significantly influence presence of tsetse flies. The model will then be used to provide probabilistic predictions of whether a change in the environmental and climatic factors will result in future increases in tsetse populations. This study examines the changes in distribution of tsetse over time in relation to important environmental and climatic variables, something not done before in South Africa.

Keywords: Abundance/richness/diversity estimation, Hierarchical modelling, Spatio-temporal statistics

Chandra P. Salgado Kent (Oceans Blueprint/Edith Cowan University/Curtin University) with Emily Evans, Rebecca Wellard and Christine Erbe

A comparison of single and bilateral asymmetrical features in mark-recapture abundance estimation of killer whales in the Bremer Sub-Basin, southwestern Australia

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Species abundance estimates are necessary for effective wildlife management and conservation, but do not often come without significant surveying costs for wide-ranging cetacean species. Consequently, many cetacean species are data deficient (IUCN Red List) with little impetus to fund their investigation. To address this shortfall, efficiencies in survey design and estimation are constantly being sought, to sufficiently reduce costs of surveying. While systematic surveys, homogeneous over time and space, are the gold post for cetacean mark-recapture estimation; vessels of opportunity are increasingly used as low-cost survey platforms. We assess the performance of killer whale mark-recapture abundance estimation using photo-ID of single identifying features; and for the first time in cetaceans, bilateral asymmetrical features from a commercial tour vessel in the Bremer Sub-Basin, southwestern Australia, in February-March 2016. Features included commonly used left and right dorsal fins, in addition to left and right eye and saddle patches. Of the 42 models fitted, half assumed constant and half individual heterogeneous detection probabilities. Preliminary detection probabilities were highest for dorsal fins, with the combination of left and right dorsal fins yielding estimates (79 with 95% HPDI of 51-161) approaching the expected. Preliminary findings suggest bilateral dorsal fin mark-recapture is an improvement over standard approaches for killer whales and cetaceans with similar features. The vessel of opportunity likely resulted in underestimates; however, estimation provides additional information over minimum cumulative numbers in the form of uncertainty. Future simulation and comparisons with systematic surveys are required to fully evaluate biases in such mark-recapture models aiming to enhance cetacean protection globally.

Keywords: Abundance/richness/diversity estimation, Capture-mark-recapture

Michael G Walsh (University of Sydney) with Siobhan M. Mor, Hindol Maity and Shah Hossain

Deforestation is associated with the landscape suitability of Kyasanur Forest disease in the biodiversity hotspots of the Western Ghats, India

Session: 06/25/2020 9:00:00 AM-10:00:00 AM

Location: #displayhall1

Human-mediated landscape change in biodiversity hotspots has been documented as a major driver of the expansion of zoonotic disease. In India's Western Ghats region the tick-borne arbovirus, Kyasanur Forest disease (KFD), has expanded rapidly beyond its historical endemic range. It has been suggested that anthropogenic pressure in the form of agricultural development and the subsequent loss of native forest may contribute to the expansion of KFD, but evidence has not yet established the association between forest loss and KFD occurrence. The current study sought to investigate the relationship between KFD landscape suitability and both forest loss and mammalian species richness to inform its infection ecology and epidemiology. Forty-seven outbreaks of KFD between 1 January, 2012 and 30 June, 2019 were modelled as an inhomogeneous Poisson process. Forest loss and mammalian species richness were both strongly associated with increased KFD landscape suitability. These results provide the first evidence of a distinct association between increasing forest loss and KFD risk. The findings also highlight the importance of forest loss in areas of high biodiversity. Therefore, this work provides strong initial support for transdisciplinary approaches to public health that incorporate forest conservation, which can be simultaneously protective of humans, animals, and the environment.

Keywords: Disease ecology, Interdisciplinary ecology, Spatio-temporal statistics

Nossaiba Baba (Hassan II University) with

Lotka-Voltera model of Aristeus Antennatus and sardine in two different areas

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2 *Student*

in this work, we describe a model of the interaction between the Aristeus Antennatus and Sardine marine species in two different areas: the first one is a preserved area against fishing and the second one is a free access fishing area. The Aristeus Antennatus in the preserved area grows according to the logistic model. If the Aristeus Antennatus population is in the preserved zone then it is protected against fishing but if not, i.e, if it is in the free acces fishing zone, it is captured. This paper has as objective to study the existence and to prove the equilibrium points stability by using eigenvalues analysis. As results, we found that the conditions that ensure the existence of the Aristeus Antennatus and Sardine marine populations are hold, and their coexistence is shown in the numerical simulations results.

Keywords: Dynamic state models, Ecological stability and resilience, Population dynamics, Predator-prey modelling

Gaetan L. B. Dupont (University of Massachusetts Amherst) with J. Andrew Royle, Muhammad Ali waz and Chris Sutherland

Towards optimal sampling design for spatial capture-recapture

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2 *Student*

Reliable estimates of population density and abundance throughout a species' range are central to ensuring the success of conservation practices. Currently, spatial capture-recapture (SCR) methods represent the most robust approach for analyzing observational data to estimate population density by leveraging information from the spatial locations of repeat encounters. As a consequence, the precision of such estimates are highly dependent on the spatial configuration and number of detectors in the landscape. Despite this knowledge, sampling design for SCR remains poorly understood. Preexisting recommendations are guided only by general principles that are ad hoc and heuristic and dependent on the use of grid-based designs. Further, in most practical applications, the terrain of the study area is logistically challenging, thereby rendering previous recommendations ineffective. To address these issues, we demonstrate the use of a genetic algorithm that minimizes any sensible SCR-related objective function to produce near-optimal sampling designs. To motivate the idea of optimality, we compare the performance of designs optimized using two model-based criteria: the probability of a capture, and the probability of a spatial recapture. We use simulation to show that these designs out-perform designs based on existing recommendations in terms of bias, precision, and accuracy in the estimate of population density. Deciding on appropriate criterion and employing the genetic algorithm will provide managers with the ability to generate their own sampling designs, which will lead to more accurate estimates of population density and improved monitoring of animal populations for species of conservation concern.

Keywords: Sampling design, Spatial capture-recapture

Shui Feng (McMaster University) with

Random Diversity Index

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

The diversity index of a population is a number that measures the number of types of individuals and how evenly distributed these individuals are among these types. It is a function of the discrete distribution of various types in the population. Diversity indexes arise in many areas including communication, economics, ecology, and population genetics. When the discrete distribution itself is random, the index becomes a random variable that serves as statistical estimators for various quantities. When the number of types is unbounded, we are led to indexes with infinite number of types. A large class of random diversity index can be constructed through the masses of random measures and the normalized jump sizes of a subordinator. In this talk, we will focus on the random Simpson index derived from the Dirichlet process and its infinite dimensional generalization, the homozygosity. Asymptotic results will be presented including the law of large numbers and central limit theorem.

Keywords: Abundance/richness/diversity estimation, Population dynamics, Population genetics, Species distribution modelling

Olivier Gimenez (CNRS) with

Recent advances in capture-recapture models with applications in conservation biology, ecology and evolution

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

1. Studying wildlife populations is challenging because not all individuals can be captured, identified and monitored exhaustively. Capture-recapture (CR) is a powerful tool to study individual life-history and behavioral traits and connect them to the dynamic of free-ranging animal and plant populations. CR is also key to evolutionary demography through the inference of demographic parameters and establishment of causal assumptions between biological processes and environment, while accounting for individual heterogeneity and imperfect detection. The past decade has seen an explosion in the development and application of CR in statistics, conservation biology, ecology and evolution.

2. We review the scientific CR literature over the last decade and analyzed > 5000 papers using bibliometric and textual analyses. In particular, we used topic modelling to identify hot topics. Data and codes available from https://github.com/oliviergimenez/capture-recapture-review.

3. We discuss recent applications of CR, including the study of life-history trade-offs and senescence, threats to biodiversity like climate change and overexploitation, dominance and parental care, foraging and anti-predation vigilance, resistance and tolerance to pathogens, overall providing a better understanding of changes in population size and composition and useful insights for management and conservation.

4. We also review recent CR methods. The last decade has been about how to mark and (re)capture animals with non-invasive methods, in particular camera trapping and genetic tagging. We have seen an uptake of state-space (SSM) and hidden Markov models (SSM with Markovian states) to estimate i) transitions between states (survival, dispersal, breeding or infection) and ii) the hidden states (disease/hybrid prevalence, sex ratio, home ranges locations). Also, there has been a growing interest in combining CR data with other sources of information on demography using integrated population models and combined data models.

5. We suggest future research and model development. New technologies produce new and more data with drones, e-DNA, PIT tags, bioacoustics, etc… In this context, survey design will remain important to collect data in ways that can inform ecological questions. We anticipate a growing interest in studying species interactions with community ecology. Other avenues of research will be spatial CR models and the combination of CR data with even more sources of information, including data on unmarked animals and telemetry data. We suspect hidden Markov models will become a unifying framework for data combination. Last, cross-fertilization between disciplines will continue, including between ecology and climate science, artificial intelligence with deep learning for signal processing and machine learning for inference, and statistics and computer science for data combination and the analysis of big data.

Keywords: Capture-mark-recapture

Nicole A. Hill (University of Tasmania) with Craig Johnson, Philippe Ziegler, Otso Ovaskainen, Scott Foster and Kerrie Swadling

Detecting, attributing and mapping ecological change in the Southern Ocean using joint species distribution models.

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

The Southern Ocean occupies ~20% of the global ocean, supports exceptional biodiversity and productive and distinctive ecosystems as well as providing a range of critical ecosystem functions. However, the physical environment of the Southern Ocean has changed over the last 30 years and will continue to do so on a time scale of decades. A basic understanding of whether, how and why entire assemblages of species have changed, and are likely to continue to change, in response to environmental and other factors is lacking for most levels of the ecosystem. Here we examine key ecological time series data of demersal fish on the highly productive Kerguelen Plateau. We use the latest developments in spatio-temporal joint species distribution modelling to detect, quantify and map species and assemblage-level changes. Preliminary results will be presented on which species have responded to environmental and other changes, what factors are important in driving these changes, and which areas of the plateau are undergoing the greatest change. We will also discuss what we have learnt thus far in applying these relatively new models and how this information feeds into management initiatives.

Keywords: Community ecology, Hierarchical modelling, Multivariate analysis/joint species distribution models, Spatio-temporal statistics, Species distribution modelling

Abhishek Singh (National Institute of Technology Hamirpur) with

Indian summer monsoon rainfall prediction: A comparison of ARIMA and ANN models in time series

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

Accurate forecasting of Indian summer monsoon rainfall (ISMR) could generate useful information for designing the strategies in order to lessen the impact of disaster caused by retreating monsoons from June through September. However it is one of the toughest challenges that the scientific community is facing today. For time series forecasting, different artificial neural network (ANN) models are recommended as alternatives to commonly used autoregressive integrated moving average (ARIMA) models. Recently, combined models with both linear and nonlinear models have greater attention. In this study, ARIMA, linear ANN, and multilayer perceptron (MLP) models are considered along with various combinations of these models for forecasting Indian summer monsoon rainfall. Comparison of forecasting performances shows that models with nonlinear components give a better performance.

Keywords: Machine learning, Model assessment/validation

Timothy L. Staples (University of Queensland) with Wolfgang Kiessling and John M. Pandolfi

Quantifying the novel ecosystem concept

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

Ecological turnover has accelerated across Earth, with altered abiotic and biotic regimes pushing ecosystems past tipping points. Natural systems that have been altered into an unprecedented, non-historic state are referred to as ‘novel ecosystems’. The paper establishing the novel ecosystem concept has been cited c. 1,000 times and has led to hundreds of subsequent papers. Despite this, the novel ecosystem concept has been criticised for multiple, vague definitions, and lack of empirical evidence. In part, this may be due to an inability to identify novel ecosystems in a reliable and quantitative way. I will outline a quantitative framework we have developed to detect novel ecological shifts in compositional time-series data. Our work so far has focused on identifying monotrophic ‘novel communities’. Our framework uses a working definition of novel ecosystems, and provides several advances compared to related techniques. Specifically, our framework (1) uses a two-factor test of novelty that allows comparison of different types of community change, (2) retains the time-ordered nature of community progression, and (3) compares observed compositional turnover to flexible, time-series-specific expectations. These advances let us pool identified novel communities across different time periods and biomes for further comparison and study. We intend to apply this framework to naturally-occurring novel communities and ecosystems from paleoecological records to study their drivers, patterns and legacy.

Keywords: Community ecology, Ecological stability and resilience, Paleoecology

Gabe O'Reilly (UNSW) with William Sherwin

New solutions for measuring mating structure from complex genes

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2 *Student*

Determining mating structure of a population is an important aspect of population genetics research. The standard for quantification of a population’s mating structure is Fis. However, Fis is a single-locus measure, so it has some major limitations when applied to multi-locus gene families. This is because current sequencing techniques are not up to the task of determining which variants are allelic at which locus in multi-locus gene families, unless your research happens to deal with a model organism. It is also common to not know exactly how many loci a multi-locus gene family has, adding more ambiguity in the process.

Because of these limitations, many gene-families that are linked to both mate choice and selection such as MHC (The Major Histocompatibility Complex) have gone unanalyzed in relation to Fis. To rectify this, I have developed an equation analogous to Fis, which can be used on a typical data output for multi-locus gene family sequencing results. This new equation utilizes Shannon’s information as its basis.

I will be presenting this equation, as well as a method to estimate a minimum number of loci in the multi-locus gene family (required for my equation). I will also present some examples of the method’s use on real data.

Keywords: Abundance/richness/diversity estimation, Population dynamics, Population genetics, Theoretical ecology

William (Bill) Sherwin (EERC BEES UNSW-Sydney) with NA

Monitoring and Forecasting Diversity: Entropy Unifies Molecules and Ecosystems

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

At all scales from molecules to ecosystems, we measure biodiversity to indicate outcomes of natural changes or threatening processes, so that we can compare these with forecasts under various management schemes. Every biodiversity level has four basic processes - dispersal, adaptation, random change, and generation of novel ecosystems, species, or genetic variants. How can we exploit this similarity? Entropy is an obvious choice, being a general forecasting and measurement tool throughout science. It is also a simple transform of the biodiversity-measure â€˜profile’: Richness; Gini-Simpson; and Shannon. Conservation managers mostly use Richness and Shannon for biodiversity measurement, and have some forecasts for MaxEnt (Shannon) and Simpson - so there is a mismatch between what is forecast and measured. In contrast, measures and forecasts in molecular ecology are now well developed for the entire profile of biodiversity-measures, within and between areas (Trends Ecol.Evol. 32:948). Shannon approaches outperform others in some important tasks, such as tracing rangeshift or invasion, and genetic estimates of dispersal for input to metapopulation models. Thus the stage is set to unify our monitoring and forecasting of these four processes that are common across all biodiversity levels, using a complete diversity profile that encompasses Richness, Shannon and Simpson. This will integrate well with the many entropic methods in studies of the physical environment.

Keywords: Abundance/richness/diversity estimation, Community ecology, Landscape genetics, Population ecology, Population genetics, Theoretical ecology

Avishek Chakraborty (UNIVERSITY OF ARKANSAS, USA) with John A. Herbert, Luke W. Naylor, William S. Beatty and David G. Krementz

Effects of Landscape Structure and Temporal Habitat Dynamics on Wintering Mallard Abundance

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

The conservation of wintering waterfowl in North America requires flexibility because constantly changing landscapes and conditions pose challenges to existing knowledge regarding waterfowl habitat use at large spatial scales. Many mallards use the lower Mississippi Alluvial Valley (MAV) for migrating and wintering habitat, making this an area of emphasis for improving management strategies for waterfowl and wetlands. Data from 25 aerial surveys were collected in the Arkansas portion of the MAV (ARMAV) from 2009-2016 to explain the abundance and distribution of mallards. We built a hierarchical spatio-temporal models with a random spatial effect and time-varying effect of landscape characteristics. Our analyses found that mallard abundance responded positively to surface water and the interaction of land cover and surface water. Models that performed best across months and years, indicated surface water, rice fields, wetlands and fallow (uncultivated) fields positively and consistently influenced mallard distribution. We constructed spatio-temporal patterns of mallard distributions across the ARMAV within and among years. Identifying regions where environmental factors drive distribution changes will be useful to improve management and conservation efforts.

Keywords: Abundance/richness/diversity estimation, Dynamic state models, Hierarchical modelling, Model assessment/validation, Spatio-temporal statistics, Species distribution modelling

Andrew N. Stillman (University of Connecticut) with Austin R. Spence, Jacob B. Socolar and Morgan W. Tingley

Population response to temperature and precipitation across 156 North American passerine distributions

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2 *Student*

Despite strong evidence that temperature and precipitation affect avian distributions, we know very little about the different effects of mean and extreme weather events on bird populations and how responses may vary across a species' geographic range. We leveraged data from the North American Breeding Bird Survey, a long-term continent-scale citizen science effort, to ask how changes in interannual weather affected yearly population changes for 156 passerine bird species across their ranges from 1980–2016. We used count data to build a metric of year-to-year population change at each survey site. Using daily climate surfaces, we then calculated local breeding-season, post-breeding season, and late-summer temperature and precipitation, as well as anomalies, for each year. We modeled the effects of climate on local population changes in a hierarchical Bayesian framework. We found that higher temperatures during the late summer (July/August) showed a negative relationship with interannual bird populations. This effect interacted strongly with the climatic niche—hotter temperatures had a stronger negative effect in the hotter versus cooler parts of a species' distribution. In addition, higher precipitation had a slightly positive relationship with bird populations across the wet and dry portions of the range. Our analysis of a 36-year continent-wide citizen science dataset suggests that birds in the warm portions of their breeding distribution may be at higher risk from climatic extremes than their cooler counterparts.

Keywords: Citizen science, Hierarchical modelling, Ornithology, Population ecology

Emily L. Weiser (U.S. Geological Survey) with

Quantifying and avoiding biases in nest survival estimates when nests are discovered after initiation and daily survival changes with age

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

Daily survival rates (DSR) are commonly measured in ecology. Often, DSR are extrapolated beyond the monitored period, such as to predict seasonal or annual survival rates of individuals or to predict hatching or fledging rates of nests that are found after initiation. However, such extrapolation implicitly assumes that DSR are constant across the period of interest, including days or nest ages that were not monitored. In contrast, nest survival has commonly been found to vary with age, even within nesting stages (laying, incubation, or nestling stages), in a variety of birds. If DSR varies with age and nests are not found at the beginning of the nesting stage of interest, the estimated probability of a nest surviving through that stage is known to be susceptible to biases. However, the biases and how to avoid them have not been well explored in the literature, and many studies of avian nest survival continue to ignore any effects of nest age. I used a simulation study to quantify potential biases in estimates of nest survival resulting from a relationship between age and DSR under a variety of age effects and ages at discovery. I used the simulations to identify a method with which biases were avoided and explore the implications for designing field studies of nest survival in wild birds. The biases quantified here will have similar implications for studies that estimate other types of daily survival rates to predict survival over a longer period than when animals are directly observed.

Keywords: Demography, Model assessment/validation

Laurel Hopkins (Oregon State University) with Ulises Zaragoza, Weng-Keen Wong and Rebecca Hutchinson

Developing habitat covariates from remotely sensed data with deep learning

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2 *Student*

Methods for collecting environmental variables for species distribution models (SDMs) generally consist of field-based methods or statistics of remotely sensed data. These statistics (e.g., mean and standard deviation of image bands) may not be sufficient for capturing complex land cover patterns and are rudimentary when compared to state-of-the-art computer vision techniques. Oversimplified representations of landscapes may prevent models from determining the impacts of fragmentation on species distributions. Given the advancements in computer vision due to deep learning, features extracted by deep neural networks have the potential to characterize habitats better than methods currently used to summarize remotely sensed data. More descriptive habitat variables are likely to lead to more informative SDMs.

In this work, we trained deep neural networks on a variety of tasks (e.g., to classify land cover from aerial images) to obtain models that can compute habitat covariates from remotely sensed images; the habitat covariates can then act as inputs to any style SDM. We compared the habitat covariates computed from deep networks to several sets of habitat covariates commonly used in SDM (e.g., statistics of remotely sensed data) by modeling bird occurrences in the state of Oregon. We modeled five species with Occupancy-Detection and Random Forest models using data from eBird.

Surprisingly, we have found little difference in model performance when predicting species occurrences with simple summary statistics versus habitat covariates computed from the deep networks. We will discuss several hypotheses to explain these results and promising directions for deep neural networks to provide informative habitat covariates.

Keywords: Citizen science, Machine learning, Species distribution modelling

Julie Vercelloni (Queensland University of Technology) with

Global patterns of community assembly on coral reefs

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

The structure of coral reef communities results from interacting evolutionary, ecological and environmental forces. How these factors interact in structuring these communities at a global scale, and how such effects might vary among biogeographical regions is unclear. We partitioned sources of reef community assemblage patterns by environmental, latent, and random factors using modern statistical methods. We then estimated how these factors related to variations in abundance and correlations among 17 functional groups on 252 coral reefs distributed across five biogeographical regions. Latent factors better explained the distributions of opportunistic functional groups like algae, whereas environmental factors better explained abundances and co-existence of hard corals. Co-occurrence patterns revealed complex interactions between coral and algae groups that were not related to environmental factors but influenced by regional biogeography. Our result show the often overlooked fact that environmental factors are unlikely to be the sole drivers of coral reef community structure, and the need to consider biogeographical variability when comparing regional declines in reef health and the potential consequences for management approaches.

Keywords: Abundance/richness/diversity estimation, Community ecology, Ecosystem ecology, Multivariate analysis/joint species distribution models

Joel Williams (NSW Department of Fisheries) with Than Knott, David Harasti, Hamish Malcolm, Melinda Coleman and Alan Jordan

Common and highly abundant species of fish are not as ubiquitous as we think

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

Common species of fish are often overlooked or removed from analysis because they are perceived as highly abundant or create issues during analysis. A fish assemblage may contain only a few highly abundant species but these few species may account for the majority of biomass and energy turnover in their ecosystem. Using existing data collected over the past ten years from baited remote underwater video (n =1,544) along the New South Wales, Australia, coastline, we selected, a priori, abundance and length data for three perceived common species. We also compiled a suite of potential predictor variables and used a full subsets GAMM approach to establish the importance of each variable in explaining the distribution of these common species. Then, select the model that best explains the variance in species distribution. The three model common species used in this study were indeed highly abundant (1-400 per replicate) and widespread (60-80 % of replicates). Yet, there was a definite structure to their distribution. The full subsets GAMM revealed depth, no-take status and reef structure best explained the distribution of each species. Most notably there was a species dependant response to marine park zoning. We conclude that, spatial management and human impacts have an influence on the distribution and size of common species of fish. The location of a reef in relation to latitude, depth and aspect also influence these species distribution. This study demonstrates that common species should not be overlooked when investigating species assemblage dynamics and marine park monitoring.

Keywords: Abundance/richness/diversity estimation, Ecosystem ecology, Species distribution modelling

Casey Youngflesh (University of California, Los Angeles) with Morgan W. Tingley

Assessing spatio-temporal morphological change in North American birds using hierarchical Bayesian models

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

Morphology is both a cause and a consequence of how organisms interact with their environments. Studying morphological change over time and space provides a mechanism by which to better understand how organisms are shaped by their environments. The vast majority of work in this area, however, has focused on among-, rather than within-species dynamics.

Using continental-scale bird capture data over a period of 26 years, we assessed intraspecific changes in bird body size and wing length over time, latitude, and elevation for 79 species of North American-breeding birds. We used hierarchical Bayesian models to quantify changes in both the trait means as well as within-population trait variances. For a subset of these species, we used spatial Gaussian process models to more finely map how these morphological traits vary across the landscape.

Results show that while some heterogeneity in responses exists across the species assemblage, in general both body size and wing length decreased with time and increased with latitude. Body size generally decreased while wing length increased with elevation. Relative rates of change follow both Bergmann’s and Allen’s Rules, though the morphological differences are likely driven by an interaction of factors, including temperature, predation pressure, migratory distance, and air viscosity. Intraspecific variance in traits generally decreased with latitude, mirroring patterns observed at the community level (i.e., lower variance in morphological traits among species at higher latitudes). This work highlights intraspecific morphological changes across time and space and has implications for better understanding morphological responses to global change.

Keywords: Hierarchical modelling, Spatio-temporal statistics, Trait based ecology

Gleb Tikhonov (Department of Computer Science, Aalto University, Finland) with Otso Ovaskainen, Jarno Vanhatalo, Harri Lähdesmäki

Faster Bayesian inference in Joint Species Distribution Models

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

Over the last decade the analytical toolset of an ecologist studying species communities has undergone major evolution. In response to the widespread understanding that analyzing species jointly rather than one-by-one provides a more in-depth insight on the community structure, many statistical approaches for joint modelling have been published, enabling coherent and rigid testing of various ecological hypotheses. Furthermore, many of such models are accompanied with documented software implementations that greatly facilitate their reusability by other researchers.

However, alongside the increasing expressiveness and complexity of joint species models, the associated model fitting computational costs have also dramatically increased. Thus, analyzing even moderate-sized community datasets with existing packages can take days to obtain a single reliable model fit.

In this work we seek to alleviate such computational load for Bayesian inference in a flexible class of joint species distribution models (JSDM), titled Hierarchical Model of Species Communities (HMSC), which principally encapsulates several other popular JSDMs. We ground our approach in latent Gaussian representation of HMSC combined with several techniques from probabilistic machine learning domain. First, we analytically exploit the specific HMSC-imposed structure for the marginal Gaussian form and blend it together with the Expectation Propagation technique to accommodate non-Gaussian observation models. Next, we consider three strategies for learning the analytically intractable parameters: Maximum Posterior estimate, Variational Inference and Hamiltonian Monte Carlo. We demonstrate our approach using simulated and real datasets and compare its performance to two JSDM R packages representing the extremes on the current model fitting techniques gradient – Hmsc and gllvm.

Keywords:

Michael A. McCarthy (University of Melbourne) with

Statistics in Biology Textbooks

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

The misunderstanding and misinterpretation of statistics in ecology (and biology more generally) is well documented. Here I review the extent to which statistics is covered in 20 leading university-level biology textbooks, and the presence of errors in interpretation and understanding of statistics. The extent to which statistics were covered in the textbooks varied substantially. However, fundamental errors were present in almost every textbook that covered statistics. The most common errors involved incorrect description of null hypothesis significance testing. This review highlights the challenges faced when teaching ecology students about statistics, and the opportunity to improve that through corrections to textbooks.

Keywords: Statistical ecology education

Rebecca Fisher (Australian Institute of Marine Science) with Pia Bessell-Browne and Ross Jones

Disentangling synergistic and antagonistic impacts of suspended sediments and thermal stress on corals using full subsets and Bayesian modelling methods

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

Understanding pressure pathways and their cumulative impacts is critical for developing effective environmental policy. For coral reefs, widespread bleaching resulting from global warming is occurring concurrently with local pressures, such as increases in suspended sediments through coastal development. Here we use full subsets non-linear generalised mixed modelling to examine the relative importance of suspended sediment pressure pathways for dredging impacts on corals and to identify the 'best' statistical models for estimating their combined impact. These 'best' models were fit within a Bayesian framework and used to assess evidence for synergistic or antagonistic cumulative effects between suspended sediments and thermal stress. We show that low to moderate reductions in available light associated with dredging may lead to weak antagonistic (less than expected independently) cumulative effects. However, when sediment loads are high any reductions in mortality associated with bleaching are outweighed by increased mortality associated with severe low light periods and high levels of sediment deposition and impacts become synergistic (greater than what would occur independently). The findings suggest efforts to assess global cumulative impacts need to consider how pressures interact to impact ecosystems, and that the cumulative outcome may vary across the range of realised pressure fields.

Keywords: Benthic light, Community ecology, Coral bleaching, Coral reefs, Cumulative impacts, Dredging, Ecological stability and resilience, Ecosystem ecology, Population ecology, Theoretical ecology, Turbidity

Brian R Gray (US Geological Survey) with Darryl I. MacKenzie, Richard A. Erickson and Fang K. Chen

Estimating among-season effects on the probability of species occupancy absent revisits among seasons

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

The probability that a species is present at (“occupies”) sampling units among multiple sampling seasons is typically estimated using dynamic occupancy models. However, such models assume sampling units are revisited among seasons. Some programs, including those that monitor submersed aquatic vegetation in North America, are interested in multi-season occupancy inferences in the absence of unit revisits among seasons. We address this issue using a multi-season elaboration of the classical (Bernoulli-binomial mixture) occupancy model where Bernoulli and binomial parameters are permitted to vary among units as well as seasons, and where the typical parameter of interest, the Bernoulli parameter, may be serially dependent among seasons. We evaluate this model using 21 seasons (years) of Eurasian watermilfoil (Myriophyllum spicatum) data and a calibration study. Estimators of linear trend in the Bernoulli and binomial means on the logit scale were broadly accurate regardless of level of serial dependence and of whether dependence was or was not modeled. Serial dependence led to decreased credible interval coverage for the occupancy trend parameter under a naïve assumption of serial independence while accommodating serial dependence under an autoregressive lag 1 (AR1) assumption led to improved credible interval coverage. Extreme bias in the AR1 parameter was confined to cases where standard deviations in among-season variation in the Bernoulli and binomial parameters were both small. Posterior standard deviations of the occupancy trend parameter, given the M. spicatum data, were substantially larger under an AR1 assumption. The model may be fit using widely-available statistical software.

Keywords: Dynamic state models, Occupancy analysis

Andrew M. Edwards (Fisheries and Oceans Canada) with Carrie A. Holt and Luke A. Rogers

Testing the use of Empirical Dynamic Modelling to forecast fish populations and provide advice to managers

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

Empirical Dynamic Modelling (EDM) has been proposed as a promising method to incorporate environmental influences into population forecasts, in particular for advising fisheries managers. It generates forecasts by empirically reconstructing the past dynamics of nonlinear systems from the data, backed up theoretically by Takens' Theorem. This avoids the traditional use of mathematical and statistical equations to define relationships that can often break down in applications. Previous studies have tested EDM for specific examples, in particular the iconic population of Fraser River Sockeye Salmon in British Columbia, Canada. Here we simulate a range of realistic scenarios to more generally test the skill and usefulness of EDM for fisheries forecasts. We compare EDM with the Bayesian approaches currently used in applications (specifically for Sockeye Salmon), and conclude whether and when it should be used to provide applied advice to fisheries managers.

Keywords: Ecosystem ecology, Integrated population models, Model assessment/validation, Population dynamics, Population ecology

David H Maphisa (South African National Biodiveristy Institute (SANBI)) with Res Altwegg and Hanneline Smit-Robinson

Dynamic multi-species occupancy models reveal individualistic habitat preferences in a high-altitude grassland bird community

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

Moist, high-altitude grasslands of eastern South African harbour rich avian diversity and endemism with contrasting habitat needs for some birds. Some of these species are rare and therefore a target for conservation. However, this area is a target for new development projects. Ingula Pumped Storage Scheme whose purpose is to argument electricity to national grid partly occupies an Important Bird and Biodiversity Area is new development in the area. The new management seeks scientific advice on how to make habitat suitable for birds and biodiversity in general. We used a dynamic multi-species occupancy model to examine the seasonal occupancy dynamics of 12 common grassland bird species and their habitat preferences. Our model accounted for detection probabilities related to time of survey and weather conditions. We estimated plot occupancy, persistence and colonisation in relation to grass height and grass cover when birds are breeding. Majority of this species showed contrasting plot occupancy in relation to grass height and grass cover but overall heterogeneous plot persistence in relation to these two habitat variables. In 9 out of the 12 species, colonisation declined with increasing grass height and grass cover. We argue that the observed overall low colonisation is a result of reduced grazing since new management took over. We conclude that some of the 12 species are good indicators of habitat suitability because they represent a range of habitat needs and are relatively easy to monitor. We suggest management use fire and grazing to create mosaic of grass heights and covers.

Keywords: Dynamic state models, Hierarchical modelling, Occupancy analysis

Natalie Jones (University of Queensland) with Rachel M. Germain, Tess N. Grainger, Monta Hickey andMargie Mayfield

The biogeography of dormancy evolution

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

The ability of plants to avoid conditions that render them vulnerable to extinction is foundational to the maintenance of diversity. In variable environments, dormancy – the production of environmentally resistant forms that can emerge when conditions improve – is a critical life history strategy that allows species to persist during unfavorable periods. Habitats have different baselines of environmental variation, which should impact the propensity of plants to enter and emerge from dormant states, yet, to date, geographic patterns in the sensitivity of plants to environmental cues remains unknown. In this global meta-analysis, we synthesize experiments that have tested the sensitivity of dormant seeds to germination cues by compiling data from experiments that tested the role of environmental conditions for the termination of dormancy. In total, we extracted the raw data from 70 studies that included 326 species across 104 plant families from around the world, then ran a mixed-model analysis using the “metafor” package in R. Our results revealed that dormancy rates are greater in extreme environments that exhibited high variability in temperature and precipitation ($p<0.0001$), specifically polar and arid sites. At the same time, other life-history characteristics explained biogeographic patterns in dormancy dynamics. Plants that exhibited physical dormancy had the highest rates of dormancy (significant dormancy type × variability interaction, $p<0.0001$), while perennial dormancy showed a weak and sometimes absent relationship with variation in environmental conditions. The results of this work suggest that the role of dormancy for coexistence is elevated extreme environments.

Keywords: Community ecology, Life-history evolution, Macroecology, Meta-analysis, Population dynamics

Natasha Karenyi (University of Cape Town) with Kerry Sink, Ronel Nel, Res Altwegg and Allan E. Clark

Imperfect detection distorts depth-related trends in marine macrofaunal species richness

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

Species richness patterns and their drivers underpin ecological and biodiversity research. Observed species richness is however dependant on both ecological and observation processes. Most species richness measures assume a perfect observation process, i.e. equal detection of species in space or time, but this is not always the case. What if species detection varies along the environmental gradient of interest? We tested three hypothesized relationships between benthic macrofaunal species richness and depth on the continental shelf of the South African west coast. The dataset consisted of 427 species from 42 replicated sites stretching from the beach to the continental shelf edge. Species richness per site was estimated with a capture-recapture heterogeneity model that accounts for variable detection probabilities. The average probability of detection decreased along the depth gradient, but the species richness increased resulting in a positively near-linear relationship between species richness and depth. Ignoring the variable species detection probabilities would have resulted in a weaker species richness-depth relationship which has implications for environmental management.

Keywords: Abundance/richness/diversity estimation, Capture-mark-recapture, Community ecology, Occupancy analysis

Juan Manuel Morales (INIBIOMA-CONICET, Universidad Nacional del Comahue) with

Linking movement, frugivory, and seed dispersal

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

Here I review the connections between animal movement and seed dispersal. Recent empirical work shows that some frugivores may favor the consumption of rare fruits with important consequences for plant diversity maintenance. The mechanisms behind such patterns are still speculative but they could be related to frugivore physiology. Progress in hierarchical data analysis tools allows us to fit joint species frugivory models where species-level movement and foraging parameters are modelled as a function of species traits and their phylogenetic relationships. We have parameterized such models with bird movement and foraging data from tropical and temperate communities. In our model, plant-frugivore interactions emerge from frugivores' behavior in a spatially explicit setting. This allows predicting how interactions rearrange after extinctions, and hence, to better quantify the vulnerability of plant species to partner loss. We can also have good estimates of frugivores' role in seed dispersal. Overall, there has been great progress in data collection and modelling but we still need a better understanding of seed retention times, and of how bird physiology influences fruit choice. Further improvements in our ability to understand and predict seed dispersal by animals would probably also require considering within and among species agonistic behaviors.

Keywords: Behavioural ecology, Movement modelling, Network ecology

Ulrike Naumann (University of Kent) with Rachel McCrea and Nik Cole

Adjusting for misclassified gender observation in a capture recapture study of Telfair skinks

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2 *Student*

Frequently, we want to adjust capture recapture based estimates for survival of a population and capture probabilities for the effect of gender. Furthermore, there is often an interest in obtaining gender-specific abundance estimates. However, for some animals, gender is not consistently determined across re-captures.

While previous methods have looked at using a category ‘unknown gender’ to deal with this or similar situations, this approach ignores that the rate of inconsistencies depends on the number of recaptures, and might also depend on true gender. This becomes an important issue if there is a relatively large proportion of inconsistencies among recaptured animals, but a large proportion of observed animals are only observed once.

Here, we propose an HMM model framework, where we will estimate gender proportion over time, gender-dependent classification rates (as male, female or unknown), and gender effects on entrance into population, survival, and temporary emigration rates. We compare an open population model with a robust design. We also evaluate the parameter redundancy of this model in order to understand its’ limitations.

We demonstrate our method on a capture-recapture study of Telfair skinks on Gunners Quoin, Mauritius. We show the improvement of this method compared with an analysis where we ignore gender. Further we compare our method to an approach where all animals with inconsistent gender are labelled as ‘unknown’ gender. Furthermore, a simulation study is performed to demonstrate the properties of our method for varying levels of gender proportions, and misclassification rates, and demographic differences across the gender.

Keywords: Abundance/richness/diversity estimation, Capture-mark-recapture, HMM, Misclassified states, Population ecology

Gavin L. Simpson (University of Regina) with

Estimating the time-varying correlation between time series using copula distributional models

Session: 06/24/2020 10:00:00 PM-11:00:00 PM

Location: #displayhall2

Where multiple time series are available, such as for multiple species at the same location, species abundance and related environmental time series, or biomass values over time at multiple locations, ecologists are commonly interested in knowing how correlated those time series are, and whether the correlation varies over time or with covariates (e.g. treatment effects). Typically, correlations are estimated either directly from the data or post hoc after estimating the trend in each series separately. Time-varying correlations between series may be estimated using moving windows of time. Instead, it would be expedient if we could estimate trends within, and correlations between, series using a single model. Here, I describe the use of bivariate copula distributional models to achieve this aim.

A bivariate copula distributional model comprises a pair of marginal distributional models, and a copula model to link them. Each marginal distributional model comprises one or more linear predictors for the location, scale, or shape of the marginal distribution. The copula model links the marginal distributions and allows the estimation of the dependence between them. Parameters of the copula function can also be modelled by covariates. In the time series setting, penalized spline functions of time may be used to estimate non-linear trends in parameters of the conditional distribution of each series and in the correlation between the series.

I illustrate the approach using time series of planktonic and benthic foraminifera in an ocean core from off the Iberian peninsular, and of desert rodent abundances from Arizona.

Keywords: Paleoecology, Population dynamics, Time series