1	ID	Science keywords	AI/ML/data science keywords	Preferred skills	ARS unit and location
		apiculture, honey bees,		knowledge of applied statistics,	
	1	pollination, stock evaluation, behavior, ecology	remote sensing, audio, temperature, activity, SQL	experience working with SQL files	Honey Bee Breeding, Genetics, and Physiology Unit
		Crop improvement, host	Hidden markov model, data	Python or Perl programming experience, Linux working environment and shell programming, interest or	Crop Production and Pest
	2	resistance, genomics	mining	exposure to bioinformatics	Control
	3	Disease vectors, Animal Health, Genomics, Genetics, Annotation	computational genomics, pattern matching, unsupervised learning		Arthropod-borne Animal Diseases Research Unit, Manhattan, Kansas
		plant genomics, plant breeding, crop wild relatives statistics and machine learning.	genome assembly, genome annotation	Unix/bash, R, and/or Python programming knowledge	Kearneysville, WV
		environmental drivers, pathogen prevalence and persistence, poultry farms, pre-harvest, broiler chicken	Bayesian MCMC modeling, logistic regression, random forest, XGBoost, supervised learning	knowledge of applied statistics, R programming, machine learning experience	Egg and Poultry Production Safety Research Unit, Athens, GA
	6	landscape ecology, climate refuge, insect pest forecasting	causal inference, machine learning, deep learning, GIS/remote sensing	knowledge of applied statistics, machine learning and GIS/remote sensing, experience with Python/R computing environment and commonly	Pest Management Research Unit, Sidney, Montana
	7	hail damage assessment, high- resolution imagery, yield deduction	computer vision, predictive modeling	Python, R, Image processing	Water Management and Systems Research Unit, Fort Collins, CO 80526
	8	biological nitrogen fixation, photosynthesis, crop improvement	genomics/transcriptomics, gene network inference	coding in one of Python/R/C/C++/etc., machine learning	Global Change and Photosynthesis, Urbana IL
	9	phosphorus, water quality, nutrient management, soil science, spatial ecology	ensemble learning, causal inference, supervised and unsupervised learning, spatial statistics	knowledge of applied statistics, experience with geospatial data, programming experience (Python, R, etc.)	Water Quality and Ecology Research Unit, Oxford, MS
	10	root phenotyping, root architecture, climate resilience, tree physiology	computer vision, structure analysis, image processing	familiarity with image data, programming experience in Python or C++, familiar with use of deep learning libraries	USDA-ARS-AFRS, Kearneysville, WV
	11	Bacteriophages, next-generation sequencing	deep learning, natural language processing	Python programming experience, NPL model-related experience etc	Produce Safety and Microbiology Research Unit, Albany CA
	12	sustainable agriculture, crop production, precision agriculture	UAV imaging, machine learning, deep learning, big data	knowledge of statistics, machine/deep learning, and remote sensing, and skills of GIS, Python and graphic user interface (GUI) programming	Genetics and Sustainable Agriculture Research Unit, Mississippi State, MS
		hydrologic modeling, conservation assessment, climate adaptation	random forest, deep machine learning, model optimization	Python programming, hydrologic modeling, water resources management	Grassland Soil & Water Research Laboratory, Temple, Texas
	14	Natural resource modeling, spatial connectivity, spatial dependency, soil erosion	Recurrent Artificial Neural Networks	Machine Learning, Python, GIS concepts	National Sedimentation Laboratory, Watershed Physical Processes RU, Oxford, MS
	15	Unmanned Aerial Systems (UAS), Sentinel-2, precision crop management	Artificial Neural Networks (ANNS) / Deep Neural Networks (DNNs) for Computer Vision, Time Series Forecasting, geospatial data analysis	Al programming experience, e.g., Python, C++, JavaScript, PyTorch, TensorFlow, geospatial data analysis	University Park, PA
	16	climate change, microbiome, ruminant livestock, methane, GHG, soil, fertilizer	bioinformatics, computational biology, random-forest ML	graduate students with multidisciplinary interests in Microbiology, Livestock Agriculture, Environment, Veterinary Medicine,	Livestock Nutrient Management Research Unit, Bushland, Texas
	17	insecticide, physiology, insect behavior, mating	computer vision, causal inference, behavior chain estimation	Python programming, image detection and automation	Center for Grain and Animal Health Research, Manhattan, KS
	18	crop improvement, phenomics, quantitative genetics	computer vision, object detection, segmentation	Linux shell scripting experience, Python programming experience knowledge of applied statistics,	Cereal Crops Research Unit, Edward T. Schafer Agricultural Research Center, Fargo, ND
	19	agriculture, effector biology, plant-microbe interactions, genomic	bioinformatics, data analytics, computational biology, omics integration	familiarity with bioinformatics tools, transcriptomics, pathway analysis, Phyton or R, interest in plant-pathogen interactions	Temperate Tree Fruit & Vegetable Research, Wapato, Washington
	20	precision aquaculture, crop protection, remote sensing, image processing	computer vision, unsupervised learning, self-supervised learning	image processing, Python programming, machine learning, GIS	Sugarbeet and Potato Research Unit, Fargo, ND
	21	Crop improvement, Biology, Agriculture, Genetics, Breeding	computer vision, active machine learning, convolution neural network, unsupervised learning, deep learning	Python or R programming experience, knowledge of applied statistics or agriculture or biology	Plant Science Research Unit, St Paul, MN
	22	plant pathology, weed science, microbial community ecology, invasion biology	supervised and unsupervised machine learning	Programming experience (any language), basic knowledge of applied statistics, introductory level coursework in microbiology and/or genetics	Fort Detrick, MD
	23	drought stress, crop physiology, remote sensing	supervised learning, unsupervised learning	experience with Python programming, specifically Sci-kit learn, Pytorch and/or Tensorflow Experience with Unix	Adaptive Cropping Systems Laboratory, Beltsville Agricultural Research Center, Beltsville Maryland
	24	crop development, food security, data findability, data accessibility	Data sharing. Data discoverability, findability, and accessibility	programming, website programming (PHP), application programming interface (API) development (JavaScript),	Crop Improvement and Genetics Research Unit, Albany, CA
	25	foodborne pathogens, assay development, long-read sequencing	bioinformatics, analysis workflow, pipeline development	knowledge of bioinformatics, Galaxy, Python, and command line	ERRC CIFP Wyndmoor, PA
	26	nutrition, ultra-processed foods, nutrients, food categorization, NOVA	multi-class random forest classifier, machine learning model, machine learning prediction	knowledge of Python 3.6.10, MATLAB 2022a, and R, ability to generate PCA plots, familiarity with the jupyter ecosystem of products	NP 107 Healthy Body Weight Research Unit Grand Forks, ND
	27	Soil moisture, Cover crop, Nutrient management, Digital Soil mapping	Support vector regression (SVR), artificial- and deep neural network	knowledge of soil physics, R/python programming experience	Soil, Water, and Air Resources Research Unit, NLAE, Ames, IA
	28	emerging diseases, zoonotic, zoonoses, biothreat, virus, pathology, ticks, Crimean Congo hemorrhagic fever, livestock	agent-based modeling, unsupervised learning, climate, geospacial, ecological	knowledge of applied statistics, Python programming experience, experience with AI/ML	ZEDRU Manhattan KS

Research summary We have two honey be activity projects that we are using to test remote sensing technologies (passive data collection techniques). One complete dataset is in-hand (pollnation esperiment) and one is in the process of beng collected lowenixtering experiment), which allows an incoming student to play with the complete dataset and to potentially apply their tearing with the other dataset. The that(completed dataset and to potentially apply their tearing with the other dataset.) use outer adtaset: ne minal completed dataset geperiment was a honey bee stock The project involves genome assembly and annotation of Mytophthora sansoneana (an emerging soykean pathogen) using short and long sequence reads. Following this step, wer use data mining to learthy effector genes in the genome that are likely responsible for pathogenicity. We also plan to compare this genome to the genomes to drute Phytophthora speciels to identify genomic signature granutationary and preprinties of effector genes) species to identify genomic signatures (particularly, their repertores of effector genes) currently, was respectively according to the state of the state of the state environmental stress and insecticide responses. The mentes will ascende use and the state genomes utilizing estimally the state of the They will be taught principles of genome assembly gain experience in annowarus processes infections caused by Listeria and Campylobacter through poultry consumption pose significan challenges to public health and the economy. The risk of these infections may excalate with th expansion of the poultry management system. This project is primarily focused on developing predictive models to identify variables and factors that could be linked to the reduction of Listeria and Campylobacter pathogens. The mentee involved in this project will gain hands on Listeria and campylobacter pathogens. The mentee involved in this project will gain hands on the project will be a strained and the project will gain hands on the project will be a strained and the project will gain hands on the project will be a strained by the project will gain hands on the project will be a strained by the project will gain hands on the project will be a strained by the project will gain hands on the project will be a strained by the project will gain hands on the project will be a strained by the project will gain hands on the project will be project will be a strained by the project will gain hands on the project will be provided by the project will gain hands on the project will be provided by the project will gain hands on the project will be provided by the provided by the project will be provided by the provided b Mormon crickle outbreaks typically originate on rangeland where infestations can result in substantial forage iosses and cause major damage when they migrate into crops. Currently, a forecast model for Mormon cricket outbreaks does not exist. Recent research to deviation and the substantial for the set of the set of the set of the set of the deviation and the set of the deviation and the set of the deviation and the set of the set of the set of the set of the deviation and the set of the set of the set of the deviation and the set of the set of the set of the deviation and the set of the set of the deviation and the set of the set of the deviation and the set of the deviation and the set of the deviation and deviation and

elevations, and thus identification of multi-generational egg beds is imperative to this research project aims to develop an integrated framework for assessing bail damage in crop fields, leveraging absorbed techniques in computer vision, statistical modeling, and data integration. The general is to provide fammes and apprometists with a reliable to that can apply and ascorately evaluate the impact of hail on mains crops and enable informed decision-makin for crop management and yield optimization. The internet will contribute to the development of Our bib studies how integras assimilation and photosymbies are coordinated in crops and model plants to achieve optimal growth. We are particularly interrested in how the relationship will be affected by climate change. We integrate technical physiological measurements with notingenomic datasets to determine the genes and metabolic processes that respond to changes in integrandose and CO2 concentration. Our goal is to identify the transcriptional regulators than to concent of the assessible to evaluate home to have a particularity to the particular physiological measurements with the operative to accentration to evaluate home and the physiological measurements with the operative to accentration to evaluate home and the physiological measurements with the operative to accentration to evaluate home and the physiological measurements with the operative to accentration to evaluate home and the physiological measurements with the operative to accentration to evaluate home and the physiological measurements with the operative to accentration to evaluate home and the physiological measurements with the operative to accentration to evaluate home and the physiological measurements with the operative to accentration to evaluate home and the physiological measurements with the operative to accentration to evaluate home and the physiological measurements and the physiological measurements and the physiological measurements and the physiological measurements a We propose to adapt a geospatial and machine learning approach developed by Dolph et al [2023] (or similar ensemble learning methods) to predict high resolution sof phosphorus (P) concentrations within the Lover Mississippi River Basin, vew il utilize an in-house database sof properties in the Mississippi portion of the Lover Mississippi River Basin, augmented wit data complet form Iterature and USS3 databases to developed nat test (an anticipated) random data complet formations and the machine and the soft and the using subject to the minimum of the production in the constraint of the constraint o

In our research project, we will develop a natural language processing-based bioinformatic AI tool to classfy bacteriophage lifecycles based on their sequences. First, the interns can help with data collection fom public databaset to set up the comprehensive training dataset and test dataset. Further, they can assist in model training with different key parameters. We have field experiments related to studies of cover crops, unitient traitements, and imgitotio for the responses of gas emission and microbiology to optimize row crop productivity to close which be the effect experiments related to addition to traditional argomonic methods, innovative which gas, for these experiments, in addition to traditional argomonic methods, innovative whiches (LUN4) offered a fileside, high-performance platform for crop growth monitoring and the second seco

VehiCleS (DAxs) offered a Telescie), faint-per remained parts in as curp grown inter-method in the Soli & Water Assessment Too (SUN) is a watershed modeling system used internationality to estimate impacts of faind management practices on water quality in complex watersheds. Anong other applications, it has been used extensively within the USDA Conservation Effects Assessment Program (CAAP) for evaluating the effectiveness of conservation practices to improve water quality in U.S. watershed. There are also many possible SWAP applications

Management of natural resources in fields and waterhelds often requires modeling of complex physical processes to guide policy and decision making, remediation design and performance, and monitoring, in a trautal systems, such processes present complex spatial and temporal dependencies. For example, generation of nucli fin a field depends on the limits, intensity, and amount of stom precipitation, and on turne varying hydradius properties of the soli. The temporation of the stom procession of the solit procession of the solit procession. The solution of the stom procession of the solit procession of the solit procession of the solit procession. The solit procession of the solit processi Although use of UAS' may be an effective strategy for targeted management practices, costs increase with spectral range, here are time consuming and impacticat to cover large acreage over time, and are impacted by a range of environmental conditions such as wind, precipitati and cloud cover. Satellites provide lower resolution imagers, but it is comprehensive over spatiand and time, and generally includes greater range of spectral bands. Our objective to story to the spatiant of the spectra spectra of the spectra bands. Our objective to story to an effective spectra spe The intern will be directly involved in an (1) ongoing meta-analysis for investigating the rumen minimized on the state of the state minimized on the state manure as an organic fertilitier, its relationship to emission, and potentially (3) investigating minimized on the state of the stat

are primed with dattle manure as an organic fertilizer, its relationship to emissions, and potentially (3) instraighting microbious differences in feedlo surfaces where water is applied The graduate student will contribute to a project on quantifying the mating behavior of insects that have been exposed to subletall does of insecticities. The goal is to develop an automated systems to track male-female interactions and determine how mating patterns are disrupted by insecticide exposed to subletall does of insecticide potential exposed on the previously recorded video and still images available and will need to determine meta-data. Measuing disease emposens as in important component of plant breeding and genetics research. Ny lab is working to impose disease measurements of a highly voltate fold and desase infection of crown acts on susceptible ext varieties elicity to the molecular interactions between that one manuface and the straing frame to the molecular interactions between that are important for characterizing response to infection and rows applications. Week ensuing the associated with Phytoplasma promi, the kalfnopper vector, and their plant host. Effectors, key proteins accreted by pathogens to manufaule host defenses, play a polarito lice in the establishment of pathogenitity. This project aims to identify and characterize effectors associated with Phytoplasma point, and the leafhopper vector, identify light on their functions and the The student will work on Al-based plant classifications for real-time weed identification and tist-specific sympa polication. Week and crog caropy appear similar in color but can be discriminated by spectral instruce in beyond visible bands, morphological features, and modest to extract those features for plant classification. The student will contribute to the CIS Maturity-based harvesting time for alla is circitation based sublestibly and ideutify and the classible policy. The sublext will contribute to the CIS Maturity-based plant theore theore a

Maturity-based harvesting time for alfalfa is critical to have a balanced high digestibility and biomass yield so that farmers can harvest maximum digestible biomass yield for maximum polft. Currently, maturity is measured by estimating the percentage of flowers, and an estimated 25% of flowering by human eyes is used to decide the harvesting time. We have developed a deepleraming model to count the number of howers from images taken by mo developed a deep-learning model to count the number of flowers from images taken by mobile Non-native imaxies weeds cause over nine billion doltars, in drings to agricultural productivity and natural resources annually. Microbes can be applied as biological control agents to to effectively manage these imaxies weeks, bub biological control agent development is limited by the rate at which candidate microbes are discovered using conventional methods. The student intern would contribute to research mined at improving our ability to detect candidate The inhibition of photosynthetic activity and metabolic changes induced by severe drought stress exposure a flowering can be remotely detected with canopy reflectance. These spectra are sensitive enough to differentiate response to drough that are mediated by genotype, environment and regration management in crops, and contain stress-associate signatures which are directly influenced by changes in leaf pigment and metabolite content that cours at climate changes in theories pigment and metabolite content that cours at the instance interveloped availability be teachings for home of events hy

nks by abiotic (e.g., which are dracely interacting block loads and an ange in rear paging in an an intraduction content con

genotypic relationships, such as what genes contribute to what crop traits, so that improved crops can be developed to withstand to challenges posed by dimate change. My lab is investigating the use of long-read sequencing for foodborne pathogen detection. The goal is to develop an enthod that reduces the time and labor needed for foodborne pathogen detection from current methods. Long-read sequencing could be highly advantageous for foodborne pathogen testing because I provides information on the whole genome of a pathogen. Therefore, species, serotype, virulence genes, and antibiotic resistance profile can all fairlier this year, a machine learning algorithm developed to predict the degreed of processing for foods using the NOVA scale (not an acronym) was published in Nature Communications. This publication included links to the source code for the foodprox. model developed by the investigators. My lab is currently working on several projects related to food processing level, and we are interested in comparing the food processing categorizations of the machine fraggian soils are charactered by dense subsurface layers that severity restrict water flow and not growth. Located in southern limits, two on-firm studies have been conducted to determine whether the adoption of annual regrass (Lalium multiforum) as a cover crop can improve change during the wet portions of the yearan reduced crop water stress during the summer for fraggian soils under com-soybean production. Pofile (60 cm) soil moisture and I have three projects that would benefit from a graduate studem. The first is the development

I have three projects that would benefit from a graduate student. The first is the development of models of the risk of distribution of Cimean Congo Hemorrhagic feer virus. There is significant concern that the virus may be equading its gradpatic range and may find new hosts. There is a need to build models using available data sets. Of particular interest is if the immary cikes if accelerable introduced to the US would be able to stabilito positions. This is the set of the

Potential A/MU/dist a science component(s) Discovering if different hone ybe estocks are more or less efficient at foraging compared to others is important to commercial beekeepers as well as almond producers. However, we hon thad the chance to develop pipelines to analyae this data yet due to understiffing and til constraints on the staff we have. A/MU/dist ascience expertise is what we need to complete project, and it also gives students a chance to learn about an we lobogical system (pollonal lete thi

Genome assembly and annotation require experience in script language programming and familiarity with Linux working environment and its shell language. Machine learning/data environment and an environment and the shell anguage. Machine learning/data incorporating AI/ML and data science expertise into this genomics project can significantly enhance the efficiency accuracy and depth of the research. These technologies automate ta construing tasks, uncover intricate genomic patterns, and provide predictive insights that contribute to a more comprehensive understanding of inset disease vectors and their responses to environmental and insecticidal atresors. Several steps in the proposed analysis ed analysis responses to environmental an user-Local as Leskola. Service a segar une proposed aimpose Genome annotación require the training of ab initio gene prediction programs that can search a genom sequence for signatures that are associated with genes. Having expertise in AVIA for this process can improve the prediction accuracy and precision of the annotation programs. Many of the current ab initio gene prediction programs are flexible, alowing for modification or

The datasets to be collected from multiple pastured poultry farms are excellent examples for statistical and machine learning analyses. The size and quality of the data, along with the scale of variables, are likely to circumvent technical difficulties that might otherwise discourage

of Variables, are intery to characteristic sciences of the second science of the sc will elucidate the spatiotemporal patterns of Mormon cricket populations and provide accurat Becidise the beneficio of image processing, automated feature extraction, and addina faion techniques, AI/ML expertise will enhance the accuracy and precision of hail damage detection and provide more eliable insights for farmers and agronomists. Machine learning models will provide a predictive capability that will allow stateholders to anticipate potential crop damage more effectively. Data science experts can ensure that the developed models and tools are using the gene expression data we have generated from multiple plant species, the student intern will perform a houts comparison of sevent machine learning network interace tools. After optimizing and running each hol, the accuracy will be compared based on their ability of predict validated fractactions and target gene expression. Sevent in wene algorithms can also incorporate "priors" based on known regulatory interactions which they claim can improve

Data science and ML expertise are needed to integrate the geospatial datasets with the soil chemistry dataset to analyze for predictive relationships. Root architectural trains and their associations with stress tolerance and crop productivity in woody peremisis remains largely unexplored. The new took developed in this project will greatly improve the throughput of root phenotyping. The knowledge of apple roots generated from the proposed work will also allow characterizing the effects of rootstocks on whole tree physiology related to stress realizing. accelerating the development of climate-stramat varieties mysougy related to strass resultance, accentrating the development to climate-shart variates activities of bacteria and play an important role in shaping the ecology and indicated on the interval of the activities. Based on their lifecycles, bacteriophages can be classified virtual phages and temperate phages. Virulent phages, the natural predictors of bacteria, ave become promising antimicrobial agents for antibiotic-resistant bacterial pathogens. Temperate phages are favorable to several applications, such as phage display, genitic Machine learning provides a model-free paradigm for high-performance crop growth process modeling for biological parameter estimation and yield prediction. Traditionally, linear regression was used to fit the data. However, the data we collected exist complex nonlinear relationships. For known nonlinearity linear regression still can be used by transformed input variables, such as ios, exponential, polynomial etc., which may be the rare case in practice. The hondpr of al. 4 and the second state of the second state of the second state of the second state. variables, solari e cig, experienta, porynomia etc., winci may be the artic case in practice. The benefit of AI, kui, and data science of SWAT modeling ise primarily in efforts to calibrate the model for applications across large watersheets. Model calibration efforts now require gra-computational aperese, which can push the practical limits of existing high-performance computers. Modern AI and MI technologies can be trained to learn how current model optimization techniques arrive at optimization activity practice.

Although natural resources management relies heavily on computational modeling of spatiall distributed physical processes, machine learning has been shown to efficiently replace expensive computations, allowing for more flexible predicting systems that fully consider the natural world complexities. The capability of recognizing contributions from spatially connect engibrors or sequences of neighbors 3 applicable to a large variety of spatial problems.

The proposed strategy includes using a super resolution CNN (SRCNN) AI model.

The projects are heavy in computational biology. Therefore, expertise in these tools and techniques are essential for the projects to be successful. Experience in next-generation expennenting and the accompanying computational pipelines for analysis is required. Many hours can be spent soring and describing behavioral data by hand, which significantly delays dissemination of information or tricked for understanding insecticide efficacy and resistan management. By using A/M/A/data science expertise, we can cut time spent hand scoring vidi and speed up the markyls of insect behavior and subletal nonequences of insecticide applications. This information is critical for the current and future development of insecticided rescuences.

Expertise in model construction and pipeline development will be necessary for model flexibili and the accuracy of final segmentation maps that serve as foundation (input) for calculation of

and the accuracy of Intal segmentation responses disease metrics. Incorporating A/IML/data science expertise into the project will not only expedite the identification and characterization of effectors but also enhance the depth and precision of understanding of the complex interactions within the patosystem. Efficient Data Analysiz AI and machine learning algorithms can streamline the analysis of large-scale onlices data, facilitating the identification of potential effectors in a more efficient and systematic manne efficient material efficiency in a more efficient and systematic manne ensurements of the interaction of potential effectors in a more efficient and systematic manne that the fast score of the potential effectors in a more efficient and systematic manne with the fast score of the score of the fast score of ofou

lacinana go e demination to potensi enclosi on su totte enclosi en so specializza name: Hin weest are a specializati transit coro production with the relati arowshof 2 into e day and populating a half million seeds particular that would devise sugarbeet fields if not managed. Machine learning (ML) based classifications can make outsray sugarbeet fields if not managed identification. High-throughput image analytics using and particular based to so meet early detection and treatment for timely weet management, reducting yield to sa metriormental

The project will benefit from Al/ML/data science expertise by applying computer vision to analyze the images, deep karning for object detection to find the flowers, and differentiating flower piest from kackground piest, his improving breeding efficiency by applying artificial intelligence algorithms to modern agriculture. The project requires computationally intense analyzes, large scale data curation, and the use of machine learning approaches. Specifically, the project will benefit from the application of established dasfitation tools for the prediction of gene more content, as well as the adaptation of recently developed machine learning algorithms to categorize microbial lifestyles.

Ittestyles. This project will use AI/ML methods to identify signature patterns in the reflectance spectrum that are strongly associated with physiological crops stress responses including leaf water opternal jan indicator for drought stress impact on the plant, photosynthetic pignement content and drought-impacted metabolities in cotton and sophean plants that were well-watered or rought-attressed ching the critical reproductive stage. The student's role in the project will be

drought-stressed during the critical reproductive stage. The student's role in the project will be This project will be a superh opportunity for a student who would like to would shapside with GrainGenes. The student will be exposed to various data management concepts such as data storage, discoverability, access, and retrieval through hands-on learning will implement a robust and a secure API that interface a distributed network of servers. We are optimizing methods to process the meat samples and extract high quality DNA for sequencing, but another important aspect of this method will be the bioinformatics workful of the valuable foot analyze the sequencing data. A babit pipeline has been established, but it would be valuable foot to have an intern that could dedicate time or fining and automating the pipeline. The goal is for a user to have the Mass approximation and the pipeline. The second sequencing list at Altern teches a report.

Currently, the GFHINC does not have any personnel currently with expertise on ML A graduat student with a background in these skills would be crucial to our ability to implement the FoodPoxt model with our current food processing categorization research. The graduate intern will contribute toward the calibration and validation of machine learning models, linear regression, support vector regression and recurrent neural network, in prediction soll water movement and soll hydraulic properties like, soil water retention curve. Main three activities of the graduate student will be () compare various machine learning model to simulate soil water retention curve of fragipan soils, (ii) training and testing of sensor data to

29 g F			Python programming skills,		The student will build models to classify features of potato tubers (sprouts/eyes, defects,
F	otato, Breeding, Quantitative enetics, Image analysis	Machine vision, Classification, Deep learning	Knowledge relating to classification/deep learning	Prosser, WA	anatomy) and/or processed products (fry quality evaluation) from thousands digital images of potato tubers and fry planks collected by our breeding program this winter (11/2023 – 4/2024)
	orage grasses, Rangeland				We are actively developing a HTP project for both turf and forage grasses using unmanned aerial systems - "drones" to estimate several plant traits from high-resolution RGB and
A	estoration ecology, Unmanned Jerial Systems UAV, High		R and/or Python programming		multispectral imagery. For many of our main dual-purpose (forage and grain) grasses, we would
	hroughput phenotyping HTP, cological Services	Deep learning, Neural networks, Supervised learning	experience, multispectral UAV imagery	Forage and Range Research Lab - Logan Utah	like to model seed yield (pounds of seed per unit area). Accurate estimations of seed yield modeled from drone imagery can help plant breeders to accelerate their plant material
-	cological services	Supervised learning	inagery	Logan otan	This project aims to quantify environmental impacts of agricultural systems with winter cover
					crops (WCC). The impacts of WCC on reducing agricultural releases are not fully understood. The performances of WCC are often spatially heterogeneous and climate dependent. The
	fe cycle analysis, cover crop,	semi-supervised sequence	knowledge of applied statistics	Hydrology and Remote Sensing	graduate student intern will integrate spatially explicit life cycle assessment, machine learning and SWAT modeling approaches to quantify environmental impacts of the WCC systems under
c	limate change, watershed	learning DNA sequence analysis,	and machine learning algorithms	Lab, Beltsville, MD	In sub-objective 3E of our in-house appropriated research project 2034-22000-015-000D,
		microbiome data analysis,			normal and drought-treated grapevine and citrus root and rhizosphere/bulk soil samples will l collected for DNA extractions. Bacterial ribosomal 16S RNA sequences will be amplified for
	ilant physiology, plant nicrobiome, plant drought	phylogenetics, Clustering, statistical testing of alpha and	knowledge of applied statistics	Crop Disease, Pests and	sequencing. Raw sequences will be demultiplexed and processed through QIIME2 for the
2 ti	olerance	beta diversity, linear models	and R programming	Genetics, Parlier, CA	identification of amplicon sequence variants (ASVs). Bacterial taxonomy will be assigned using
			knowledge of applied statistics,		Step 1: This aspect of the project focuses on using image processing techniques to analyze the color spectrum of blueberries and muscadine grapes. The aim is to classify the fruits based on
	!		Python programming experience, and machine	Southern Horticultural lab.	their color variations, which may indicate different stages of ripeness or quality. This classification can be achieved by capturing high-resolution images of the fruits and applying
3 C	rop improvement, omputational biology	machine learning	learning	Poplarville, MS	digital image processing algorithms to extract color features. Step 2: The second part of the
	ig data, database, data uration, data integration,	computer vision, causal	knowledge of applied statistics, Python or comparable language		The intern would be working with the results of a National Agricultural Library (NAL) - Nationa Plant Germplasm System (NPGS) Rayyan search to extract publications with phenotypic and
b	reeding information nanagement system (BIMS),	inference, agent-based	programming experience, use of		genotypic data associated with small fruits (strawberry, raspberry, blackberry, blueberry, cranberry) and pear. The data from these publications would then be extracted, converted to
	reeding data management	modeling, unsupervised learning, machine learning pipeline, etc	Al tools for data extraction and manipulation, etc	National Clonal Germplasm Repository, Corvallis, Oregon	specific templates to upload to and make available through public databases (GRIN-Global,
					Our research projects all relate to the data we collect and disseminate in USDA's FoodData Central (https://fdc.nal.usda.gov/), integrated data system that provides expanded nutrient
		text mining, natural language		Beltsville Human Nutrition	profile data and links to related agricultural and experimental research. We have two data
	ood composition, nutrition	processing, data mining, data modeling	programming experience, knowledge of applied statistics	Research Center, Beltsville, Maryland	projects that would greatly benefit from support of a graduate student intern as follows: 1. Research Literature Review. This project involves using AI for text mining and natural language
5 10	bod composition, nathtion	modeling	knowledge of applied statistics	ivial yiallo	Grape viral diseases cause major economic losses worldwide. The most common viruses in
			knowledge of applied statistics,	San Joaquin Valley Agricultural	grape-grow regions are grapevine fanleaf virus, the grapevine leafroll viruses, red blotch viruse and the grapevine vitiviruses. High-throughput sequencing (HTS) has been widely used for plan
		computer vision, bioinformatic	Python programming	Sciences Center, Parlier,	viruses detection and discovery. Commercial software packages are usually costly and lack full
6 P	lant disease management	workflow	experience, machine-learning	California	annotation capability. In this project, we are seeking to establish standard bioinformatic The primary task for this project is to develop an algorithm that automatically measures width
					and length of oysters based on a semi-standardized group photograph. The secondary task, if time permits, is to develop an algorithm that identifies an individual oyster based on a
		image analysis, image	knowledge of image analysis/recognition AI/ML		photograph of that individual at an earlier time period (smaller size). We have collected image
7 a	quaculture, oyster	recognition	techniques	Orono, Maine	of oysters at several time points in the grow-out cycle for manual image analysis (measuring The National Agricultural Statistics Service and Economic Research Service recently released th
					Crop Sequence Boundaries geospatial tool that maps the agricultural fields and historical crop
Ι.	andscane Ecolomy Con-	Clustering, Regionalization,	Knowledge of applied statistics,		sequence since 2007. This project would use this new tool and the SCINet geospatial common data library to conduct a clustering and regionalization analysis to understand how crop
BR	andscape Ecology, Crop lotations, Remote Sensing	Feature Extraction, Unsupervised Learning	Python programming experience, R (optional)	Mandan, ND	sequence decisions cluster together in the Northern Great Plains. To answer, for example, if
					As part of an interdisciplinary group of ecologists, virologists, entomologists, and informaticiaa at the USDA ARS, we explore the spread of arthropod-borne livestock diseases towards better
R	vestock disease ecology,	causal inference, data			management practices. Vesicular stomatitis is one such disease that quasi-periodically spread northwards from endemic regions in south central Mexico to cause large outbreaks in horses
	ontinental disease spread, limate, drought, early warning	assimilation, random walks, Bayesian statistics	programming (e.g., R, Python), version control (GitHub)	ABADRU Manhattan, KS	and cattle in the United States. Our group links this spread to environmental conditions that
					Amyelois transitella, commonly known as the navel orangeworm (NOW), is the most damaging
	rop production & protection.		programming experience, knowledge of applied statistics.		agricultural insect pest for almonds, pistachios, and walnuts in the U.S. The systems approach by ARS scientists in Parlier also involves sterile insect technique (SIT) investigations with
s	terile insect technique, navel	computer vision, deep learning,	commitment to use automated	Commodity Protection and	collaborators to solve the problem with NOW in tree nut production in California. This researc supports the collaborative NOW Program between California Department of Food & Agricultu
0 0	rangeworm	neural networks	imaging software & hardware knowledge of applied statistics,	Quality, Parlier, California	supports the consolitative wow Program between cantonna bepartment of Pool & Agricultu
			Python, SAS programming		Depending on the intern's interest and skill-set, Dr. Thompson has two available projects with
p	recision nutrition, disparities,	causal inference, agent-based	experience, familiarity with advanced statistical methods	Children's Nutrition Research	large datasets: a videogame study that promoted healthy nutrition to elementary-aged childre (n=400); and an online obesity prevention intervention designed for 8-10 year old Black girls
1 d	ligital interventions	modeling, data visualization	and data visualization techniques	Center, Houston, TX	(n=324).
					The student will apply and modify AI/ML algorithms to extract machine-actionable format from imagery of already scanned record logs of about 50 agricultural field stations records in 29
		Image processing, environmental		National Soil Erosion Research Laboratory (NSERL), West	States. These records from the 1940s and 50s were the foundation of the famous Universal Sol Loss Equation (USLE), the widely used, first quantitative erosion prediction technology. The go
	o-Text-Conversion, Soil Erosion, Conservation	modeling, process-based modeling	Python and R programming experience	Lafayette, IN	of this project is to develop, train, and validate algorithms with an existing partial digital data
					The student will work on a combination of high-throughput phenotyping by imagining analyse to evaluate effects on plant health of diseased and water-stressed citrus and grapevines. The
	rop improvement, viticulture,	causal inference, unsupervised	knowledge of applied statistics,		automated approaches include obtaining measurements of discoloration of leaves (yellowing
	netabolomics, genomic, ihenotyping	learning, canonical discriminant analysis	Python programming experience, image analysis	Crop Disease, Pests and Genetics, Parlier, CA	browning), plant size, and plant architecture (i.e., leaf and branch spacing). The student may also develop automated programs to measure differences in fungal cultures to allow quicker
		statistical analysis by AI, machine			We have all of the R code written for the data analysis of the first sequence of 88 runs and are
		learning for big data statistical			in the process of writing those results for publication. We are now ready to expand the data
	pidomics, bovine milk nutrition,				analysis to the full set of all 88-run sequences that we have run by LC-MS as part of the Dairy
d	lairy forage improvement, dairy	analysis, R programming for analysis of bovine milk, big data	R programming (required),	Beltsville Human Nutrition	Grand Challenge. So far, we have 17 sets of 88 runs, each set representing four replicates of tw
d	pidomics, bovine milk nutrition, lairy forage improvement, dairy ig data	analysis, R programming for	R programming (required), RStudio, interest in AI, ML	Beltsville Human Nutrition Research Center, Beltsville, MD	Grand Challenge. So far, we have 17 sets of 88 runs, each set representing four replicates of tw sets of six samples from different times in the feeding study plus five replicates of six Our laboratory works on the production of antimicrobial peptides, called bacteriocins by
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This will provide cross-discipline training opportunities for the student and the PI (Feldman). The A/MA/data acience mode/s/olutions will be applied directly in the context of our postato breeding program. Healts and utility will be communicated to AKS and state university cooperators as well as stakeholders at regional and national meetings. We envision a processis in which deep leading models can be developed and validated to automate the estimation of seed yield directly from drove imagery. Seeding vigid from grass is a challinging to dreat temporal signals in this straing created summer imagery that can be used to model future (end of seasors) seed yield. In addition to being able to detect these signals and the set in the strain and the strain of create these signals and the set of the se The graduate student intern will build, train and deploy semi-supervised sequence learning The graduate subern meet will own, it and an deputy semi-supervised sequence rearing models to predict life cycle environmental impacts of the winter cover crops systems under future climate. First, the intern will build and compare semi-supervised sequence learning models like vanilla recurrent neural network, long short-ferm memory and gated recurrent units to detect all hidden relationships between the features of the in-house datasets. The ets. Then, the

From the 16S sequencing data, we need to extract useful information such as microbial species constitution, taxonomy, diversity, and changes in response to drought treatment. Analysis of these microbiome data needs the expertise in AVML/data science. International control of the constraints and the constraints and enthocyanics expected to be presented in the expertise in AVML/data science. The constraints from large datasets of frait images and corresponding find uality data. Automation through AVML can process large volumes of image data rapidy, which is beneficial for large-sciela gatochural operations. Machine learning models can uncores there and relationships in the data that may not be immediately apparent. offering deeper insights into The Rayson assarch results cover all corpos included in the MRCS and will need to be fittered for the orgo of interest to this project. Once the publications on the corpo of interest are fuentified. Algrogramming tools would be needed to exact the data and formait is for upload into the databases. These methods will be used across the NPGS system for the other corps we preserve. The result science all could be able to identify the best AVML methods for mining and synthesizing information that best accomplicities the gails of the project. The Historical Review of Analytical food Composition will require data lacence experience and knowledge in data mining and data modeling. The database includes a diverse collection of connected but not

Currently available software packages are costly and lack full annotation capability. With the contribution of a graduate student carrying AI/ML/data science expertise, we can reduce the data analysis cost and customize the bioinformatic pipelines for virus detection and discover

This project involve image analysis and recognition that is prohibitively slow, labor-intensive, tedious, or impossible to complete manually. *AIML*/data science expertise would help in developing tools that efficiently accomplish this process for both researchers and industry. This project involves answering a simple question with complex multidimensional data. Deall with such complex and variety of data tayles and identifying the most influential variables to develop efficient models cannot be handled by traditional methods, hence these advanced AJML methods. An individual with AJML data science expertise will be able to condense this information so that it can be used by producers to better understand the rotational options in momentors to that it can be used or produces to better threestants international options vescular at somalities is a complex disease system, featuring multiple likely incurved or speci that have different ecological constraints; guasi-periodic outbreak frequency; and suspected biases in mandatory and centralized periods. AVML data science play a crucial of felling spatial and temporal observation gaps and creatively generating hypotheses of facilitation a constraints on disease pread-egsectively when systematically updated with the disease and the disease international provides and the systematical science of the section of the disease and the disease international provides and the disease and the dis pecie

This project will bring precision agriculture to the ST component of the NOW Program by tearing down barriers to the flow of field data for ARS researchers and collaborators. Maxima throughput using a robust AI algorithm will enhance the accuracy of decision-making by CDFA and APHIS-PQ. NOW ST operations could be optimized to benefit the tree nut industry in th

For both projects, AI/ML will be used to identify digital phenotypes – i.e., characteristics associated with greatest change. This information will help identify for whom an intervent this type is most likely to be effective. An intern would help run the analyses, interpret the results, and assist with manuscript development – i.e., they would be an active participant the team meetings

the team meetings. AVML techniques can aid the extraction of digital records from imagery of scanned handwritter records. Commercially available software and external services are either too costly or cannot be trusted to be processed without argin club and procession and information extraction for quality assumance purposes by companying the data with validated handronial records of cory leids, soils assumance purposes by companying the data with validated handronial records of cory leids, soils

Al/ML/data science benefits this research by allowing faster, more precise measurements to occur. Currently, measurements of plant health are often on a subjective scale (such as 0-5), which is dependent on the human observer. Developing a Al/ML pipeline to make measurements will lead to more objective, consistent and precise results. AI/MI /data science benefits this re

All of the code is written in R, which is free, and open-source, bringing "data science to the masses". The gap in knowledge is the need for more free, widely available applications of R to real-world examples of lipidenci data analysis, with all data freely available on line with all code free and downloadable, which is a primary gap of this project. We beleve machine learning could be an essential tool for identifying genetic elements which positively or negatively regulate bacteriorin production within 5. thermophilus strains. Within our collection we have strains that 1: anarulary produce. 2() and be induced to produce, or 3) cannot produce bacterioring, even though they appear to possess the necessary gene clusters. We beleve that computational analysis of the sequenced genomes could assis in predicting the statist in predicting the sequence of the sequence of the sequence of the sequence of the security of the sequence of the sequence of the security of the security of the security of the sequence of the security of the security of the sequence of the security of the sec

Unfortunately, the GC-MS library is generic and non-specific to chemical pathways. Therefore, computational, and intelligent systems may advance efforts to identify these compounds and satis in the development of chemical or physical means of momoal. The above project would benefit from AI expertise with the development of a machine learning agorithm to test formalismost and similaring and 3D printing, input parameters would potentially include protein type (sodium caseinate, micellar casein, casein and whey protein toolare muk) protein connentration, cross-linking type, fat contemt, plasticize content, etc. Model outputs would likely be parameters including yield stress to characterize flowability and characterize integrations and stress including yield stress to characterize flowability and characterize integrations and stress including yield stress to characterize flowability and characterize integrations and the stress including yield stress to characterize flowability and the stress integrations and the stress including to the stress of the stress of the stress in the stress of the stress in the stress of the stress Model outputs would likely be parameters including yield stress to characterize flowability and boch artificial integrees (A) based high-throughput phenotyping platforms can significantly increase the effectiveness of germplasm evaluation. For example, time to court tiles of a few tousands of genotypes would take a month while this platform (noce developed) can reduce 1/10 of the total processing time. It takes time to develop a platform; however, once it is developed, it will allow us to effectively and princicly evaluating genetic performance of yield The groiget described would genity benefit from data science expertise given the substantial sea and complexity of the datasets, practicularly the factaonic over poduts. An intern with applied data science skills could optimize tools like the Rangeland Analysis Platform for processing and integreint this data. You only for the current project but also for future applications in assessing treatment effectiveness. This expertise would streamline data analysis. Artificial intelligence methods are just starting to be applied to the analysis of genomic data. Areas of interest include genome annotation, gene family curation, automated genome scaff curation, and protein conformation prediction. Having a student learn what A thook could be incorporated into and/or developed for beenome.100 would speed up productivity and create new knowledge.

new kiloweage: Analyses of large sequence data requires helps from computational expertise. Our lab is in the frontline of biology research and working on using ML approach to further advance. Xyelela Ulerihacter research. This is stated in our current CRIS plant (0342-2000-015-0000) sub-objective BL: Characterize metagenomes of Xyelela spp. and "Ca. Liberbiacter sept." Interdet amples using markine learning (ML Jocusing on Improvement of taxonomic likerification.

Development of the ML approach for anomaly detection will require assimilating and evalu large data sets for subtle nuances reflecting critical changes in pig behavior associated with

large data sets for subter matters remeans annumber of the set of extraction is optimized, Generative Adversarial Networks with different hyperparameters can irrigation and water management is a complex decision make by humans with limited data, particularly under a changing climate. Pic have access to proprietary 10 m resolution, repeated every A fins thema's, hyperspectral, and multispectral data (only visentiss in USA) with access). The use of these proprietary data in this project will further advance water-carbon-energy deficiency gains in water-deficit systems. Thial reservations in the US have limited information

ugh both postdoctoral scientist co-mentors have applied some natural language essing in their projects, neither are trained as a computer scientist (both are nut

scientists). Will cervids are susceptible to a transmissible and invariably fatal prion disease called Chronic wasting disease (CWD). CWD-infected animals tend to drift away from their herd mates, males are disproportionately infected with CWO at higher rate, and CWD infected females, produce fewer fames. In principle, Al and machine learning approaches may be used to identify wild recivid and measure female/awar national approaches may be used to identify wild cervide and measure female/awar national approaches may be used to identify wild measure female/awar national approaches and the second approaches may be used to identify wild measure female female fame rational approaches and the second approaches and the second approaches and the second and the second approaches and the second approaches and the second measure and the second approaches approaches and the second approaches approaches and the second approaches approac

57		code modules, data extraction, conversion of data to model readable formats, high performance computing	ability to code modules in programming languages such as Python, R or MATLAB, basic understanding of high- performance computing and Big	Sustainable Water Management	The candidate will aid in developing a module to project the outcomes from existing hydrodogical models like Agricultural bolicy Environmental Extender (APEX) into the future using different climate scenarios from global circulation models (GCM) recommended by the Intergovernmental Panel on Climate Change. To do this the candidate will a) collect the climate data from various ources, b) develop or ugrade module to convert the data to the model	An intern with A/ML/data science expertise would greatly benefit this project by expediting a lot of our data mining and data conversion time. By shorening the link between obtaining the climate data from GCMs and producing outputs from different climate scenarios in a calibrated model, we will be able to more efficiently and effectively produce visualization tools for climate scenario analyses through statistical inferences that ald stakeholders in decision-making in a
58	crop genetics and genomics, crop improvement, polyploids, genetic introgression, plant- pathogen interaction	variant calling, SNP-machine learning, deep learning	knowledge of bioinformatics, experience in programming languages such as Python, R, and Perl	Dawson, Georgia	The research project to which a graduate student intern could contribute, is part of the pennut genetics and germplasm development program at the National Pennut Research Laboratory. The program has generated genome and transcriptome data for a variety of peanut species with different pixely levels and genome types. One of the objectives of this project is to identify and anotate generic variants, primarily single nucleotide polymorphisms and bort insertion-	The development of variant calling pipelines, together with machine learning-based variant relinement, will all in the accurate identification of true SNs in peands with different levels of genome complexity. The incorporation of ML algorithms will also increase the precision of SNP discovery in wild diploid relatives of peanut, particularly those with genomes that are relatively distant from currents vaniable references. High-confidence SNPs/INDES could serve as
59	diapause, dormancy, overwintering, stress, transcriptomics, gene expression	artificial neural networks, decision trees, support vector machines	R and/or Python programming experience, applied statistics, machine learning	Insect Genetics and Biochemistry	Dozens of transcriptome studies have borne insight into the mechanisms that facilitate insect dormancy: a life stage that is critical for the proper management of a variety of economically important species. However, tools for identifying conserved patterns of gene expression among these large transcriptomic datasets are not well developed, making valuable comparative analyses of these publicly available data not feasible. Therefore, we propose the development of events and the state of th	The first Cenetics and Biochemistry Research Unit has an extensive background in stress physiology and using transcriptomics to investigate the mechanisms underlying complex phorotypes. However, our Unit tack separience applying machine learning to investigate these mechanisms at a broader scale. Additionally, these machine learning techniques are applicable to a variety of other big-data' projects currently underway and planed for our Research Unit .
60		robotic AI, machine learning, vision Transformers, long-short- term memory networks, PDE networks	knowledge of statistics,	Genetics and Sustainable	Solh health is the key to ensuring the sustainability of agriculture and climate resilience. A preeminent challenge to improve soil health is the lack of accurate and widespread data and models for robust assessment. We propose Markine Learning (ML) techniques to develop, calibrate and validate models for measuring soil health parameters using robotic spectroscopic sensors. The graduate student intern will contribute to the Japorthm design, data analysis, and	Big data, antificial intelligence, and machine learning are powerful tools that rely on high quality data input, particularly when working with complex, interconnected datasets in agriculture- duitisource high throughput algorithms to process effectively. This research will utilize advance state-of-the art dee neural networks (including Vision Instorformes, Iong-Stor-Term Memory).
		data analysis, linear regression, statistical power, machine learning, data visualization, Python programming	Python, data visualization, dashboards, familiarity with applied statistics What is your approach to mentoring and why would you be a strong mentor	Systematic Entomology Laboratory, Washington, DC & Beltsville, MD	Biological invasions cost billions in loss of ag-important crop commodiles, and this project aims to evaluate the predictive power of existing pest interception data to articipate high-risk arthropod biological invasions. We aspire to generate a predictive machine learning model that leverages >1.6M port- and border-intercepted arthropod records (e.g., commodity, year, season, country of origin, and taxonomy) to identify patterns within the interception data to arthropod tectors of the season and the interception data to the season and the season an	