

Abstracts for the 11th Annual Graduate Student Symposium in Ecology
February 10, 2018

Session I: Community Ecology & Ecosystem Indicators

Vadim Karatayev, UC Davis Graduate Group in Ecology

Playing with fun ecology problems

We know that local communities can shift suddenly among distinct states, but what does this process look like in large, demographically open ecosystems like coastal reefs or grasslands? I use a simple, dynamical community model of California's giant kelp forest communities to gain insights into both this general question and the spatial and temporal scales at which socioeconomically undesired urchin barren states can arise as a result of fishing and disturbances. The bottom line is that the makeup of a local community (i.e., its ecological state) often determines which dispersers (e.g., seeds, larvae, adult animals) manage or choose to settle there. Consequently, sudden shifts among alternative stable states can happen at small scales even in demographically open communities.

Adam Pepi, UC Davis Graduate Group in Ecology

Elevationally biased avian predation as a contributor to the spatial distribution of geometrid moth outbreaks in subarctic mountain birch forest

Background/Question/Methods

Population dynamics and interactions that vary over a species range are of particular importance in the context of latitudinal clines in biological diversity. Theory suggests that increased amplitude in population fluctuations with latitude and elevation may be related to the decreased importance of generalist natural enemies relative to specialists. Winter moth (*Operophtera brumata*) and autumnal moth (*Epirrita autumnata*) are two species of eruptive geometrids that vary widely in outbreak tendency over their range, which generally increases from south to north and with elevation in Fennoscandia. The predation pressure on geometrid larvae and pupae over an elevational gradient was tested. The effects of background larval density and bird occupancy of monitoring nest boxes on predation rates were also tested. Predation on larvae was tested through exclusion treatments at 20 replicate stations over four elevations at one site, while pupae were set out to measure predation at two elevations at three sites.

Results/Conclusions

Larval densities were reduced by bird predation at three lower elevations, but not at the highest elevation, and predation rates were 1.9x higher at the lowest elevation than at the highest elevation. The rate of predation on larvae was not related to background larval density or nest box occupancy, though there were more eggs and chicks at the lowest elevation. There were no consistent differences in predation on pupae by elevation. These results suggest that elevational variation in avian predation pressure on larvae may help drive elevational differences in outbreak tendency, and that birds may play a more important role in geometrid population dynamics than the focus on invertebrate and soil predators of previous work would suggest. This work aligns with previous theory in that lower impacts of generalist predators at higher elevation may contribute to more extreme outbreaks, though from other work there is no evidence of a correspondingly greater impact of specialist natural enemies at higher elevations

Ann Holmes, UC Davis Graduate Group in Ecology

Species in a bucket of water: Environmental DNA and conservation

Conservation requires sampling in the wild, but endangered species are often hard to find. Traditional methods of sampling may also harm sensitive populations. A relatively new approach called environmental DNA (eDNA) sampling uses trace DNA to detect fish and other aquatic species in water. eDNA may enable more sensitive and less invasive sampling in the wild, and the field is growing rapidly. However, the approach is not "one size fits all." Lessons learned from an ongoing project to design an eDNA sampling protocol for endangered fish in the San Francisco Estuary may be helpful for designing eDNA sampling protocols for other aquatic species. Target species and environment must be considered in eDNA sampling. eDNA protocol choices in the field and laboratory can affect detection rates or even the ability to detect target species. Experimental work is valuable for determining the most effective protocol, and for reducing the likelihood of false positive detections from contamination. Appropriate eDNA protocols may increase detection accuracy and improve the ability to accurately interpret eDNA detections. With appropriate protocols, eDNA sampling may indeed prove a valuable addition to the conservation toolbox for many aquatic species.

Rebecca Walker, UC Davis Graduate Group in Ecology

Clues in the soil: using nitrogen isotopes to model global patterns in nitrogen cycling

Denitrification removes biologically available N from ecosystems and thus controls the biosphere's N balance, with implications for air quality, human health and climate change. Estimates of the global soil denitrification flux are highly uncertain. Process-based models constrained by empirical isotopic evidence are as a key tool for quantifying this flux. These models use the soil $\delta^{15}\text{N}$ budget, soil moisture, and N input data, to quantify NO , N_2O and N_2 emissions from denitrification. However, this method is limited by incomplete understanding of how isotopic expression of denitrification varies across known controls, including organic carbon (C) and nitrate (N) availability. We present a quantitative assessment of isotope effect expression of soil denitrification across a range of C and NO_3^- availabilities. This experiment tests the hypothesis that isotopic expression of soil denitrification (a kinetic process) increases with NO_3^- availability (reaction substrate) and decreases with increasing availability of organic C (electron donor). Periods of both net consumption and net production of nitrate were observed, yet only the net consumption events had significant isotope effects. Isotope effects ranged from 2–22‰. Isotopic enrichment increased with increasing C until a threshold of 10% soil organic C was reached, after which only a small isotope effect was observed. This indicates that C availability is a key driver of variability in the isotope effect of denitrification. Isotope effects measured in this study were less than those used in current models, suggesting that the global denitrification flux is underestimated.

Keynote Address:

Dr. Meg Lowman, California Academy of Sciences

Using Canopy Research as a Hook to Inspire Forest Conservation

Session II: Anthropogenic Impacts on Ecological Systems

Maya Almaraz, UC Davis Department of Land, Air and Water Resources

Agriculture is a major source of NO_x in California

Nitrogen oxides (NO_x=NO+NO₂) are a principal component of poor air quality, aiding in the formation of ground-level ozone and ammonium nitrate aerosols that contribute to lung disease, premature death and natural ecosystem damages across the globe. In California, regulatory policies have limited fossil fuel sources of NO_x pollution; however, recent findings have suggested that soil NO_x emissions from the state's extensive agricultural regions have been overlooked. We use three approaches to constrain soil NO_x emissions for the state of California: 1) an Intergraded Model for the Assessment of the Global Environment (IMAGE) to estimate the magnitude and spatial distribution of soil NO_x emissions; 2) airborne observations of atmospheric concentrations from agricultural soils combined with surface emissions estimates; and 3) a meta-analysis of empirical observations among different land use types. We hypothesize that, a) biogenic emissions of NO_x are substantially greater than the California Air and Resource Board's estimate of zero, and that b) soil NO_x emissions are an important source of atmospheric NO_x, particularly in agricultural regions of the state where large amounts of fertilizer are applied. The results are largely convergent: NO_x emissions from cropland soils represent a significant fraction of California's total NO_x emissions (~25-41%). Emissions of NO_x from cropland soils totaled 161,100 tons N y⁻¹. While emissions from natural ecosystems were relatively small (1.0 kg N ha⁻¹ y⁻¹), NO_x emissions from cropland soils averaged 19.8 kg N ha⁻¹ y⁻¹, with the highest fluxes in hot and arid regions of Southern California. These estimates are consistent with empirical observations, which typically fall between 1-10 kg N ha⁻¹ y⁻¹. Surface emissions estimates of cropland soils generated a summertime NO_x flux of 12.4 kgN ha⁻¹ y⁻¹, contributing ~47% to the overall NO_x concentration measured by aircraft. Our results suggest the need to adopt statewide policies to limit NO_x emissions from California agriculture, thus benefiting human and ecosystem health in rural areas.

Jessica Rudnick, UC Davis Graduate Group in Ecology
California Farmers' Voices on Nitrogen and Water

Ryan Bourbour, UC Davis Graduate Group in Ecology and Avian Sciences
Raptor feather mercury trends in time and space across North America

Mercury (Hg) contamination from anthropogenic sources is widespread and can be detected in even the most remote ecosystems of the world. When Hg becomes biologically available and enters food webs, top predators can be vulnerable to toxic levels of exposure. Raptors are apex predators in a variety of ecosystems and are known to be useful as sentinels for environmental contaminants over large geographic regions. However, little is known about how Hg exposure in North American raptor populations differ among species, feeding guilds, through time, and across the continent, especially for raptors feeding in terrestrial food webs. To investigate raptor feather mercury trends, we compiled archived breast feathers collected from 10 species during autumn migration to analyze feather Hg concentrations of raptors representative of different habitats and feeding guilds in North America.

Matt Thorstensen, UC Davis Graduate Group in Ecology

To breed or not to breed? That is the question (of white sturgeon conservation aquaculture)

Captive breeding programs are challenged by maintaining genetic, phenotypic, and behavioral characteristics in managed populations. Conservation aquaculture, in captivity breeding fish, has dealt with several negative genetic impacts on wild populations such as loss of genetic diversity, domestication selection, and inbreeding. We present a study where two sampling methods are compared in a conservation aquaculture program for white sturgeon, *Acipenser transmontanus*, with the goal of minimizing genetic diversity loss and maximizing the number of breeders

represented in reintroduced cohorts. Egg and larvae based sampling where young are repatriated into their native habitat after rearing in hatcheries is found to preserve more genetic diversity and represent more breeders than broodstock-based aquaculture. These results provide the first comparison of number of breeders between broodstock and repatriation-based methods with respect to a hatchery program, and provide a framework for both other conservation aquaculture programs and captive breeding in general.

Session III: Wildlife Conservation & Management

Jennifer Brazeal, UC Davis Graduate Group in Ecology

Assessing deer population responses to a high-severity wildfire in the Sierra Nevada using non-invasive genetic sampling

William Hemstrom, UC Davis Graduate Group in Ecology

Rapid adaptation during establishment and spread in invasive Three-spined Stickleback in the Deschutes River, Oregon: from introduction to adaptation

Adaptation during the establishment and spread phases of species invasion is thought to be critical to invasion success. However, since introduction is often accompanied by a population bottleneck, the adaptive potential of invaders are often constrained by limited genetic diversity. Three-spined stickleback were introduced into the Deschutes River system in central Oregon in the 1980s and have since spread throughout the system, where they have flourished despite substantial ecological heterogeneity. Based on 2b-RAD sequence data taken from six sub-populations, we found evidence that a novel chromosomal inversion was swept dramatically up in frequency twice as the species spread across the system and that a selective sweep at another region of the genome likely happened during the period when the population was still establishing, despite low initial genetic diversity. This study provides evidence that macro-evolutionary events such as chromosomal rearrangements can be provide critical adaptive capacity and promote invasion success

Martha Wohlfeil, UC Davis Graduate Group in Ecology

Potential mechanisms of within-season elevational movement of songbirds

Frank Fogarty, UC Davis Graduate Group in Ecology

Riparian area, fragmentation, and breeding birds in the Great Basin

In much of the Great Basin, montane riparian areas exist as small islands within the larger, arid landscape. Although riparian areas cover <1% of the total land area in the Great Basin, more than 50% of breeding bird species in the region are associated with riparian habitats. These riparian areas occur mostly in canyons, either along the canyon bottom or in the form of seeps, and are fragmented due to both natural processes and human activities. I am evaluating the extent to which the total area of riparian vegetation and the degree of fragmentation of this riparian area explains both species richness and beta diversity in breeding riparian bird species, as well as the likelihood that a given riparian species is present in a given canyon.

My study area was 24 canyons in four mountain ranges (the Shoshone Mountains, Toiyabe Mountains, Toiyabe Mountains, and Monitor Range) in Eureka, Lander, and Nye counties in Nevada. I am using bird point count data collected from 2001 to 2015 and derived land cover data from the National Agriculture Imagery Program. The total riparian area in each canyon ranged from <1- 430 hectares and we detected a total of 114 species on point counts. I calculated total average annual species richness for each canyon. Additionally, I selected a subset of 16

migratory species that were both associated with riparian land cover and confirmed breeders in our study area. I calculated species richness on that subset and modeled the likelihood of occurrence for each individual species at the canyon level as a function of both total riparian area and fragmentation. I also modeled the effect of riparian area and fragmentation on beta diversity using non-metric multidimensional scaling.

Preliminary results suggest that both the total area and fragmentation of riparian habitat within a canyon may be a strong influence on whether migratory birds establish breeding territories in that canyon, even when the available habitat is much larger than the area of an individual bird's territory. Riparian fragmentation explains more variance than total riparian area for both species richness and the likelihood of occurrence for most individual species. These results also suggest that there may be maximum thresholds of riparian fragmentation within a canyon beyond which some species are unlikely to occur. Riparian areas in the Great Basin are expected to further contract and fragment in the coming century, as climate change increases aridity in the region and human demand on water in arid regions increases. Therefore, understanding these relations and thresholds may have implications for conservation and management of species reliant on riparian areas.

Posters:

Jaelyn Aliperti

*Litter translocations by yellow-bellied marmots, *Marmota flaviventris**

Tom Batter

Using a predictive model to develop an efficient sampling design for population estimation of tule elk using fecal DNA in Colusa and Lake Counties

Jennifer Brazeal

Evaluating the use of non-invasive genetic spatial capture-recapture for estimating elk population density

Recently, the use of spatial capture-recapture models (SCR) to estimate wildlife population density has increased. Non-invasive genetic sampling methods, the collection of genetic material left in the environment, are particularly useful for obtaining sufficient sample sizes for SCR for wide-ranging species. However, accuracy of SCR estimates for a given species is difficult to assess without comparison to a known population number. In addition, current SCR models assume independence in animal movement, an assumption that group species (e.g., elk) would violate. In the Central Valley, California, a population of tule elk (*Cervus canadensis nannodes*) resides in a 3.5 km² enclosure at the San Luis National Wildlife Refuge, and is surveyed seasonally. From July 14th to September 1st, 2016, we collected 484 fecal samples, identifying 71 individuals, compared to 72 elk counted during the most recent survey (July 22, 2016). We assessed the effects of sampling effort and density on precision of estimates by subsampling different numbers of sample grids and elk. SCR results were robust to violations of the assumption of independence of movement, producing unbiased estimates at different sampling levels. We found that the number of samples was a good predictor of RSE, and would be a useful adaptive sampling measure for attaining a desired level of precision for fecal DNA SCR studies.

Amanda Coen

Proposal - Simulating the effects of landscape and population on wildlife spatial-temporal genetic patterns

Human land use affects how animals move across landscapes and how their populations are structured. Measuring genetic diversity and differentiation is useful for determining the impacts of landscape change on the degree of connectivity between populations. Yet efforts to inform conservation may be confounded if genetic patterns represent past signatures of gene flow and not the current degree of connectivity. The genetic composition of a population does not immediately stabilize at a new equilibrium after a change in connectivity. The speed with which changes in genetic composition are detectable is influenced by the degree to which the landscape resists movement, in addition to dispersal capability, population size and genetic diversity at the time of disrupted gene flow. Understanding whether landscape resistance or population characteristics have greater influence on spatial genetic patterns and the temporal speed with which they develop is important for wildlife management in an increasingly human modified environment. Using the individually-based simulation program CDPOP, I will run factorial simulations with varying landscape resistance and population configurations to examine lags in detecting disrupted gene flow between simulated populations.

Annelise Del Rio

Effects of low oxygen and high temperature on Chinook salmon physiology and development

Climate change and drought can lead to increased temperature and decreased dissolved oxygen in rivers. In the Central Valley, rivers are typically managed for salmonid survival based on temperature; however, oxygen saturation is another critical factor for managers to consider. Salmon embryos are particularly susceptible to high temperatures and low oxygen given that conditions within a redd, or nest, can differ from those of the river itself. To investigate how temperature and oxygen as single and combined stressors affect the survival and physiology of early life stage Chinook salmon, we reared embryos from fertilization to the fry stage under low temperature and high oxygen, low temperature and low oxygen, high temperature and high oxygen, and high temperature and low oxygen. Fish were sampled at four stages during development to test their upper thermal tolerance and low oxygen tolerance, measure growth, and analyze biochemical responses. Fish reared in low temperature or low oxygen developed more slowly than those in high temperature or full oxygen. Embryos reared in low oxygen had significantly reduced hatching success and the multiple stressor treatment with high temperature and low oxygen had greatly reduced hatching success. Acclimation to warm temperature or low oxygen increased thermal tolerance. Acclimation to low oxygen during development increased tolerance to low oxygen, while high temperature reduced low oxygen tolerance. These results demonstrate the importance of water management strategies that consider other abiotic stressors in addition to temperature to promote survival of early life stage Chinook salmon in the Central Valley and further explore the interaction between temperature and oxygen on fish physiology.

Breanna Martinico

Merlin (Falco columbarius): Population genetics in the post-DDT era

In the mid-1900s, Merlin populations experienced range-wide declines due to eggshell thinning caused by persistent organic pollutants (DDT and DDE). After DDT was banned, North American Merlins steadily recovered without any focused conservation efforts. However, little is known about how the genetic diversity and population structure of this species has been affected by this bottleneck event. Additionally, little is known about how historic events, such as past glaciation, have shaped the demographic history of this species. To investigate population structure and phylogeography of Merlins in North America, we collected blood or breast feathers from 272 Merlins from 13 migration banding sites. We used 24 polymorphic microsatellite loci for population genetic analyses and a 569 bp sequence of the COI gene of the mitochondrial

DNA for phylogenetic analyses. We found that Merlins have a unique demographic history compared to other North American raptor species and that DDT likely played a large role in shaping contemporary population structure. Future targeted genomic studies will help to identify additional fine-scale patterns of differentiation and selection.

Linda Mendez

How to study power in socio-ecological systems?

Amy Michaud, UC Davis Entomology and Nematology

Snail-mediated dispersal of plant-parasitic nematodes

Dispersal is a fundamental phenomenon with significance for individuals, populations, and communities. Dispersal of parasites has fitness consequences with respect to dissemination among hosts. *Helix aspersa*, the brown garden snail, is common in California and especially in agricultural settings. As snails move and feed, they encounter and potentially consume a diverse array of meiofauna. If snails consume plant-parasitic nematode propagules (eggs or infective juveniles) present in their food, and the nematodes survive the passage through the digestive tract, viable nematodes may be moved from the natal location and deposited in the feces some distance away. Plant-parasitic nematodes are small, and have limited capacity to disperse independently, such that snails could represent a long-distance dispersal mechanism. Here we report that egg masses of the root-knot species, *Meloidogyne javanica*, were consumed by snails, that the recovered egg from feces were viable, and that the infective juveniles that hatched from those eggs were able to infect new host plants. Snails were allowed to feed for 5 days on carrot discs upon which had been placed intact nematode egg masses. Snail fecal pellets were collected daily and disrupted in water by bombardment with zirconia/silica beads. The resultant aqueous suspension was diluted and a subsample of eggs, infective juveniles and other nematodes was enumerated using a dissecting microscope. A subsample of fecal pellets were placed on Baermann funnels, and were sampled every 24 hours for up to 10 days to quantify viability by monitoring egg hatching. A subsample of the freshly hatched infective juveniles were added to tomato seedlings and the roots were evaluated for galling after 6 weeks. We recovered eggs from fecal pellets within and up to 48 hours after ingestion of egg masses. These eggs hatched for up to 10 days. In 61% of the samples of eggs from which juveniles were hatched, those juveniles successfully infected and induced symptoms in those host plants (gall formation). These data demonstrate that eggs that traverse the digestive tract of *H. aspersa* can hatch viable infective juveniles. Snails may act dispersal (potentially phoretic) hosts of plant-parasitic nematodes and represent an underrecognized means of dispersal.

Sophie Preckler-Quisquater

Assessing selective introgression of nonnative red fox genes into the genomic background of the native Sacramento Valley red fox

The Sacramento Valley red fox (SVRF, *Vulpes vulpes patwin*) is endemic to the northern Central Valley of California, and is considered a Species of Greatest Conservation Need due to the apparent decline in abundance from historic levels, the recognition of its low genetic effective population size ($n=50$), and its restricted and sparse distribution. Along with habitat loss, hybridization with nonnative red foxes of captive-bred origin has been identified as one of most significant threats to the persistence of the SVRF. Genetic monitoring during 2007-2017 indicated the presence of gene flow from the nonnative population into the native SVRF population. To the extent that the diffusion of nonnative genes into the native population is

random (i.e., neutral with respect to selection), gene flow appears relatively low. However, if particular nonnative genes are positively selected for in the native population (i.e. invasiveness genes), these could potentially be transferred at a far greater rate than were observed for neutral genes and become fixed. Selective introgression of nonnative genes could potentially transform functional aspects of the SVRF's biology, affecting its fundamental niche and, consequently, its role in the greater ecological community. Selective introgression also can also be a habitat-specific phenomenon. For example, nonnative red foxes are frequently associated with wetlands, where SVRF were not historically known to occur; yet today they have been observed within these novel habitat types. Thus, in the next phase of this research, we plan to use emerging genomic techniques to identify regions of the SVRF genome potentially reflecting selective introgression of nonnative red fox genes.

Aviva Rossi

Comparing the Niches of Three Sympatric Montane Squirrel Species

Species that overlap in physical space are often separated along niche space parameters. We evaluated the niche space of three sympatric high-elevation ground-dwelling squirrels, yellow-bellied marmot (*Marmota flaviventris*), Belding's ground squirrel (*Urocitellus beldingi*), golden-mantled ground squirrel (*Callospermophilus lateralis*). Our survey area encompassed the alpine and subalpine region of the Sierra Nevada in California. We used Ecological Niche Factor Analysis (ENFA) to quantify multivariate niche using an index of marginality and specialization, along axes of several climate and habitat variables. This allowed us to identify which of those variables are important predictors of each species presence. We also compared species use of niche space, as well as identified areas of niche space overlap and differentiation between the three considered species. This poster presents the results of the ENFA.

Julea Shaw

Strip-seeding: a novel grassland restoration strategy Sarah Stinson: Metabarcoding of freshwater invertebrates for biomonitoring

The prevalence of invasive annual grasses and the difficulty of establishing native perennials makes restoration of California grasslands challenging. Recently, strip-seeding has been proposed as a novel, cost-effective strategy to address these persistent challenges to restoration success. Strip seeding is a spatially-patterned seeding method that involves seeding in linear patches across a site. The method is expected to reduce cost of seed, increase native establishment, and reduce invasive species cover within seeded areas. However, strip seeding has never been formally tested in western grassland systems and it is unclear how initial configuration may alter the plant community and dispersal of desirable species to unseeded areas. We examined the utility of strip seeding by seeding native perennial bunchgrass mixes in different strip width configurations (seeding coverage from 0% - 100%) in fall 2012 in Davis, CA. In spring 2016, we measured the community diversity and abundance across transects in seeded strips and in unseeded between-strip areas. There were no significant differences in plant communities among strip seeded treatments, but there were differences between plant communities in strip seeded treatments and controls. Native grasses successfully established in all seeded strips with cover similar to those in the 100% seeded treatment (~31%). Average native cover in unseeded areas was only slightly lower than in seeded areas (~27%), however non-native cover was higher in unseeded areas than in seeded areas (~60% vs ~31%). Therefore, strip-seeding is an effective method for establishing native species, but control of non-natives in unseeded areas will require further management.

Sarah Stinson, UC Davis Graduate Group in Ecology

Metabarcoding of freshwater invertebrates for biomonitoring

Freshwater invertebrates are important consumers of phytoplankton and ample food sources for organisms at higher trophic levels. They are useful as bioindicators due to their wide tolerance ranges to altered water quality. Traditional taxonomic identification is limited by the life stage and condition of each specimen, however. This can reduce the predictive power of inferences made about water quality, potentially limiting the usefulness of the tool. Access to taxonomic expertise can be another bottleneck in this process. Innovative molecular technologies such as metabarcoding are cost-effective methods for scientific monitoring and analysis of ecosystem characteristics, reliably quantifying patterns of diversity and community composition. DNA can be used to identify a wide range of taxa, even at very low densities, providing taxonomically comprehensive, efficient, and verifiable data. The increased taxonomic resolution obtained from metabarcoding could reveal losses in intraspecific genetic diversity or losses of cryptic species. This will require the creation of a robust and relevant sequence database to match sequences to taxonomy. The overall goal of this project is to evaluate the effectiveness of DNA metabarcoding to characterize aquatic invertebrate communities for biomonitoring, relative to traditional methods. My objectives are to 1) create a DNA sequence database of invertebrate biodiversity of the California bay-delta and its tributaries, 2) evaluate species richness and population genetics information obtained from metabarcoding to inform long-term monitoring. H1: Genomic techniques will enhance the taxonomic resolution and coverage of traditional biomonitoring, and provide information relevant to understanding population dynamics. H2: Community structure will vary between sampling sites, with sensitive bioindicator taxa absent from sites with a history of contaminant exposure. Preliminary Results show that the choice of DNA extraction and amplification methods produce high quality/quantity DNA sequences from preserved voucher specimens. The C01 primers are appropriate for a wide range of taxa found in the Delta. The molecular methods produce data that is suitable for establishing the database. Taxonomic identification is on-going, with assistance from expert taxonomists at UC Davis.