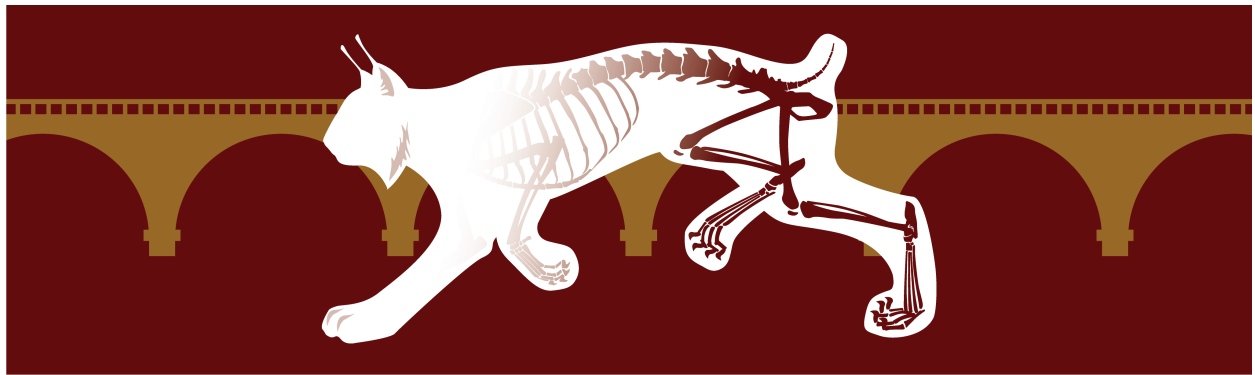


96TH ANNUAL MEETING
OF THE
AMERICAN SOCIETY OF
MAMMALOGISTS

24-28 JUNE 2016

UNIVERSITY OF MINNESOTA
-MINNEAPOLIS, MINNESOTA-



ASM • 2016 • MPLS

ABSTRACT BOOK

The 2016 American Society of Mammalogists Annual Meeting logo features a Canada lynx, a Minnesota native mammal. The transition in the depiction of the lynx represents different but related fields of study in mammalogy, from morphology to behavior. The Stone Arch Bridge, a Minneapolis landmark, and the maroon and gold coloring nod to the conference location at the University of Minnesota-Twin Cities. The logo was designed by Carmen Martin, a Minnesota-based artist who practices scientific illustration, observational drawing, sculpture, and graphic design.

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AMERICAN SOCIETY OF MAMMALOGISTS (ASM)

The American Society of Mammalogists (ASM) was established in 1919 for the purpose of promoting interest in the study of mammals.

AN OVERVIEW

In addition to being among the most charismatic of animals, mammals are important in many disciplines from paleontology to ecology and evolution. We, of course, are mammals and thus are in the interesting position of studying ourselves in quest of a greater understanding of the role of mammals in the natural world.

The ASM is currently composed of thousands of members, many of who are professional scientists. Members of the Society have always had a strong interest in the public good, and this is reflected in their involvement in providing information for public policy, resources management, conservation, and education.

The Society hosts annual meetings and maintains several publications. The flagship publication is the *Journal of Mammalogy*, a journal produced 6 times per year that accepts submissions on all aspects of mammalogy. The ASM also publishes *Mammalian Species* (accounts of individual species) and *Special Publications* (books that pertain to specific taxa or topics), and we maintain a mammal images library that contains many exceptional photographs of mammals.

We encourage you to peruse the ASM web site for information about mammals and the American Society of Mammalogists. Check out our interesting history by clicking on the Our History tab on the Archives Committee page. We hope it will stimulate your interest in mammals and further your appreciation of their importance.

ASM LEADERSHIP

The ASM is led by a group of scientists who are elected by the membership.

ASM COMMITTEES

Much of the work that the ASM does is accomplished through a large number of volunteer committees. These committees work to further the aims of the Society and the science of mammalogy as a whole.

ASM ENDORSES HUMAN DIVERSITY

The ASM is dedicated to ensuring the opportunity for active, equal participation in all ASM functions by all members, regardless of gender, race, ethnic background, age, physical disabilities, or sexual orientation.

<http://www.mammalsociety.org/>

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WELCOME

Welcome to the 96th annual meeting of the American Society of Mammalogists!

This is one of our best-attended meetings in 25 years, so the next few days promise to be exciting, busy, and fun. For new members, this will be a wonderful opportunity to meet fellow mammal enthusiasts and to share in the latest findings regarding mammalian biology. For long-term attendees, it's a chance to catch up with old friends as well as welcome newcomers to the pack.

In addition to a full slate of contributed papers and talks covering the latest research in mammalogy, we have scheduled symposia on two important themes: the use of digital "big data" to further understanding of mammals and the application of morphometric techniques to studies of mammalian ecology and evolution. The first should be of interest to anyone who uses online databases in their work and will highlight not only existing resources but also indicate how you can participate in the growing digital world of mammalogy. The second will demonstrate how emerging technologies such as CT-scanning are creating new opportunities to study morphology, including application of morphometric data to diverse aspects of research on mammals. These symposia will take place on Monday, 27 June but at different times so that you can attend both.

As part of our Society's commitment to research training and professional development, we are again hosting several pre-meeting workshops, which will take place on Friday, 24 June, the day before the regular meeting program begins. These events include a workshop on geometric morphometrics that is co-sponsored by iDigBio and a workshop aimed at helping members to navigate the often-challenging balance of professional and personal responsibilities. To read more about these workshops, please see the information posted on the meeting website.

With regard to oral presentations, we have a great roster of plenary session speakers. During the first plenary session, we will hear from some of our outstanding student members, including the 2015 recipients of the Hornaday Award (José González-Maya), the Shadle Fellowship (Silvia Pavan), and the ASM Fellowship (Kayce Bell). At the second plenary, we will hear from a stellar group of more established mammalogists, including the 2015 recipients of the Merriam Award (Bruce Patterson), Leopold Award (Andrew T. Smith), and Grinnell Award (Robert Dowler). The meeting will conclude with a capstone presentation by Dr. Ali Swanson, who combines research on the community ecology of African taxa with innovative citizen science projects to promote the conservation of all mammals – non-human and human – in the areas in which she works.

No ASM meeting would be complete without some socializing! We will kick off this important component of the meeting on Friday night, with an opening reception in the Bell Museum. Come check out the museum, greet old friends, and welcome new members to the meeting. On Saturday night, we will hold a student mixer, which is an important opportunity for this group of attendees to get together and share ideas and experiences. Sunday is the picnic, which will take place at the Nicollet Island Pavilion, located along the shore of the Mighty Mississippi. Monday night will begin with a poster session and segue to a social and our annual auction, proceeds of which go to support the Future Mammalogists Fund. Come, have some beer, and bid on some the fantastic memorabilia that will be available. We will end the meeting with our second Closing Social and Awards Ceremony, to be held at the McNamara Alumni Center. This will be an informal event intended to give everyone one last chance to visit with each other and to participate in recognizing the outstanding achievements of some of our members.

In closing, I would like to thank our sponsors, exhibitors, and advertisers. Their support is critical to the success of many of our annual functions. Please take some time during the breaks and socials to stop by their tables and displays and be sure to let them know how much you appreciate their participation.

Enjoy the meetings,

Eileen Lacey
President, American Society of Mammalogists

ACKNOWLEDGEMENTS

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LITERATURE ONLY



ABSTRACTS

1^{E,TA}: A multi-method approach to understanding and mitigating human-carnivore conflict in Meibae Community Conservancy, Kenya

Adriana M. Casillas*, Beth A. Kaplin, and Mary Wykstra

Department of Environmental Studies, Antioch University New England, Keene, NH 03431 USA (AMC, BAK); Forestry and Environmental Studies, Yale University, New Haven, CT 06520 USA (MW)

Human-carnivore conflict (HCC) is a serious and complex issue threatening predator populations and local livelihoods on a global scale. Across Africa, active persecution by humans based on real or perceived threats to themselves or their livestock is a leading cause in the disappearance of medium-to-large predators outside of protected areas. Improving our understanding of HCC by scientifically evaluating potential mitigation strategies is critical to establishing sustainable management and conservation efforts, and thus the future of apex predators. In this study, we investigated 'actual' versus 'perceived' conflict inside Meibae Community Conservancy (MCC), Kenya, via comparison of formal interview data with evidence from foot patrols and camera traps set around homesteads. Additionally, we tested the effectiveness of two different light systems (solar-powered Lion Lights and 6-volt Foxlights) as possible non-lethal, predator deterrent methods. We used frequency of visitation data to determine the impact of light systems on species. Our findings suggest the Lion Light system has the potential to significantly decrease visitation by all species, including spotted hyena (*Crocuta crocuta*) which is the most problematic, and least tolerated livestock-raiding predator in MCC. This project was successful due to the growing interest and support from the local community and, although HCC environmental conditions and socioeconomic factors are often site-specific, may provide useful information for mitigating conflict in similar areas and help guide future studies. This research was supported by Annie M. Alexander Award awarded to Adriana Casillas in 2015.

2^{E,TA}: Is vomeronasal system evolution in bats is a one-way street?**

Laurel R. Yohe* and Liliana M. Dávalos

Department of Ecology & Evolution, Stony Brook University, Stony Brook, NY 11794 USA

Mechanisms for pheromone communication occur in the vomeronasal system in mammals and are well conserved, as vomerolfaction has critical roles in social communication. These mechanisms include pheromone detection by vomeronasal receptors (V1Rs) and signal transduction via Transient receptor potential cation channel 2 (Trpc2), an ion channel indispensable for vomerolfaction. Surprisingly, most bats lack a functioning vomeronasal system, exhibiting degraded vomeronasal morphology and pseudogenized Trpc2 and V1Rs, despite a nocturnal lifestyle and gregarious behaviors. New World Leaf-nosed bats, a family well known for its diet diversity, are one curious exception. Whether phyllostomids retained or regained vomeronasal function through time remains unclear. We obtained V1R profiles from the vomeronasal transcriptome of a diversity of phyllostomids and sequenced Trpc2 in over 100 bats. Phyllostomid V1Rs are orthologous with the dog and horse, and resulting gene trees provide no evidence of bat-specific vomeronasal receptors. Most non-phyllostomids show independent pseudogenizing mutations of Trpc2, while phyllostomids show strong purifying selection to maintain a functional Trpc2. Through sequence simulations, we determined purifying selection of Trpc2 and V1Rs has been prevalent throughout the evolutionary history of phyllostomid bats and it was unlikely Trpc2 was reactivated. Thus, phyllostomids have maintained vomeronasal function since the divergence with other Laurasiatherians. These results also imply the chemosensory system is a crucial sense for some bats, a modality often underappreciated in light of other extreme bat sensory adaptations. This research was supported by a 2015 Anna M. Jackson Award and a Grants-In-Aid of Research awarded to Laurel Yohe.

3^{TA}: Reassessing the phylogeny, biogeography, and diversification of Madagascar's tenrecs (Tenrecidae)**

Kathryn M. Everson*, Voahangy Soarimalala, Steven M. Goodman, and Link E. Olson

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Madagascar is renowned for the strikingly high endemism of its native biota, including 100% endemism of its extant terrestrial mammals. About 20% of these are tenrecs (Tenrecidae), small- to medium-sized placental mammals (2-1800 g) often described as an extraordinary example of adaptive island radiation. Tenrecs have a tumultuous taxonomic history, which has caused much confusion about the relationships among the major tenrec lineages and about the number and timing of colonization events to Madagascar. Here we present the largest molecular study of Tenrecidae to date (11 genes, 9,584 nucleotides) and the first to include all recognized species in a phylogenetic reconstruction. This comprehensive phylogeny allows us to make three important taxonomic revisions, and provides a much-needed backbone for placing newly recognized species, which have been named at a rate of nearly one every two years since 1992. We also estimate divergence and colonization times using six fossils, including several that have never been used as calibration points. Finally, we estimate the rate of diversification (i.e., speciation, dispersal, and extinction) with respect to habitat association. This research was supported by an A. Brazier Howell Award awarded to Kathryn Everson in 2015.

4^{TA}: Elucidating the evolutionary consequences of mammalian sociality

Jeremy Chase Crawford

Department of Integrative Biology and Museum of Vertebrate Zoology, University of California at Berkeley, Berkeley, CA 94720 USA

Biologists have long hypothesized about the potential costs and benefits of sociality, which have been broadly characterized in terms of tradeoffs between direct and indirect fitness that may allow animals to overcome particular ecological constraints. Of the specific costs putatively linked to group living and complex social organization, increased exposure to communicable disease may be the most important, as pathogen exposure and disease susceptibility are two of the greatest influences on reproductive success. Attempts to explicitly demonstrate the consequences of sociality by comparing pathogen or parasite prevalence among social and solitary species have historically proven difficult, as divergence among species is often commensurate with divergence among their respective pathogens and parasites. Rather than attempting to quantify differences in immune pressures by assessing pathogen or parasite prevalence, I have endeavored to quantify those differences by measuring evolutionary response to immune pressures at the molecular level. To accomplish this, I utilized a comparative analysis that leverages genome-wide transcript sequences from social-solitary species pairs along distinct mammalian lineages, each separated by 75-95 million years of evolution. By inferring ancestral sequence states for these transcripts, I was able to estimate and then compare rates of evolution among social and solitary lineages. These analyses demonstrate that relatively social and solitary mammals experience distinct evolutionary pressures, with genes involved in a diversity of immune functions evolving significantly faster in social species. This research was supported by an Elmer C. Birney Award awarded to Jeremy Crawford in 2015.

5^{}: Distribution of mammal functional diversity at different scales: implications for conservation**

José F. González-Maya

Proyecto de Conservación de Aguas y Tierras, ProCAT Colombia/Internacional, Carrera 13 # 96-82, Of. 205, Bogotá, Colombia

Mammals are one of the key groups in the functioning of ecosystems, and yet one of the most threatened. Loss of their populations and consequent functional loss can potentially represent a major threat to global ecosystem's functioning. The aim of this work was to evaluate patterns of functional diversity (FD) at different scales, its spatial variation and main determinants at global, regional and national levels, as well as its relationship with intervention and endangered species. We found that mammal FD varies globally with clear patterns similar to SR, but influenced by ecological scale; threatened species significantly influence FD globally (60-70%). Regionally, human intervention and species at risk are the main determinants, where certain ecoregions have already suffered drastic FD loss and others are more likely to suffer it due to extinction. Nationally, FD differs from SR and is strongly influenced by composition, environmental, biogeographic and anthropogenic determinants, also showing spatial mismatch. Global variation and convergence can be the response to environmental filtering as well as extraordinary trait convergence in assembling communities according to ecosystem type. Our results have implications for conservation prioritization and planning, the differential impact of human intervention

and the need to explore the spatial variation of the species-ecosystem relationship and its drivers. Functional diversity should be a measure considered in future conservation schemes allowing better resolution for decision-making. This research was supported by a William T. Hornaday Award awarded to José F. González-Maya in 2015.

6^{E,TA}: Disentangling lousey relationships: a phylogenomic perspective on host-parasite coevolution**

Kayce C. Bell

Department of Biology, Museum of Southwestern Biology, University of New Mexico, Albuquerque, NM 87131 USA

Climate and host demographic cycling often shape parasite genetic diversity and host distributions. Comparative phylogenetic and phylogeographic approaches can elucidate processes that impact parasite evolution beyond strict host associations. We used 900 genomic loci to investigate the history and genetic structure in two sucking lice (Anoplura), *Hoplopleura arboricola* and *Neohaematopinus pacificus*, that only infect western North American chipmunks (Sciuridae: *Neotamias*). We also estimated chipmunk phylogenetic relationships using 3500 ultraconserved element (UCE) loci from across the genome. Given the high species diversity within *Neotamias* and a history of climatic cycling across western North America, we predicted that lice would contain divergent lineages structured by both host affiliation and geography. For both lice species, we recovered clades largely associated with a set of related host lineages (i.e. single host species or host species complexes) suggesting some level of codiversification. However, the relationships among the host-associated lineages vary between the two lice species. Comparison of the phylogenies reveals different histories of association with chipmunks for these two ectoparasitic species. These outcomes suggest that diversification of different parasite species inhabiting the same niche is being impacted by processes beyond host diversification. This research was supported by an ASM Fellowship awarded to Kayce Bell in 2015.

7^F: Source-sink dynamics and sex-specific dispersal patterns in wolverines of the Yukon Territory

Dianna M. Krejsa*, Sandra L. Talbot, George K. Sage, Thomas S. Jung, and Joseph A. Cook

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Climate change is quickly affecting all parts of the biosphere, with particular fast and adverse effects to high-latitude biological communities. As a wide-ranging circumboreal carnivore, the wolverine (*Gulo gulo*) is an ideal species for studying responses to perturbation. This species has a dynamic history of contraction into glacial refugia and post-glacial expansion during the repeated Pleistocene glacial events. More recently, anthropomorphic impacts including furbearer harvest, climate change and habitat transformation have resulted in a total loss of 37% of the wolverine's historic range in the last century. Our research uses 17 microsatellite loci and mitochondrial sequence data to investigate dynamics across 300 sampled individuals and five populations to inform conservation and harvest strategies for wolverine. We are also using these data to explore potential barriers to gene flow under scenarios of changing conditions in the Yukon Territory, Canada as well as adjacent areas in Central and Southeast Alaska. We explore sex-biased dispersal patterns of wolverines within the Yukon in light of similar analyses of wolverines conducted in a resource-poor (tundra) region of Alaska (e.g., Brooks Range and Seward Peninsula). As a large carnivore of northern latitudes, wolverines are an excellent focal species for conservation monitoring, and like the polar bear, are a compelling symbol of high-latitude communities that are being impacted by fast-advancing climate change.

8^{}: Marmots in the Great Basin: strong persistence over eight decades suggests resilience to climate change**

Chris H. Floyd*, Andrew Rankin, Alison Shulte, Morgan Freeburg, Breana Meyer, and Rachel Schwartz
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Among the most striking effects of climate change are the upslope shifts in distributions of montane species and the concomitant loss of populations in the lower-elevation portions of the species' range. Montane species may become increasingly prone to local extinction as warming continues. The impacts of climate change could be especially severe in the Great Basin, where the cool, mesic environments favored by montane species are situated on island-like mountains surrounded by arid lowlands. These species include the yellow-bellied marmot (*Marmota flaviventris*). To assess the extent to which marmots in the Great Basin have persisted over the last several decades, we conducted field surveys and searched archived field notes to compile location information over two periods: historic (1929–1945) and modern (1999–2015). For the latter, we used E. R. Hall's notes from his mammal surveys in Nevada. The modern surveys included 18 of the 26 sites where Hall documented marmots. At 17 of the 18 sites, we confirmed the modern presence of marmots. Some lived in environments that were highly modified by humans or very arid compared to typical marmot habitat. One arid, low-elevation site had a talus slope that emitted near-freezing air but—contrary to Hall's prediction—did not seem to support or attract marmots. Our findings suggest an eco-physiological flexibility that will allow marmots to tolerate the effects of climate change.

9: Environmental factors and population demography in big-eared woodrat, *Neotoma macrotis*

Virginie Rolland, William D. Tietje*, Arjun Srivathsa, Anne Y. Polyakov, and Madan K. Oli

Department of Biological Sciences, Arkansas State University, State University, AR 72467 USA (VR); Department of Environmental Science, Policy, and Management, University of California, Berkeley, CA 94720-3114 USA (WDT, AYP); School of Natural Resources and Environment, 103 Black Hall, University of Florida, Gainesville, FL 32611 USA (AS); Department of Wildlife Ecology and Conservation, 110 Newins-Ziegler Hall, University of Florida, Gainesville, FL 32611 USA (AS, MKO)

In arid and semi-arid environments, water is a limited resource and changes in temperature and rainfall patterns can have profound impacts on species that inhabit such resource-restricted environments. In the context of climate change with projected increases in the frequency of droughts in the Southwest US, the long-term population viability of some wildlife species may be threatened. We investigated the population dynamics of the big-eared woodrat (*Neotoma macrotis*) in mixed woodland of coastal-central California. We used a 20-year biannual capture-mark-recapture dataset (1993-2014), and applied Pradel models to estimate capture probability, apparent survival, and realized population growth rate. Capture probabilities differed between seasons and sexes; they were higher for females than males, and higher in the spring than in the fall. The monthly population growth rate was 0.999 ± 0.0002 (SE), indicative of a stable population, although it varied over time (from 0.935 to 1.126). Monthly survival was higher for females (0.922 ± 0.001) than males (0.909 ± 0.001), higher in the fall (0.927 ± 0.001) than in the spring (0.907 ± 0.002), and increased over the study period. We also quantified the effects of resource availability, local weather conditions, and global climatic patterns on woodrat demography to better predict the viability and resilience of small mammal populations in resource-restricted environments under future climate change.

10: Population demography and environmental drivers in brush mouse, *Peromyscus boylii*

Arjun Srivathsa, Anne Polyakov*, William Tietje, Virginie Rolland, and Madan K. Oli

School of Natural Resources and Environment, 103 Black Hall, University of Florida, Gainesville, FL 32611 USA (AS); University of California, Department of Environmental Science, Policy, and Management, Berkeley, CA 94720-3114 USA (AP, WT,); Department of Biological Sciences, Arkansas State University, State University, AR 72467 USA (VR); Department of Wildlife Ecology and Conservation, 110 Newins-Ziegler Hall, University of Florida, Gainesville, FL 32611 USA (AS, MKO)

In arid and semi-arid environments, primary productivity tracks the highly variable patterns of rainfall events and temperature. These patterns can have pronounced and often little understood consequences for population dynamics of small mammal populations that thrive in resource-restricted environments. We investigated population dynamics of brush mice in a mixed blue oak-coast live oak woodland of coastal-central California. We used a 20-year biannual capture–recapture dataset (1993 to 2014), and applied Pradel's models to estimate capture probability, apparent survival, and realized population growth rate. Capture probability varied seasonally with higher detections in fall and for females. Although the population was stable during the study period with a monthly-realized population growth rate of $0.993 \pm$

SE 0.000, population growth rate varied over time from 0.680 ± 0.054 to 1.449 ± 0.083 . Overall monthly survival was 0.802 ± 0.005 , but this parameter also exhibited variation over time and differed between sexes, with estimates ranging from 0.530 ± 0.063 to 0.948 ± 0.030 . The monthly recruitment rate varied from 0.000 to 0.539 ± 0.083 . We tested the relative impacts of resource availability, temperature, and rainfall regimes on vital rates. Preliminary results show that survival was positively correlated with a one-session lag in temperature ($r = 0.270$). In our talk, we will evaluate results in relation to the future viability of brush mice in its highly variable and resource-restricted environment.

11: Interactions between red foxes and Arctic foxes as lemming cycles dampen at the Arctic's edge

James D. Roth *

Department of Biological Sciences, University of Manitoba, Winnipeg, Manitoba, Canada

Climate change has been implicated in dampened lemming cycles and expansion of mammalian predator ranges in the Arctic, both of which could strongly affect tundra predators and disrupt Arctic food webs. I examined dynamics of Arctic fox (*Vulpes lagopus*) and red fox (*Vulpes vulpes*) populations and their response to changing prey availability near Churchill, Manitoba, where tundra meets boreal forest and the ranges of these foxes overlap. Provincial harvest records indicate Arctic and red fox populations historically fluctuated in synchrony, and fox den surveys in the 1990s found reproductive success of both species was highly correlated with fluctuating lemming numbers. Recent mark-recapture estimates, however, suggest lemming populations are consistently low and no longer fluctuating. While Arctic foxes previously dominated the harvest, recently Arctic fox numbers are declining relative to red fox numbers, and their populations are becoming decoupled, as pup production of Arctic and red foxes has been inversely related in recent years. Red foxes have also been observed more commonly using tundra dens historically occupied by Arctic foxes. These observations suggest red foxes may be responding favorably to the warming climate and may eventually usurp arctic foxes from the edge of the tundra and displace them further north. The food web consequences of this displacement, and potential implications for reproductive success of Arctic-nesting birds and population dynamics of small mammals, remain to be seen.

12: Arctic fox dens provide a winter refuge for collared lemmings at edge of the Arctic

Jacqueline S. Verstege* and James D. Roth

Department of Biological Sciences, University of Manitoba, Winnipeg, Manitoba, R3T 2N2 Canada (JV, JR)

Predators may impact prey through mechanisms other than predation. Arctic foxes (*Vulpes lagopus*) create small-scale disturbances by digging burrows and concentrating nutrients on their dens through excrement and prey remains, which promotes growth of tall shrubs and grasses atypical on tundra. In winter, thick snow drifts accumulate leeward of raised vegetation. Increased snow thickness and decreased snow density provide greater insulation for lemmings (*Dicrostonyx* sp), which live beneath snow during winter. Yet much of the tundra is covered in thin and hard-packed snow, limiting suitable overwinter habitat for lemmings. Consequently, if taller vegetation on fox dens promotes greater snow insulation, then lemming activity, reflected in the number and distribution of winter nests, should increase on fox dens compared to surrounding areas. Our results suggest fox dens near Churchill, Manitoba have taller vegetation, snow with greater insulation, and greater lemming activity compared to control sites (200 meters from dens). Thus fox dens may provide a winter refuge for lemmings, despite the presumed greater predation risk. Lemmings are important prey for many Arctic predators and their removal would greatly restructure terrestrial Arctic food webs. Decreased snow quality with climatic warming may have dampened lemming population cycles throughout the Holarctic. Understanding interactions between lemmings, their predators, and snow conditions may better illuminate the effects of climate change on food web interactions in the Arctic.

13: Why do the boreal forest ecosystems of northwestern Europe differ from those of western North America?

Rudy Boonstra*, Harry P. Andreassen, Stan Boutin, Jan Hušek, Rolf A. Ims, Charles J. Krebs, Christina Skarpe, and Petter Wabakken

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The boreal forest is one of the largest terrestrial biomes on Earth. Conifers normally dominate the tree-layer across the biome, but other aspects of ecosystem structure and dynamics vary geographically. The cause of the conspicuous differences in the understory vegetation and the herbivore-predator cycles in northwestern European from those in western North America presents an enigma. Ericaceous dwarf-shrubs and 3-4-year vole-mustelid cycles characterize the European boreal forests whereas tall deciduous shrubs and 10-year snowshoe hare-lynx cycles the North American ones. We will discuss plausible explanations for this difference and conclude that it is bottom up: winter climate is the key determinant of the dominant understory vegetation that then determines the herbivore-predator food web interactions. The critical unknown for the 21st Century is how climate change and increasing instability will impact these forests, both with respect to the dynamics of individual plant and animal species and their community interactions.

14: Population variability complicates the accurate detection of climate change responses

Christy M. McCain*, Tim Szewczyk, and Kevin Bracy Knight

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Assessments of species' responses to climate change (CC) have underestimated the importance of interannual population variability (PV). Researchers assume sampling rigor alone will lead to an accurate detection of response regardless of the underlying population fluctuations. Using population simulations across a realistic, empirically-based gradient in PV, we show that moderate to high PV can lead to opposite and biased conclusions about CC responses. Between pre- and post-CC sampling bouts of modeled populations as in resurvey studies, there is (1) a 50% probability of erroneously detecting the opposite trend in population abundance change and nearly zero probability of detecting no change. (2) Across multiple years of sampling, it is nearly impossible to accurately detect any directional shift in population sizes with even moderate PV. (3) There is up to 50% probability of detecting a population extirpation when the species is present. (4) Under scenarios of moderate to high PV across a species' range or at the range edges, there is a bias towards erroneous detection of range contractions. The frequency and magnitude of population peaks and troughs greatly impact the accuracy of our CC response measurements. Many small mammals with even modest PV may be inaccurate 'canaries in the coal mine' for CC without pertinent demographic analyses and additional repeat sampling. Such PV impacts urgently need more careful consideration in design and analysis of CC responses.

15^{TA}: Genetic consequences of recolonization by black bear (*Ursus americanus*) into the western Great Basin

Jason L. Malaney*, Carl W. Lackey, Jon P. Beckmann, and Marjorie D. Matocq

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Many species of mammals are facing declines and during the mid-twentieth century, several populations of large-bodied mammals were significantly imperiled. Fortunately, some have rebounded including black bear (*Ursus americanus*) that recently recolonized the western Great Basin. In this study, we examine genetic variation in source and recolonized areas to understand the genetic consequences of natural recolonization. We genotyped 449 bears at 19 microsatellite loci to measure patterns of genetic differentiation, gene flow, and effective population sizes. Using Approximate Bayesian Computation (ABC), we show that, as expected from long-term field survey data (census), genetic variation of western Nevada black bear retain a signature of demographic decline followed by rebound. When compared to

the source area, recolonized populations are minimally differentiated, have lower effective population sizes, and reduced allelic diversity, but fail to show significant signals of genetic bottlenecks. Furthermore, populations now experience asymmetric gene flow with disproportionate emigration from the source area. Taken together, our results provide strong support for a genetic connectivity model that can be best described as a metapopulation. Our results highlight the need to develop management approaches uniquely tailored to support connectivity of black bear in newly recolonized areas. However, more broadly, these results imply there are unique challenges on the horizon for understanding genetic consequences of imperilment followed by recolonization, including complications in maintaining connectivity for many mammals now facing declines.

16^{TA}: Insights from comparative genomic analyses in a non-model organism – *Elephas maximus*

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Elephants are primitive placental mammals (superorder Afrotheria, order Proboscidea) characterized by several unique traits such as primitive placenta, long snout, poor eyesight, exceptional memory, intelligence and olfactory sense, complex social behavior, tusks, large body size, etc. The Asian and the African elephants have a shared evolutionary history dating back about 7 million years ago; yet they exhibit species-specific differences. Functional genetic analyses of these traits would provide interesting insights into their evolution. However, such studies in 'non-model' organisms is severely restricted. Comparative sequence analyses overcomes many limitations, but the availability of genome and transcriptome sequences is essential for such analyses. We sequenced the whole genome and blood transcriptome of an Asian elephant, *Elephas maximus*, to ~20x and ~35x coverage respectively. Comparative sequence analyses with the available reference genome of the African elephant and the mammoth genome identified 1.9 million single nucleotide variants (SNVs) specific to the Asian elephant, of which 7155 map to protein coding regions and 1859 result in non-synonymous mutations in 1514 genes. A significant subset of these genes is involved in olfaction. We have created a valuable resource that opens up tremendous opportunities for exploring species-specific evolutionary changes at a genome wide scale. Our findings have broader implications in furthering our understanding of genetic and evolutionary processes among Elephantids, as well as Afrotheria and across all mammals.

17^{E,TA}: Long-term pair bonding and monogamy: are coyotes faithful even in high population densities and cities?

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Social and genetic mating systems vary among species based on factors such as life history strategies, population densities, and environmental conditions. However, sociogenetic monogamy is rare in species, especially in areas of high intraspecific densities or areas with clumped resources. Previous research during 2000-2006 on coyotes in the Chicago Metropolitan area reported sociogenetic monogamy and long term pair bonding. However, over the last ten years the population has increased, with smaller home ranges and an abundance of potential mates among alpha pairs. Animals living within the urban core have also been extensively tracked, and city conditions pose unique stresses which require coyotes to change behaviors and travel long distances to small scattered areas for available resources. We tracked an average of 40 radio-collared coyotes per year and located over 60 litters of their pups from 2007-2015 to determine mating systems. By changing to a polygamous mating system or from life time monogamy to serial monogamy, coyotes would be able to diversify their offspring to optimize reproductive fitness and avoid inbreeding. However, through telemetry data we were able to determine that social monogamy is still present. Microsatellite data from litters that were sampled also suggests that both long term pair bonding and genetic monogamy also still occur, even within high densities and highly urbanized landscapes.

18^{E,TA}: Genetic diversity and population structure of the riparian brush rabbit: potential impacts of habitat fragmentation

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Biodiversity can be driven and limited by a changing landscape. This is evident in the California Floristic Province, where millennia of geologic change molded one of the world's most biodiverse regions. Over the last century, the Great Central Valley of this region has experienced extensive habitat loss and fragmentation due to land use change. Over time, changes in habitat size and connectivity can impede gene flow among populations and accelerate genetic drift within populations, resulting in long-term evolutionary consequences. As with other species endemic to the once-widespread riparian forests of California's Great Central Valley, the riparian brush rabbit (*Sylvilagus bachmani riparius*) has suffered dramatic population declines. We used mtDNA sequencing and nuclear microsatellite variation to quantify population history and patterns of genetic subdivision among remaining *S.b. riparius* populations. Shared haplotypes across the current range of *S.b. riparius* suggest historic gene flow among populations. However, nuclear genetic variation supports two distinct genetic clusters within the subspecies, suggesting recent divergence within this taxon, consistent with the history of fragmentation across the region. Habitat suitability analyses show limited opportunity for natural dispersal across portions of the extant range, but provide guidance for critical areas of restoration. This study along with those of other mammals occupying remnant habitats of the Great Central Valley strongly support the need for restoration of natural corridors of connectivity across this highly altered landscape.

19^{TA}: Evolutionary analysis of *Taenia* spp. tapeworms from Mongolia using morphological and molecular techniques

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Diverse mammal/faunal assemblages occur in regions within Mongolia not only because of the convergence of different biomes, but also because of the presence of discontinuous/isolated alpine and larch forests. Few studies have compared both morphology and molecular analyses to distinguish new species or construct phylogenies. Cestodes of the family Taeniidae are a monophyletic group that use herbivorous mammals as intermediate hosts and carnivorous mammals as definitive hosts. Because of the importance of this group to the health of both human and domestic animals and because of the relative commonness of *Taenia* larvae in mammals, we focused our efforts on the larval forms of *Taenia* in Mongolia. We identified larval forms of cestodes of the family Taeniidae using standard morphology of the hooks combined with multivariate morphometric techniques and phylogenetic analyses utilizing three different mitochondrial genes to explore the diversity of species of *Taenia* throughout the southern part of Mongolia. Of species representing five mammalian orders (Artiodactyla, Erinaceomorpha, Lagomorpha, Rodentia, and Soricomorpha) nine species of Taeniidae were collected, including seven species of *Taenia*, one species of *Versteria*, and one species of *Echinococcus*. With accurate small mammal host-parasite data, and a comprehensive database on the presence/absence and distribution of the species, it is now becoming possible to establish the level of anthropogenic threat to at-risk species, and to classify regions or faunas for conservation efforts.

20^F: Characterizing adaptive immunogenetic variation in the salt marsh harvest mouse, *Reithrodontomys raviventris*

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Adaptive immune system variation is frequently characterized in endangered species to assess the potential of limited populations to respond to disease. We have isolated the first adaptive immune system

locus from the salt marsh harvest mouse, *Reithrodontomys raviventris*, in the major histocompatibility complex (MHC, Class II DRB). *R. raviventris* is endangered due to habitat limitation and disruption. Because this species is endemic to San Francisco Bay Estuary marshes, the response of *R. raviventris* to wetland restoration and management may be used as an indicator of ecosystem health. Patterns and levels of adaptive genetic variation can serve as a metric to monitor this response. To measure baseline levels of genetic diversity, populations were sampled throughout the range of *R. raviventris*. Individuals were sequenced at the mitochondrial cytochrome b locus and cloned and sequenced at the MHC locus. Preliminary results show regional differentiation at both mitochondrial and MHC loci, particularly between northern and southern populations. Populations are functionally differentiated at the MHC locus, with unique alleles present in at least 5 of 7 sampling areas, suggesting potential local adaptation. Low allelic variation in southern populations may indicate limited adaptive potential. Genetic data can be used to prioritize conservation efforts and to aid habitat management and restoration design, determining if populations should be connected by habitat corridors or preserved as separate adaptive units.

21: Population genetics and a draft genome of the greater bamboo lemur (*Prolemur simus*)

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Madagascar is home to over 100 species of lemurs, all of which are endemic. Of these, over 75% are classified as endangered. The bamboo lemurs (Family Lemuridae) are unique among lemurs in their ability to consume bamboo for a large portion of their diet. The greater bamboo lemur has experienced an extreme population decline due in part to slash and burn agriculture, illegal logging, and being hunted for food. This species is listed as critically endangered, and has an estimated total population of less than 1,000 individuals. Here we evaluate genetic structure within two populations of greater bamboo lemurs across a riverine biogeographic barrier. We genotyped 11 microsatellite loci, from individuals distributed in two forests separated by approximately 300 kilometers of discontinuous forest cover. We also sequenced a genome to a depth of 100X from one individual, and typed fecal samples to determine allelic dropout. We aim to identify if population structure exists between the sampled populations, and combine the information with whole genome data to identify the demographic history of this species. The microsatellite data in combination with the genome will allow us to identify how informative various markers are for this species, and identify regions of excess homozygosity or positive/directional selection. Preliminary results of whole genome analyses will be presented. This data will allow us to implement appropriate management strategies for this species.

22^F: Population genetics of *Canis latrans* in New York City

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Canis latrans (Coyotes) have increased their range across the United States and are now inhabiting the most densely populated cities. In order to determine how Coyotes are moving across the highly urbanized landscape of New York City, we collected scat samples from several parks within the city. We extracted DNA from the samples and used microsatellite markers to create individual genotypes. We then examined the relatedness between individuals in order to ascertain the presence of family groups and to estimate individual movement patterns. We found evidence of first-order relatedness within and between parks, implying the presence of several family groups, as well as migration and gene flow of Coyotes within New York City.

23^{TA}: Skeletal injuries in small mammals: a multi-species assessment of injury type and prevalence

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Skeletal injuries in wild animals can impact survival, reducing an individual's ability to avoid predation and compete for resources. Recent studies of skeletal injuries in small mammals are limited to an individual or

a single species. Our study takes a comparative perspective, looking across a suite of small mammal species to determine whether certain traits such as eating behavior and locomotion type, as well as age can affect the occurrence of skeletal injuries. A total of 2884 skeletons of seven representative small mammal species collected at Bartlett Experimental Forest, New Hampshire were inspected for injuries and aged. These species were binned together based on trait groups and compared across groups to determine significant differences in occurrence of injuries using a chi-square goodness of fit test. Skeletal injuries in the forelimbs, skull, pelvis, and fibula showed significant differences across trait groups. These bones can affect survival of a species differently based on their traits, whereas injuries in bones that affect all species similarly (ribs, tails) did not show significance across trait groups. This suggests that traits such as eating behavior and locomotion type do impact the occurrence of injuries. Age showed a significant difference, with older animals amassing more injuries; evidence that injuries are acquired throughout a life time, not associated with a certain age.

24: 3D analysis of embryonic and fetal development in little brown bats (*Myotis lucifugus*)

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Mammalian embryonic development is an exceedingly complex morphogenetic process. The development of external features and internal organs is described for 14 embryonic and fetal *Myotis lucifugus* specimens ranging in crown-rump length (CRL) from 6.9 to 21.3 mm. These wild-caught specimens correspond to stage 16L through fetal stages of the timed pregnancies of phyllostomid *Carollia perspicillata*. Additional comparisons are made with published fetal stages of *Rousettus amplexicaudatus*, *Miniopterus natalensis*, and *Molossus rufus*. Allometric trends with respect to wing development are made with respect to CRL. Three-dimensional analysis of internal structures, such as the cochlea, molar teeth, heart, liver, and lung development, are made using micro-CT scans and the 3D segmentation software ITK-SNAP. This late embryonic and fetal staging system yields a wealth of information useful in comparative, functional, and developmental morphology of *Myotis lucifugus*.

25: See how they run: convergence in locomotory adaptations between and among myosoricine and soricine shrews (Soricidae)

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Stereotypical adaptations for a more fossorial existence among scratch-digging mammals include shortening and broadening of metapodials and proximal and middle phalanges of the hands and feet with corresponding lengthening and broadening of distal phalanges and claws. Some of the most impressive variation is in the humerus, which generally exhibits expanded processes for the origin and insertion of larger muscles involved in moving soil. Morphological studies of limb skeletons among shrews (Eulipotyphla: Soricidae) have revealed graded transitions in these adaptations along a scale from more ambulatory to more fossorial locomotory behavior. Both more ambulatory species and more fossorial species are present in each of the three subfamilies of the Soricidae, and skeletal morphology exhibits convergence between more fossorial members of the Myosoricinae and the Soricinae. Convergence also is apparent between genera within subfamilies and between species within genera. Hence, postcranial morphology within the Soricidae appears to be constrained to certain generalized morphological paths along an ambulatory-fossorial gradient.

26: Substrate and limb evolution: a global ecomorphological analysis of ruminant unguals

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Ruminants (i.e. giraffe, deer, antelope) are found in a variety of environments despite sharing a simplified unguligrade morphology of two weight-bearing digits per hoof, a discrepancy that calls for closer study of morphological variation with respect to habitat. This research seeks to analyze ungual plantar shape and area across the suborder and determine if trends are ecologically, phylogenetically, or body size driven. Our study includes 720 unguals from 93 ruminant species that are distributed globally across a spectrum of habitats and substrates (i.e. wet, ecotone, rocky and dry). Unguals were photographed in plantar view and subjected to 2D geometric morphometrics; outlines with 100 evenly spaced semilandmarks were Procrustes superimposed to produce shape variables for subsequent analysis. Results show that, regardless of taxonomy, species which live on fluidly unstable substrates (i.e. snow or sand) tend to have overall blunter ungual shapes with flatter surfaces- most likely to prevent the animals from sinking into the dynamic surface. Furthermore, this effect is strong in wild animals, but muted in captives suggesting that the specialized ungual shape is a plastic response to substrate. Essentially, results from this study will be used to develop an analog, which will be used for ecometric comparison to fossil unguals to allow for the reconstruction of paleoenvironments and the elucidation of mammalian response to climate change across the Cenozoic.

27^E: Difference in walking motion among soricomorphs of Japan and Taiwan

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The Order Soricomorpha contains a multitude of species occupying various ecological niches and modes of life: such as terrestrial, subterranean and semi-aquatic. Specializations and convergences for each life-style are found among genera and species. Especially, diversifications of the limb morphology which may reflect their motions have been reported among the group. However, relationship between the limb morphology and the limb motion are yet to be studied. We studied the relationships between limb morphology and walking motions in 13 soricomorph species (9 species of 6 soricid genera and 4 species of 3 talpid genera) from Japan and Taiwan during 2014–2016. We video-captured their walking motions and compared the motions among the species. Our result showed that the species in the same family species shared many locomotor features, however, the species in different families employed different locomotor styles: soricid species employed semi-digitigrade or semi-plantigrade in both fore- and hindlimbs; talpid species employed semi-plantigrade or plantigrade in hindlimbs, but were walking on the tiptoe or on the radial margin of the manus in the forelimbs. These results suggest that motional characters differ among family in soricomorphs, and they may related with their musculoskeletal systems. Therefore, the limb postures and muscle architectures are also being compared among species by using CT-scans and dissections.

28^E: Predicting locomotion from vertebral morphology: a case study of terrestrial carnivorans

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Studies of morphological correlates of terrestrial locomotor strategies have focused extensively on the appendicular skeleton. Nonetheless, specialization of locomotor strategies are expected to result in adaptive variation of vertebral morphology. The Order Carnivora displays a wide range of locomotor and hunting strategies among its approximately 280 species. Moreover, many carnivorans with similar hunting or locomotor specializations are not closely related and are thus ideal for revealing true relationships between form and function irrespective of phylogenetic relationships; they allow for testing of similarity in multiple, convergent lineages. Five separate measurements: centrum height (CH), spinous process height (SH), centrum length (CL), transverse process width (TW), and total vertebral height (TH) were taken of all cervical, thoracic, and lumbar vertebrae from 60 specimens representing 42 fissiped species. Cervical vertebra 7 was used to standardize measurements and reduce effects of size disparity. In very few cases, missing values due to damaged vertebrae were estimated using mean values from two adjacent vertebrae. Specimens were categorized into five different locomotor strategies: arboreal,

scansorial, cursorial, non-cursorial, and semi-fossorial. Measurements were subjected to Principal Components Analyses to examine patterns in overall variance. Discriminant Function Analyses (DFA) were then performed to reveal vertebral differences and assess predictive reclassification of locomotor categories. DFA results revealed locomotor type can be predicted with high accuracy ($\geq 97.5\%$) regardless of taxonomic alliances and for all measurements.

29: Ecomorphological variation in the limbs of small-bodied “generalists:” a test case with voles

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Small-bodied, non-volant mammals (<100g) are often characterized as having a more generalized body plan lacking pronounced skeletal adaptations when compared to larger-bodied locomotory specialists. However, this has rarely been tested quantitatively. We predict that patterns of morphological disparity related to ecological function will emerge when comparing similarly sized, phylogenetically related small-bodied species. Arvicoline rodents occupy a wide range of niches (aquatic to arboreal) and provide a unique system for testing this prediction. We generated 20 shape indices from 19 postcranial measurements of five small-bodied arvicolines that represent a continuum from fossoriality to arboreality. Results from univariate and multivariate analyses show significant variation in postcranial morphology among the five species. Evidence of arboreal adaptation in *Arborimus longicaudus* is especially strong, with extended digits of the manus and pes, increased forearm length, and gracile limb bones clearly separating this species from the more terrestrial forms. This study provides evidence of ecomorphological disparity within a (superficially) morphologically conserved radiation of small-bodied mammals, highlighting the importance of size and scale in inferring adaptive phenotypic variation.

30^F: North American rodent tooth morphology reflects fine-scale ecology

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μ CT allows production of high-resolution 3D models that facilitate homology- and orientation-free holistic measures of functional morphology. We μ CT-scanned crania and mandibles for >130 species of North American rodent to correlate fine-scale diet and functional tooth morphology. To create idealized tooth models, we extracted enamel and dentin isosurfaces for lower right tooth rows and cropped tooth meshes to the functional crown. Using these models, we compared a large suite of novel and published ecomorphological methods including relief indices (RFI), orientation patch count, Dirichlet normal energy, and volumetric hypsodonty indices. Dental topographic analyses yielded variables including molar slope, average aspect, and curvature when teeth were analyzed as landforms in ArcGIS. We used stepwise discriminant function analysis to identify which of the 300+ variables per species were informative and to classify each species into one of seven diet categories (granivore, folivore, rootivore, invertivore, frugivore, omnivore, and mycophage). We correctly classified more than 85% of species by jackknife cross-validation using eight variables including volumetric enamel-dentin ratio, vertical complexity, RFI, and ArcGIS measures. Intriguingly, “misclassified” species were often classified in the category of documented fallback foods. Intraspecific variation among replicates was relatively low, though some morphologies were more wear-sensitive. Ultimately, this work aims to compare ecomorphological measures, elucidate how natural selection shapes morphology, and serve as a calibration dataset for reconstructing diet from tooth morphology in other mammals.

31: Mammalogy courses in the 21st century: a question of balance

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Mammalogy courses have been, and continue to be, an important aspect of training for future mammalogists. I attempted to survey a cross-section of mammalogists and mammalogy students about their perceptions of mammalogy courses in order to examine changes in course design and content over the past several decades. I also sought viewpoints on what aspects of mammalogy courses most influenced students. Results of over 210 responses revealed, among other things, a clear pattern that field experiences for students have been an important component for mammalogy courses, both recently as well as further in the past. Historically, mammalogy courses have included overnight field trips that often involved collection and preparation of mammal specimens, as well as other activities for observing mammal communities. There has been a loss of this field component in some mammalogy courses, although most continue to provide students with some field experience. As some field aspects of mammalogy courses have been lost, there has been a concomitant increase in classroom technologies that have provided students with a wealth of images and videos of mammals and their behaviors. Maintenance of field-based activities in mammalogy and advances in technology in the classroom both should continue to be important elements in the teaching of mammalogy courses in the future.

32: Science informing policy: case studies on plateau pikas (*Ochotona curzoniae*) and American pikas (*O. princeps*)

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Useful conservation policy must be predicated on scientific research. I review two cases that highlight the sometimes difficult translation of scientific evidence into appropriate policy. The plateau pika (*Ochotona curzoniae*) occupies the high alpine meadow grasslands of the Tibetan plateau. Plateau pikas are considered an agricultural pest and have been widely poisoned for decades. Managers assume that pikas cause rangeland degradation, consume vegetation that could otherwise be utilized by livestock, and foster increased erosion. My work over the past 30 years contradicts these assumptions: the plateau pika is a keystone species as well as an ecosystem engineer, and its presence reduces erosion potential, enhances biodiversity, and promotes ecological sustainability on the fragile Tibetan grasslands. I review the resistance of policy-makers in China to my findings and highlight the progress that we have recently made in halting the wholesale poisoning of this species. The American pika (*O. princeps*) of the intermontane West in North America provides another example of conservation policy not informed by research. Because pikas are sensitive to warm temperatures, claims are being made that global warming is threatening American pikas with extinction. Scientific evidence does not support these claims, but does demonstrate the need for careful evaluation of the biology of pikas (and all species) at their range boundaries to better understand and predict their potential responses to a changing climate.

33: Critical episodes in the evolution of South America's mammal faunas

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The South American mammal fauna is both diverse and distinctive. Its extended development was staged and shaped by alternating periods of continental interchange and utter isolation. Paleontologists have long recognized that South American Land Mammal Ages comprise three discrete "strata," each characterized by unique faunal elements. Stratum 1 contains Gondwanan relicts and lineages that crossed a transitory landbridge from North America; most are now extinct, and only certain marsupial lineages and xenarthrans remain. Stratum 2 is marked by the appearance, in the midst of South America's Cenozoic isolation, of hystricognath rodents and primates as waifs with African ancestry. Stratum 3 coincides with the arrival of numerous taxa from North America as the Central American Seaway receded and the Panamanian Isthmus emerged, triggering the Great American Biotic Interchange. South America's outstanding fossil record, especially from Patagonia, documents and calibrates many of these events. However, taphonomic biases have long limited the resolution and scope of paleo- reconstructions for small mammals and the wet tropics, a crucial limitation in view of fauna-wide richness patterns and body-size distributions. Recent studies with small mammals, many involving DNA-based phylogenies of living forms, illuminate these events and often do so in unexpected ways.

34^{TA}: Looking over the edge: population dynamics of an endangered peripheral squirrel population

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Traditional wisdom states that peripheral populations are more vulnerable to extinction through stochastic events. Despite increased risk, peripheral populations are conservation priorities as the distribution of endangered species often tends to contract to peripheral zones of historic range rather than toward the core. Trailing-edge populations and mountain isolates, which may become more common as climate change drives range shifts, are an important area of inquiry. The red squirrel (*Tamiasciurus hudsonicus*) is predicted to recede from its southern border in response to climate-induced habitat change. The most southerly population, the Mount Graham red squirrel (MGRS; *T. h. grahamensis*), is endangered and has been isolated on Mount Graham, Arizona, since habitat shifts created this sky island 8-10,000 years ago. We use long-term monitoring data from the MGRS to test the hypothesis that peripheral populations display distinct demographic patterns from core range populations. We analyze the demographics of this species using survival and reproduction schedules and compare the outputs to published demographic studies of core-range populations. Results suggest that higher adult mortality, compared to the core range, and associated impacts on reproductive output cause this peripheral population to operate differently than core populations. Understanding differences in demographic function between peripheral and core populations is key if management strategies are to be effective in supporting this endangered subspecies and others in the face of increasingly common range shifts.

35^{E,TA}: Small mammal responses to bison reintroduction in one of the world's most threatened ecosystems**

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Tallgrass prairie restoration often centers on reestablishing native vegetation with only minor efforts directed to the fauna that inhabit these areas. Reinstating traditional disturbance fire and bison grazing regimes is a critical component to the active management of tallgrass prairies. Understanding the role of small mammal populations and how they are affected by varying grazing and fire management strategies can assist in the holistic evaluation of restoration efforts in sites currently undergoing active restoration. *Peromyscus* and *Microtus* species play an important role in the upper trophic level dynamics of tallgrass prairie ecosystems through influencing the vegetation structure via herbivory and as prey for larger fauna. Mark and recapture data has provided a landscape-scale test for how prairies with different management strategies recover from stressors and disturbances. Abundance and diversity are correlated with more floristically diverse remnant quality sites. Preliminary results indicate that *Peromyscus* species prefer areas more frequently burned while *Microtus* species prefer less frequently burned sites. Seasonal fluctuations in small mammal community composition occur at all sites, with more species accumulating as summer transitions to fall. Sites grazed by bison had a change in community composition in the first year after bison reintroduction, although these data are still preliminary. Prescribed burning is associated with an increase in the number of unique individuals captured within any site, regardless of age or grazing influence. This research was supported by a Grant-in-Aid of Research awarded to Angela Burke in 2015.

36^{TA}: Simultaneous characterization of diet, parasites and host genetics for Southeast Asian mammals using fecal metagenomics

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A large number of mammal species are in steep decline due to habitat loss and degradation. Yet, we know so little about their natural history, that habitat enhancement or ex situ conservation are not feasible. We argue that there is a need for new methods for the rapid collection of natural history data relevant for conservation. Here fecal samples are useful as they contain DNA from the host, its diet and gut parasites. We demonstrate that direct shotgun sequencing of fecal DNA (metagenomics) allows simultaneous characterization of these aspects. We developed bioinformatic methods and tested them using a case of known diet and a complex digestive system of a colobine primate (red-shanked douc langur *Pygathrix nemaeus*). We applied these techniques to the critically endangered banded-leaf monkey (*Presbytis femoralis femoralis*) in the wild in Singapore. Our methods revealed a diverse diet of 53 plant species, which corroborated well with field observations. We also characterized gut parasites including *Strongyloides* and found a low genetic diversity in the population. We will describe our current research on other species of conservation concern in Southeast Asia, including the critically endangered Tonkin-snub nosed monkey (*Rhinopithecus avunculus*), Sunda pangolin (*Manis javanica*) and leopard cat (*Prionailurus bengalensis*). Additionally, we will discuss the challenges faced, particularly the lack of representation of species from the tropics in public databases and our efforts in augmenting these.

37^{E,TA}: Employing $d^{13}C$ analysis of ancient sea otters to quantify environmental change in a nearshore ecosystem

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Sea otters (*Enhydra lutris*) are key members of coastal communities, which are highly productive and threatened ecosystems. We analyzed the $d^{13}C$ of essential amino acids (AA_{ESS}) from ancient sea otters to track changes in a California coastal ecosystem in the late Holocene (~3500 ybp – present). Specifically, we focused on evaluating the importance of kelp forests in this system through time. In nearshore marine ecosystems different producer groups (e.g., kelps vs. microalgae) have highly distinct $d^{13}C$ values. Since only primary producers and microbes can synthesize AA_{ESS} , consumers typically route them directly into tissues without isotopic fractionation. Consequently, the $d^{13}C$ values of AA_{ESS} in top consumers can provide a ‘fingerprint’ of the dominant producers in the local food web. We analyzed bone collagen from late Holocene sea otters from two southern California islands – San Nicolas and San Miguel. We also characterized the baseline AA_{ESS} $d^{13}C$ profiles for modern producer groups: kelp (*Laminaria* and *Nereocystis*), green algae (*Ulva*) and red algae (*Neorhodomela*). We used isotope mixing models to quantify the contribution of each algal group to ancient sea otter AA_{ESS} . We found ancient sea otters were predominantly feeding in ecosystems driven by kelp production; in some instances, an estimated 90% of consumer AA_{ESS} were derived from kelp. These findings suggest that at these sites kelp forests may have been more extensive in the late Holocene than they are today.

38^E: Surface texture discrimination by bats: implications for reducing mortality at wind turbines

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It has been hypothesized that bats come into contact with wind turbines because turbines provide or are perceived to provide important resources. Recent studies have shown that bats misidentify artificial smooth surfaces to be water and that bats approach wind turbine towers with the same posture as bats drinking at water. Thus, if tower surfaces were textured rather than smooth, we predict that bats would spend less time in the rotor swept zone investigating the towers, thereby reducing overall collision risk. Using wild-caught bats, we conducted behavioral experiments in a flight facility in 2014-2015 to identify a texture that bats showed little or no interest in approaching. We presented bats with 8 treatment surfaces (smooth metal, smooth painted, 3 textured surfaces that varied in particle density, applique, and woodchip) and recorded contacts with each surface as well as the number, timing, and distance of passes made by bats at each surface. We found that bats made contact with all smooth surfaces, but not with textured surfaces. Furthermore, as gap distance between particles increased, bats made more

passes over the surface. Our findings revealed that bats showed little interest in textured surfaces with a higher density of particles. These results were used to inform a texture coating that can be applied to turbine towers (operational and manufacturing stage) as mitigation for bat fatalities at wind facilities.

39: Return of the American marten (*Martes americana*) to Vermont

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Prior to the reintroduction of the American marten into the Green Mountain National Forest in southern Vermont, the last reported marten was from a 1954 sighting by a wildlife biologist. Some of the 115 tagged martens released from 1989 to 1991 initially established home ranges near the release sites but others dispersed great distances and were trapped or found dead on roads as far away as Maine and Connecticut. The last confirmed sighting of any tagged marten was in 1994 and the reintroduction was later declared unsuccessful. By 2010, however, martens were being reported both in Southwestern and Northeastern Vermont by trappers. Examination of D-loop sequences has detected 5 different haplotypes present in Vermont and New Hampshire samples. The southern Vermont population shows significant differentiation from both the Northeastern Vermont and northern New Hampshire populations. Three haplotypes are shared between these two latter populations; however each also has a unique haplotype. Population exclusion tests utilizing a small number of microsatellite loci were not able to exclude either the Northeastern Vermont or the northern New Hampshire populations as sources from which the Southwestern Vermont population could have been derived. Examination of marten from Maine and New York, the reintroduction sources, and additional microsatellite loci are expected to demonstrate that the southern population is a remnant of the "unsuccessful" reintroduction.

40: A status report on the Tasmanian devil

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The Tasmanian devil, *Sarcophilus harrisii*, the world's largest marsupial carnivore, with adult males weighing 9-12 kg and females 20 percent less, is restricted to the Australian island state of Tasmania. Devil populations have fluctuated in the past 150 years for unknown reasons, reached unprecedented highs in the 1980s, but then, starting in the mid-1990s, animals began dying from a disease that came to be called "devil facial tumor disease (DFTD)." Apparently transmitted by bites between aggressive adults at carcasses or during mating conflicts, the tumors grow rapidly, causing death within 6 months. Originating in the northeast corner of the state, DFTD spread south- and westward at ~7 km per year, threatening the survival of the state's iconic mammal (they had already lost the larger Tasmanian tiger). DFTD is a transmissible cancer, the cells of which are not recognized by the immune system, have unique karyotypes, grow rapidly, and cause death by starvation and secondary infections. By 2015, the disease had swept across 80-90% of the State, but pockets of populations remain, probably throughout its former distribution. One population response to lower densities is that young grow more rapidly and females attaining 6 kg are breeding a year earlier than before. However, such females are likely to breed only once before becoming diseased, compared to 3 times in healthy females, thereby shortening generation times.

41^E: Habitat selection of sympatric lagomorphs supports competition hypothesis, provides management suggestions for a declining lagomorph

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Once common, the New England cottontail (NEC, *Sylvilagus transitionalis*) is now restricted to five populations at the periphery of its historic range. The NEC is a shrubland obligate, with early successional

forest loss widely recognized as the driver of NEC decline. Initiatives to create early successional forest patches throughout the Northeast are ongoing; however, NEC population recovery may be hindered by degraded forest communities and competing species. Invasive flora including Japanese barberry (*Berberis thunbergii*) and multiflora rose (*Rosa multiflora*) now dominate Northeastern shrubland, altering forest structure and quality. Moreover, the non-native eastern cottontail (EC, *Sylvilagus floridanus*), which has been naturalized in NEC habitat, has broad habitat requirements, which may confer a competitive advantage. We studied seasonal habitat selection of sympatric NEC and EC in New York. NEC habitat selection was positively correlated with density of multiflora rose and Japanese barberry, but EC habitat selection was negatively correlated with rose, suggesting removal of invasive vegetation may be detrimental to NEC. Selection varied seasonally, with both species of cottontail selecting higher shrub stem and barberry density in the winter than in the summer, suggesting possible competition. These results also indicate patches of grassland or sparse shrubland may be seasonally beneficial when juxtaposed with dense overwintering habitat. Exploiting such selection differences when managing habitat may lead to restored areas that favor NEC over EC.

42^{E,TA}: Using dental microwear to detect intraspecific variation in two canid predators**

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The quantification of microscopic wear patterns etched into tooth enamel by food during mastication is a powerful technique commonly used to classify foraging behaviors of both extant and extinct species. While dental microwear has shown success in detecting differences between species, less attention has been focused on the potential for this analysis to reflect intraspecific dietary variation. However, identifying intraspecific variation is critical for quantifying complex ecological interactions and could dramatically increase understanding of processes such as trophic cascades. Using museum specimens of coyote (*Canis latrans*) and gray wolf (*Canis lupus*) collected within the Pacific Northwest over the past century as a case study, we tested the ability of dental microwear to differentiate among life history, spatial, and temporal variation in diet. Three-dimensional scans of the m2 hypoconid occlusal surface were analyzed using scale-sensitive fractal analysis. Anisotropy and complexity of microwear, corresponding to degree of carnivory and omnivory respectively, were calculated for each specimen. Ordination techniques were used to determine the ability of specimens to cluster with respect to a priori variables. Preliminary results suggest dental microwear can reveal intraspecific variation in diet, particularly among temporal scales. These findings indicate the potential for dental microwear studies to yield more detailed reconstruction of dietary niche and environmental context both today and in the past, allowing for inference regarding causes and trajectories of ecological regime shifts. This research was supported by Grants-In-Aid of Research awarded to Brian Tanis in 2015.

43^{E,TA}: Spatial network approaches to characterize metacommunity structure of Neotropical bats in Colombia**

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How species assemble into communities depends on environmental factors, biotic interactions and species dispersal abilities. The metacommunity approach evaluates the degree to which these three determinants integrate to produce spatial variation in species composition at regional scales. A common characteristic of metacommunities is that they are composed of compartments (i.e., distinct groups of sites with similar species composition) that may correspond to modules (i.e., a group of sites with more connections among themselves than with other sites) within a network framework. Moreover, we were interested in whether metacommunities exhibit network modularity and whether modules correspond to environmental gradients. We examined a bat metacommunity from the Colombian coffee-growing ecoregion to evaluate whether modules correspond to elevation or different kinds of land cover. We assessed modularity with an agglomerative hierarchical clustering analysis and related these results to elevation and land cover attributes. Modules were most associated with elevation. Common species

exhibited a pattern similar to the overall network, whereas rare species exhibited a more fragmented network with fewer connections among sites. Determining if communities form modules within metacommunities and which environmental characteristic corresponds to those modules will help elucidate the mechanistic determinants governing metacommunity assembly, such as dispersal potential, physiological constraints, or habitat selection. This research was supported by a Grants-In-Aid of Research awarded to Cristina Rios-Blanco.

44: Impacts of a tornadic blowdown on small mammals inhabiting eastern deciduous forest in western Pennsylvania

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Tornados are common natural weather phenomena shown to highly influence ecosystem structure/function. A tornado struck the area of Ligonier, PA in 2012, creating a path of severe canopy damage 8 miles long. Thereafter, experimental forest management of blowdown areas was initiated, included salvage logging, no salvage logging, and control (unaffected forest). Our objective was to examine impacts of a tornadic blowdown and subsequent forest management on the small mammal assemblage in affected forest. The forest small mammal assemblage was composed mainly of *Peromyscus leucopus* and *Clethrionomys gapperi*, with 7 other species being trapped less frequently. Trapping success has averaged >30% per trapping season. More small mammals were found in the blowdown area than expected. Seasonally, small mammals were more likely to be found in the blowdown area in the fall (61%) than in the spring (36%). Small mammals in the blowdown area had lower body masses, skewed sex ratios, and lower reproductive activity compared to those in control areas. Age, sex, and body mass differences of the two most frequently trapped small mammals were seen in the salvage treatment compared to the other treatments. Although these mammals all strongly prefer forested habitat, the added complexity of the ground cover seems to make the non-salvaged blowdown area one of opportunity for small mammals willing to occupy it.

45: Bottom-up pulses and desert rodent dynamics across shrubland-grassland ecotones

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Shrub encroachment is common in arid environments worldwide but effects on biodiversity are equivocal. In southwestern USA, Chihuahuan Desert grasslands have experienced a long-term encroachment by shrubs including honey mesquite (*Prosopis glandulosa*). Shrub encroachment could interact with precipitation to alter the role of bottom-up pulses of productivity on desert rodents. We asked whether the total abundance and biomass of desert rodents changes with mesquite encroachment for a community dominated by granivorous heteromyids. We also asked whether the links between precipitation, aboveground net primary production (ANPP), and rodents differ among ecological states. We addressed these questions with 11 years of data from the Jornada Basin LTER site in southern New Mexico. Temporal variation in rodent abundance and biomass was extreme, and we observed strong but expected shifts in community composition with shrub encroachment. However, we detected no evidence of degradation: rodent abundance increased with shrub cover, and rodent biomass was unaffected. ANPP depended on summer and winter precipitation, and on the previous year's ANPP (a legacy effect), but was unrelated to shrub cover. Rodent abundance and biomass were best predicted by lagged summer precipitation (+), winter precipitation (-), and an interaction between summer precipitation and shrub cover (+). Our results suggest shrub invasion can make desert rodents more sensitive to precipitation variability, which may increase under climate change, creating even more pronounced temporal dynamics.

46^E: Invasive *Bromus tectorum* experiences biogeographic enemy release from generalists

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Perhaps the most well-known explanation for the success of invasive plants in novel environments is enemy release, which predicts that 1) invasive plants are limited by natural enemies in the native range but not the non-native range, and 2) native plants in recipient communities remain limited by their natural enemies. Despite considerable empirical attention, very few studies have fully tested these predictions. In addition, we know of no studies that fully test the enemy release hypothesis with respect to generalist herbivores. Because potent generalists could be present in both the native and recipient communities of translocated plants, theory indicates that escaping generalists should be an essential aspect of enemy release. We tested whether invasive cheatgrass (*Bromus tectorum*) experienced enemy release from an important guild of generalists (granivorous rodents) using experimental exclosures and seed additions in both the native and non-native range of cheatgrass. If enemy release occurs, 1) local rodents should limit cheatgrass in Iran (the native range) but not in North America (the non-native range), and 2) local rodents in North America should limit native grasses more than cheatgrass. We found that rodent exclusion improved cheatgrass establishment in Iran but had no effect in North America, and rodent exclusion in North America improved native but not cheatgrass establishment. These results suggest that invasive cheatgrass experienced enemy release from an important group of generalist granivores.

47^{}: Trophic cascades mediated by gray wolves (*Canis lupus*) reduce seed predation by rodents**

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Trophic cascades initiated by the removal or reintroduction of apex predators can lead to important, often unanticipated, changes in the dynamics of lower trophic levels. While consumption by predators can alter abundance and diversity of prey, fear of predation can also alter prey behavior, resulting in behaviorally mediated cascades that may rival or exceed the effects of cascades generated by changes in prey consumption. We examine the untested hypothesis that gray wolves (*Canis lupus*) generate trophic cascades that ultimately affect seed consumption by granivorous rodents. Specifically, we couple a large-scale study of seed removal at 22 sites over two years with a scent-manipulation experiment to understand whether wolves release foxes (*Vulpes vulpes*) from competition with coyotes (*Canis latrans*), leading to changes in the abundance, activity, and behavior of rodent granivores within sites located in wolf territories. We observed reduced seed predation in high wolf occupancy areas compared to areas with low wolf occupancy. The addition of predator scent cue similarly reduced seed predation in low-wolf sites, yet did not significantly affect seed predation in high-wolf sites. By altering patterns of rodent granivory, wolf-mediated cascades may influence vegetation composition. Our results suggest decreased seed predation in high-wolf areas may be the result of behavioral changes in rodent foraging mediated by wolf presence, highlighting the importance of accounting for nonconsumptive effects in evaluating effects of top-predator cascades. This research was supported by Grant-in-Aid awarded to Jennifer Chandler in 2015.

48^F: Temporal patterns of species co-occurrence along a climate and habitat gradient

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Many factors influence biodiversity and the structure of ecological communities, including environmental filtering (climate and habitat) and biotic interactions (e.g. competition, facilitation). One approach for identifying the mechanisms of community assembly is the analysis of non-random species co-occurrence patterns, including both negative associations (segregations) and positive associations (aggregations). In heterogeneous landscapes it can be difficult to determine whether associations are due to shared abiotic limits and habitat specificity (environmental filtering) and/or biotic interactions. We analyzed co-occurrence of 31 Great Basin small mammal species along the elevational gradient (~1,000 m) of the Toiyabe Range, Nevada during both modern and historical time periods. To differentiate between abiotic limits, habitat specificity, and competition, we compared patterns at two spatial resolutions: the site level and among microhabitats within sites. Very few non-random species pairs were observed at either scale during both eras. However, significant aggregations and segregations were detected. Over time only four significant associations persisted, indicating great temporal instability between species pairs, a result only

partially reflected in species range shifts. These preliminary analyses suggest the majority of species co-occur randomly despite our expectation that environmental filtering would be a strong factor along the elevational gradient. Additionally, our results suggest a stronger role for environmental filtering than biotic interactions, but both likely contribute to asynchronous species responses observed over the last century among Great Basin mountain ranges.

49: Rodent community response to removal of small and large herbivores in a semi-arid grassland

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Through their grazing and clipping activities mammalian herbivores can have profound effects on plant community composition and vegetation structure in semi-arid grasslands. These changes indirectly alter availability and quality of habitat and food resources for rodents. In autumn 2012 we established a large-scale, herbivore exclosure experiment at the Central Plains Experimental Range in north-central Colorado to investigate the effects of small and large herbivores on woody plant encroachment in the face of climate change. Plots consisted of five replicated units of four 0.20-ha plots, which differed in their accessibility to cattle and rabbits (*Lepus californicus*, *L. townsendii*, *Sylvilagus audubonii*), singly and in combination. In 2015 we live-trapped rodents in all 25 plots to examine changes in the rodent community in response to three years of herbivore removal. Ord's kangaroo rats (*Dipodomys ordii*) were captured most frequently and across all treatments, followed by harvest mice (*Reithrodontomys megalotis*, *R. montanus*) and prairie voles (*Microtus ochrogaster*). The presence of the latter two groups likely reflected high plant cover following the usually wet spring in 2015 (155% of long-term average). Cattle grazing had the largest effect on rodent abundance, with 2-3 times more individuals captured in plots without cattle. Species richness was similar across treatments (S=4) except that cattle-grazed plots without rabbits were dominated by kangaroo rats. Patterns will be compared to results from sampling planned for May 2016.

50^F: Molecular evolutionary analysis of the American pika (*Ochotona princeps*)

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American pika (*Ochotona princeps*) are small winter-active mammals inhabiting alpine environments. As the American pika occupies a niche characterized by hypoxia, these animals are an excellent system to use for detecting genetic changes associated with adaptation to these conditions. American pika populations were located at lower elevations during glacials, and shifted upslope during interglacials. In this scenario, pikas would have experienced increased selective pressure to develop adaptations to hypoxia. Here, we use a candidate gene approach to identify molecular signals of adaptation in the American pika genome. We first examined the sequences of 54 candidate genes for adaptation in two subspecies of *O. princeps* using draft genomes available from public databases. We constructed phylogenies using the two *O. princeps* alleles and homologs from other mammal species, and then used the CODEML module of PAML to detect evidence of selection along branches in the phylogeny. Four genes (EHHADH, IGF-1, TGF- β 1, and NOS2) showed evidence of adaptation in these analyses. We then resequenced portions of these four genes in 25 individuals from across the species' range, and analyzed the resulting data using frequency-based tests of non-neutral evolution. These tests have provided additional support for positive selection in the EHHADH, IGF-1, and TGF- β 1 loci. These loci represent strong candidates for further study of adaptation in this system, including examination of their functional role in the response to hypoxia. This research was supported by a Grants-In-Aid of Research awarded to Andrew Rankin.

51^{TA}: Genomic signatures of evolutionary processes on cetacean evolution: footprints of the return to the sea

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Cetaceans are among the most specialized mammals and are completely dependent and adapted to an aquatic environment. The adaptation to this lifestyle has required complex changes of physiological systems, behavior and morphology. The paleontological history of 50 millions of years of evolution is well-documented, but less known is the molecular trajectory behind the transition from land to sea. Identifying genes that have been subjected to selection pressure during cetacean evolution would greatly enhance our knowledge of the ways in which genetic variation in this mammalian order has been shaped by natural selection. This talk will present results from a genome-wide scan for positive selection and case-by-case analysis of candidate loci associated with adaptation to a fully aquatic life from a terrestrial life. Regarding the case-by-case analysis, we studied the molecular evolution of globin genes (hemoglobin and myoglobin) given their important role in hypoxic adaptation. Also, given the importance of hair loss in cetacean lineage to aquatic adaptation, we combined the available genomic information with phylogenetic analysis to conduct a comprehensive analysis of the evolutionary patterns of keratin gene clusters. Taken together, the genome-scanning and the candidate genes analyses provide a first insight into the type of biological processes that have been targets of selection in cetacean evolution.

52^{TA}: Phylogeographic analyses of the meadow vole (*Microtus pennsylvanicus*), a widespread North American mammal

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The glacial events of the late Pleistocene played an integral role in shaping the contemporary distribution of mammals in North America, leaving a genetic signature that may be used to infer the spatial and temporal impacts of this dynamic time period. We examined the evolutionary and demographic history of the meadow vole (*Microtus pennsylvanicus*) with a multilocus phylogeographic approach to elucidate how historical biogeography may have led to contemporary genetic structure. Our results support 4 major mitochondrial clades: (i) a western clade with individuals from Alaska, British Columbia, and northern Canada, (ii) a central clade in Alberta, Saskatchewan, Manitoba and along the Rockies into northern New Mexico, (iii) an eastern clade in the eastern Canadian provinces and along the Appalachians to North Carolina, and, (iv) a Florida clade consisting of a single relict population highly divergent (4%) from the all other clades. The eastern and western clades are further geographically sub structured with a north/south split. Individuals on Admiralty Island in the western clade are also distinctive. Demographic analyses support a scenario of population expansion in the central and western clades and stable populations in the eastern clade. Our results implicate that climatic shifts during and following the Pleistocene played an important role in the genetic differentiation of the meadow vole.

53: The evolution of covariance in the catarrhine cranium

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Phylogenetic relationships among living Old World monkeys and apes were largely resolved decades ago based first on easily identified morphological synapomorphies and later through genetic and genomic analyses. Such agreement does not extend to the fossil record, however, and in particular there is ongoing debate over the status of a diverse group of small-bodied catarrhines from the early Miocene of Africa: the so-called “dendropithecoids.” Related to this is contention over the ancestral catarrhine cranial morphotype: whether the crown catarrhine ancestor more resembled *Hylobates* and *Colobus*, or *Pongo*, *Victoriapithecus*, and *Sadaanius*. To help inform our understanding of early catarrhine cranial evolution, I utilized geometric morphometric analyses to study patterns of covariation among extant apes and monkeys. Based on thirty-four 3D landmarks collected from large samples of 55 catarrhine subspecies, I identified the primary vectors of covariation within each taxon for both males and females, and compared these using a series of multivariate statistical techniques. Among female crania, the dominant patterns of covariation within subspecies were remarkably consistent with phylogenetic relationships, particularly

among apes. Male crania exhibited patterns of covariance that were inconsistent with phylogeny. These results specifically identify a *Colobus-Hylobates* model of the ancestral catarrhine morphotype, and likewise have important implications for interpreting the selective forces underlying sexual dimorphism in living catarrhines.

54^E: Convergent evolution of venom targeted nicotinic acetylcholine receptors in mammals that survive venomous snake bites

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Honey badgers (*Mellivora capensis*) prey upon and survive bites from venomous snakes (Family Elapidae), but the molecular basis of their venom resistance is unknown. The muscular nicotinic cholinergic receptor (nAChR), targeted by snake alpha-neurotoxins, has evolved in some venom-resistant mammals to no longer bind these toxins. Through phylogenetic analysis of mammalian nAChR sequences, we show that honey badgers, hedgehogs, and pigs have independently acquired functionally equivalent amino acid replacements in the toxin-binding site of this receptor. These convergent amino acid changes impede toxin binding by introducing a positively charged amino acid in place of an uncharged aromatic residue. In venom-resistant mongooses, different replacements at these same sites are glycosylated, which is thought to disrupt binding through steric effects. Thus, it appears that resistance to snake venom alpha-neurotoxin has evolved at least four times among mammals through two distinct biochemical mechanisms operating at the same sites on the same receptor. This is the first comparative work demonstrating convergent adaptive response to snake venom in mammals, and suggests that venomous snakes may be an overlooked but significant influence in the ecology and evolution of ophiophagous mammals.

55: Quantitative morphological convergence and divergence of carnivorous rodents from the Indo-Pacific

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Convergence – the independent acquisition of similar characters across different lineages that did not share a common biological background – is a prime example to demonstrate the strength of extrinsic factors that might deterministically shape phenotypic evolution. Rodents of the family Muridae have migrated from Asia to the major landmasses of the Indo-Pacific archipelago (IPA) multiple times since the Miocene. These small to medium-sized mammals have spread over most of the IPA, where they occupy many terrestrial niches. Their ecological diversity is facilitated by a remarkable array of morphologies, including some associated with unique niche shifts toward an animalivorous diet. Our study focuses on four independent acquisitions of animalivory in the Indo-Pacific using an exhaustive murine sampling for this region and provides a rare quantification of phenotypic diversity of a mammal adaptive radiation. Our analyses demonstrate quantitative convergence and disparity among the independently evolved animalivoran IPA murines.

56^E: Sperm competition and relative testes size in three species of ground-dwelling squirrels

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Sperm competition is a post-copulatory evolutionary process that can affect sperm production, and consequently reproductive success. The operational sex ratio (OSR) is often used as a measure of the level of sperm competition or sexual selection intensity. In species where sperm competition is intense (high OSRs), males have larger testes size probably to produce more sperm. The objective of our study was to compare relative testes size and sperm traits in three species of ground squirrels with different life histories and levels of sperm competition. We examined sperm concentration, motility, vitality and testicular traits in a non-hibernating continuous breeder (Cape ground squirrel, *Xerus inauris*) from southern Africa (N=20), a second species that is a non-hibernating seasonal breeder (Barbary ground squirrel, *Atlantoxerus getulus*) from Fuerteventura, Spain (N=20) and a hibernating seasonal breeder (Richardson's ground squirrel, *Urocitellus richardsoni*) from Winnipeg, Canada (N=20). While all species are promiscuous, Richardson's ground squirrels have lower operational sex ratios compared to the other two species. Relative testes size, sperm concentration and sperm motility were higher in the African ground squirrels. Sperm vitality was higher in Cape ground squirrels and lower in both seasonal breeders' species. Cape and Barbary ground squirrels invest strongly in a post-copulatory selection, maximizing their sperm competition compared with Richardson's ground squirrels. This research contributes to our understanding of post-copulatory sexual selection.

57: Southern sea otter (*Enhydra lutris nereis*) mitogenomes do not predict diet specialization or tool use

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Southern sea otters, *Enhydra lutris nereis*, were hunted to near-extinction by the fur trade but have partially recovered. Individuals exhibit dietary specialization, focusing on 1 of 6 major prey types (abalone, crab, mussel, clam, urchin and snail) and use tools to access very hard-shelled invertebrate prey. We sequenced mitogenomes of 43 otters with known diets and frequencies of tool use. In the d-loop, we found 2 haplotypes: 1 new and the previously described haplotype C. In the entire genome, we found only 4 haplotypes. At least one individual with each haplotype used tools at least once. Our 2 most common haplotypes contained individuals with multiple diet types and individuals that did and did not use tools on a regular basis. The dispersion of diet types and tool use across sea otter matriline contrasts with dietary specialization and tool use (sponging) in Indopacific bottlenose dolphins (*Tursiops aduncus*), in which tool use and its associated diet type (small cryptic fish) are confined to a single matriline in each area. Tool use in dolphins is probably a recent innovation dating back approximately 120 years. Tool use in sea otters is likely much older, as very hard-shelled prey, such as snails and large clams, are not easily accessed without the use of tools, and the Miocene ancestors of sea otters had already developed bunodont teeth, indicating an invertebrate diet.

58^{E,TA}: Outmaneuvering climate change: behavior buffers a small, arid land mammal against thermal extremes

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Understanding behavioral responses of animals to the thermal environment is of increasing importance under changing climate regimes. Our objectives were to quantify behavioral thermoregulation strategies in a small, arid land mammal to test the hypotheses that individuals would exploit thermal refugia and alter activity patterns seasonally and daily as a function of the thermal environment. We radio-collared 52 pygmy rabbits (*Brachylagus idahoensis*) to identify rest site selection during summer and winter and evaluated the influence of multiple factors using conditional logistic regression and information theory. We also fitted 24 rabbits with accelerometers to quantify activity seasonally, during daily periods (dawn, day, dusk, and night), and in relation to daily extreme temperatures. During summer, rabbits selected rest sites that were cooler than unused sites and strongly avoided high levels of solar radiation. In winter, however,

proximity to a burrow was the only significant variable affecting rest site selection. In both seasons, activity was characterized by high crepuscular peaks, but contrary to our expectations, was not related to daily high or low temperatures. Sex and moon phase significantly influenced activity patterns, suggesting high levels of flexibility in timing of activity. These behaviors may provide thermoregulatory options that potentially buffer pygmy rabbits and other small mammals against a changing climate. Managing heterogeneity within landscapes to provide thermal refugia also may support long-term conservation of vulnerable mammals.

59^E: Wolves hunting beavers

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Beavers (*Castor canadensis*) can be a significant prey species for wolves (*Canis lupus*) in boreal ecosystems due to their abundance and vulnerability on land. However, how wolves hunt beavers in these systems is largely unknown because observing predation events is challenging. We inferred how wolves hunt beavers by identifying kill sites via clusters from Global Positioning System collared wolves in and adjacent to Voyageurs National Park, Minnesota. We identified 22 sites where wolves from 4 different packs killed beavers from April 2 to November 5, 2015. We classified these kill sites into 8 categories based on the beaver habitat type in which the kill occurred. Seasonal variation existed in types of kill sites as 7 of the 12 (58%) kills in the spring occurred at sites downstream from dams and on shorelines while 8 of the 10 (80%) kills in the fall occurred near foraging trails and canals. From these kill sites we deduced that the typical hunting strategy has 3 components: 1) waiting at areas of high beaver use (e.g. feeding trails) until a beaver comes nearby 2) using vegetation or the dam for concealment, and 3) ambushing the beaver by cutting off access to water. By identifying kill sites and inferring hunting behavior we have provided the most thorough description of where and how wolves hunt and kill beavers available.

60: Habitat specific fitness consequences of sociality in *Octodon degus*

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Theory predicts that social group living, a form of sociality in which individuals live in relatively long-lasting, stable groups should persist if living together results in greater net benefits compared to living alone. To fully understand the adaptive significance of sociality, it is crucial that we examine intraspecific variation in the fitness consequences of group-living within the same populations and between populations. Moreover, we need to tease apart the fitness benefits of different components of sociality, including group size and social network structure. The objective of this study is to determine how ecological variation influences sociality-direct fitness relationships in the common degu (*Octodon degus*), a plurally breeding rodent endemic to central-north Chile. In 2014 and 2015, I quantified two components of degu sociality (group size, social network strength) and the per capita number of offspring weaned by adult females in two populations characterized by extreme differences in food availability and predation risk: Bosque Fray Jorge National Park (71°40'W, 30° 38'S, altitude 200 m) and Estación Experimental Rinconada de Maipú (33°23'S, 70°31'W, altitude 495 m). My aim is to determine the extent to which ecological variation (food abundance, predation risk) and social variation (group size, group composition) predict the reproductive success of degus within and between sites. This research was supported by a Grant in Aid of Research awarded to Madeline K. Strom in 2014.

61^{E,TA}: Risky rabbits: evaluating responses to food and fear by a specialist and generalist herbivore

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When selecting foraging patches, herbivores are faced with multiple risks imposed by their environment such as the risk of consuming food that does not meet their daily energy requirements, the risk of toxicity from plant secondary compounds, and the risk of predation. Because these risks operate simultaneously, animals must make tradeoffs when selecting foraging patches. To understand how animals trade off food and predation risks, we manipulated both in a series of experiments with pygmy rabbits (*Brachylagus idahoensis*) and mountain cottontail rabbits (*Sylvilagus nuttallii*), which differ in their size, ability to digest fiber and detoxify toxins, and use of burrows. In these experiments, rabbits were given a choice between two foraging patches that varied in the amount of fiber, toxins, level of exposure to predators, and distance from a burrow. Using the method of paired comparisons, we estimated and compared relative risks and tradeoffs both within and between species. Fiber, toxins, exposure to predators, and distance from a burrow all increased the risk of patches for pygmy rabbits, whereas only fiber and toxins did so for cottontails. Pygmy rabbits traded off food quality for safety whereas cottontails traded off safety for food quality. This study provides a functional understanding of how the quality of food and predation risk influence habitat use by these rabbits, advancing our ability to assess habitat quality for mammals across landscapes.

62^{E}: Do stress and behavior shape responses to environmental change in two co-occurring chipmunk species?**

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Climate change is an extensive and ever-increasing source of environmental challenge for wildlife. Climate-attributed range shifts have been documented for many species, but the mechanisms behind these shifts are largely unknown. In particular, the physiological and behavioral components of range shifts remain largely unexplored, particularly for terrestrial wild mammals. This study compares behavior and stress hormone levels in two species, the lodgepole chipmunk (*Tamias speciosus*) and the alpine chipmunk (*T. alpinus*), which have exhibited divergent range responses to a century of climate change in Yosemite National Park, CA: while the elevational range of *T. alpinus* has undergone a significant upward contraction, the range of the partially sympatric *T. speciosus* range has not changed appreciably. To test predictions about the roles of physiological stress and behavior in explaining elevational range boundaries, we quantified fecal glucocorticoid metabolite levels and used acceleration loggers to quantify activity patterns in different parts of these species' ranges. By pairing these datasets with individual-level data (e.g. body condition, reproductive status) and habitat information (e.g. temperature, ground cover), we examined relationships among environmental variation, behavior, and stress. Collectively, these analyses promise to generate new insights into the factors dictating species ranges as well as improve our understanding of why species vary in their spatial responses to environmental change. This research was supported by an ASM Grant-IniAid of Research awarded to Talisin T. Hammond in 2013.

63: Altitude- and sex-specific variation in roosting behavior and thermoregulation of *Myotis lucifugus*

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Little brown bats (*Myotis lucifugus carissima*) are common summer inhabitants of Yellowstone National Park (YNP). These high-elevation populations of *M. l. carissima* survive in energetically challenging environments. We examined roosting behaviors and thermoregulatory patterns of bats at four sites located at relatively lower elevations (1,890 – 1,981 m asl), and one site at a relatively higher elevation (2,377 m asl). We sampled 6 non-reproductive females, 15 pregnant females, 3 lactating females, 2 post-lactating females, and 5 non-reproductive males during the summers of 2013, 2014, and 2015.

Reproductive females and some non-reproductive females formed maternity colonies in buildings, where the reproductive females exhibited daytime and evening bouts of torpor. Solitary males inhabited natural roosts such as cliffs, talus slopes, and dead trees, and remained torpid for most of the day. All females recorded in natural roosts maintained higher body temperatures (mean 32.20°C ± .19) than females in building roosts (mean 30.14°C ± .05), and did not enter deep torpor. Roost switching among buildings was common among the reproductive females we sampled. Our research suggests that buildings containing maternity colonies are crucial for reproduction and summer survival in little brown bats in YNP by allowing the facilitation of energy savings and maturation of neonates in this species.

64^{E}: Quantifying variation in fungivory by eastern chipmunks (*Tamias striatus*)**

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During the summer season, eastern chipmunks (*Tamias striatus*) are fungivorous, although the type and amount of fungi consumed may change both spatially and temporally. Understanding this variation in fungal consumption is important because fungivory leads to dispersal of mycorrhizal spores in forests. We quantified the diet of eastern chipmunks in the White Mountains of New Hampshire to determine 1) if fungivory varied across the summer season, among forest types, or relative to truffle abundance and 2) whether methods used to quantify diet provide comparable signals of fungivory. We used fecal microscopy to determine spore loads of mycorrhizal fungal genera and stable isotope analysis ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) of both hair and feces to quantify bulk fungal contribution to diet. Based on microscopy, fungal richness in fecal samples increased as local truffle richness increased, with eastern chipmunks consuming over 18 different genera. Isotopic analysis of both feces and hair indicate that fungal contribution to bulk diet increased from June through August. Additionally, all three analyses suggest that fungal consumption was greatest in softwood forests where truffles were most abundant. Based on the diversity and amount of fungi consumed, and their occurrence in both hardwood and softwood forests, eastern chipmunks may be especially important as dispersers of mycorrhizal spores across forest gradients. This research was supported by a Grants-in-Aid of Research awarded to Ryan Stephens in 2015.

65: Managing and preserving the University of Alaska Museum's rapidly growing Genomic Resources Collection

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The University of Alaska Museum (UAM) has maintained a frozen tissue collection for over two decades. The UAM-Genomic Resources (UAM-GR) collection was traditionally housed in ultra-cold mechanical freezers. In 2007, half of the collection was transferred to LN2 produced on site. In 2015, UAM was awarded an NSF grant to complete the transition to LN2 cryopreservation. Currently, the majority of the ~200,000 cryovials housed in UAM-GR are mammal tissues, including the largest and fastest-growing collection of marine mammal samples in the world, fresh tissues from SE Asian and African species, and enormous numbers of Alaskan, Canadian, and eastern Russian voucher-associated taxa. Historically, samples from UAM-GR have been used primarily for studies of evolution, systematics, population genetics, conservation, ecology, toxicology, and zoonotics. More recent loans have supported research in transcriptomics and population genomics. UAM-GR's extensive use by the scientific community is due in part to the relatively early adoption of LN2 and the sophisticated object-tracking abilities of Arctos. Arctos (<http://arctosdb.org>) is an online relational database for managing and serving museum specimen data and is currently used by some of the largest natural history collections in North America. The functionality of Arctos significantly enhances our ability to track, quantify, and communicate the impact of museum specimen-based research.

66: Lack of habitual movements by the Yucatan squirrel (*Sciurus yucantensis*) in Belize, Central America

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Tropical squirrels have received considerably less study than their counterparts in temperate regions, likely due to the historic distribution of researchers, but also because northern squirrels appear more amenable to study. To address this imbalance, I conducted a pilot investigation into the basic ecology of the Yucatan squirrel (*Sciurus yucatanensis*) in Belize, Central America, during 2014-15. Camera-station and live-trap transects showed the animals were present in a variety of forest types (savannah-oak scrub, transitional, and rainforest), but less than 40 detections occurred in over 25,000 camera hours, and repeated detections at the same trap station were exceedingly rare. Focal observation data (including one telemetered animal) showed little repetitive movements or patch use over successive days. An analysis of putative nest sites showed no bias towards any particular tree type or patch density. Further, animals were observed feeding on a wide range of food types (both cultivated and wild) suggesting food is not likely a limiting factor, and hence the need for definitive home ranges. Hoarding has not been detected, even though an experimental test of cache pilfering showed greater rates of pilfering in temperate forests. Overall, the need for patch familiarity/resource defence may be weak in this species compared to temperate zone squirrels. This work provides preliminary insight into the ecology of this animal, while highlighting the difficulties in studying tropical forest squirrels.

67: Home ranges and burrow activity of *Peromyscus polionotus* in southeastern Georgia

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Oldfield mice (*Peromyscus polionotus*) were often studied by early mammalogists as they are readily found in early successional habitats in the southeastern United States. Past studies primarily relied on live-trapping techniques to explore population biology and life history attributes of this species. From these studies, we learned that oldfield mice are obligate burrowers and functionally monogamous. However, movement patterns and burrow use of oldfield mice are not easily or precisely studied using traditional trapping methods. Our study evaluated the movement patterns of oldfield mice within three similar early successional habitats using radio telemetry. We sampled 45 wild mice (21 females, 24 males) over the winter, spring, and summer seasons of 2014-2015. Some but not all of these individuals were paired. Paired individuals were often seen foraging in close proximity. Mouse burrows were characterized by a clumped distribution pattern in all habitats. The distribution pattern was not related to obvious habitat differences. Individual mice within the “colonies” had overlapping territories with each other but not with mice in other areas of the same field. In all seasons, paired males and females had overlapping territories and shared burrows. Mice were found more often in burrows during nightly telemetry in the winter and spring compared to the summer months. In winter, multiple individuals were found together in the same burrow.

68^F: Dispersal of American martens in Minnesota, USA

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Dispersal is an important process that influences gene flow and meta-population dynamics. Direct observations of dispersal are rare for many mammal species because collecting information on dispersal is challenging, particularly for secretive species. Our objectives were to quantify dispersal rates and distances for American martens (*Martes americana*) in northeastern Minnesota, USA. We radio-collared 150 martens from 2008-2015 and used net-squared displacement from the initial trap site to classify individuals as resident or dispersing martens. We identified 46 dispersing martens. Most dispersing martens were juveniles (N=30) or yearlings (N=10), but we also documented dispersal in adult martens (N=6). Dispersal typically occurred during late winter or early spring (Late February-early May), although some martens were dispersing when they were captured and radio-collared (December-February). Mean dispersal distance was 12.2 km (median: 4.77 km; range: 0.8-130 km). Distribution of dispersal distances was leptokurtic. Most martens (N=38, 83%) dispersed less than 15 km while a few martens dispersed long distances (85-130 km). There was no difference in dispersal distances of juveniles (\bar{x} = 11.9 km) and

yearlings (\bar{x} = 18.3 km; p = 0.24), but juveniles and yearlings dispersed longer distances than adults (\bar{x} = 3.5 km; p < 0.01). Dispersal timing and distance may have been influenced by increased access to available territories following harvest by fur trappers.

69: Bridging mammalogy, molecular markers, and outreach in Ecuador

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Ecuador has more than 400 species of mammals, and it is considered one of the most diverse countries in the World. Unfortunately, Ecuador is also a country where little scientific research is done. We are currently working on two projects, driven by the premise that education at all levels of instruction must be improved to efficiently train more researchers and contribute to the literacy, conservation, and development of the country: 1) Developing an on-line encyclopedia of Ecuadorian mammals to provide easy-to-access information about all the species present in the country. This information is targeted to a broad audience, comprising all levels of formal education (K-12 and university). This on-line encyclopedia is MammaliaWeb Ecuador, and presents information of natural history, etymology, taxonomy, distribution and high quality photographs. 2) Establishing a collections-based research program on the use of molecular markers to answer questions related to ecology and evolution of mammals and their pathogens. This program has so far yielded the discovery of cryptic species within the rodent *Chilomys instans*, and assessments of the amount of molecular data available for Ecuadorian mammals. With these two initiatives we are creating resources to help in the education and research training of Ecuadorian students.

70^{E,TA}: Using stable isotopes to detect responses to environmental change in parapatric ctenomyid rodents

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Understanding how interspecific differences in a community play out in response to historical environmental changes provides a useful foundation for predicting the evolutionary and conservation outcomes of future changes in environmental conditions. Ecological studies have increasingly utilized stable isotopes to gain insights into the diets, and hence, the floristic composition that historical populations of mammals utilized. Here, we report on the use of stable isotope analyses of rodent teeth to explore the potential role that interspecific differences in response to past environmental changes have played in shaping observed differences in genetic structure between two parapatric species of ctenomyid rodents. Previous research has revealed that both abundance and genetic diversity have declined over the last 12,000 years for *C. sociabilis*, a group-living habitat specialist, but not for *C. haigi*, a solitary habitat generalist. We analyzed the carbon and oxygen stable isotope composition of molars from modern and paleontological specimens of *C. sociabilis* and *C. haigi*. Our data indicate that the floristic landscape in this region of Patagonia has changed markedly over the past 12,000 years, and as it did *C. sociabilis* and *C. haigi* shifted their diet in response to this change. Based on these findings we suggest that future studies explore potential interspecific differences in response to the same environmental variables, to understand observed temporal differences in abundance and genetic diversity in the study species.

71^F: Population augmentation provides nominal genetic and demographic rescue for an endangered carnivore

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The intentional movement of mammals to reintroduce extirpated populations or augment declining ones is an important conservation tool. Augmentations, in particular, are frequently used to restore species of conservation concern, and may constitute up to a third of all translocation attempts. Carnivores are regularly targeted for such augmentation efforts, but quantitative assessments of these efforts are rare. In Wisconsin, American martens (*Martes americana*) were reintroduced and subsequently augmented, yet remain a state endangered species. To evaluate this restoration effort, we sampled martens before and after augmentation, used genetic mark-recapture and parentage analyses to quantify stage-specific vital rates, and conducted population viability analyses with and without augmentation. Surprisingly, we found that translocated individuals did not contribute genetically or demographically to population recovery. Indeed, we found that translocated individuals had lower heterozygosity and higher inbreeding coefficients than did the recipient population, and translocated females accounted for only 17% of the maternity assigned to contemporary offspring during parentage analyses. Moreover, demographic models revealed that augmentation had little effect on population persistence, which was instead driven by intrinsic population attributes such as recruitment. Our findings question augmentation as a primary conservation strategy for carnivores, and suggest management should first focus on enhancing natural population processes such as immigration and juvenile recruitment before utilizing costly and controversial measures like augmentation.

72: River otter population decline in coastal Alaska is associated with shifts in oceanic conditions

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Marine carnivores occupy high trophic levels and show numerical responses to changes in prey abundance. Thus, their population status may provide an index of ecosystem productivity and responses to climatic shifts. Coastal river otters (*Lontra canadensis*), a harvested furbearer in Alaska, mainly feed on nearshore marine fishes. We used non-invasive genetic sampling and spatially-explicit capture-recapture models to estimate river otter densities in southcentral Alaska over the past decade. We then assessed the relation between changes in otter density and environmental processes in the North Pacific using biotic and climatic data. Our results show a significant decline in river otter densities between surveys conducted in 2006 and 2009 and more recent ones in 2012 and 2014. The period of higher abundance was characterized by lower sea surface temperatures and winter upwelling. The corresponding stronger recruitment of age-3 classes of Pacific herring (*Clupea pallasii*) was only weakly correlated with otter numbers. The subsequent otter population decline followed a return to warmer conditions, although the shift in river otter densities did not temporally match a basin-scale North Pacific regime shift. Our results indicate population responses to local shifts in oceanic conditions. In view of projected increases in North Pacific sea surface temperatures and marine carnivore distribution shifts, this raises concerns for the resilience of Alaska coastal ecosystems and warrants increased caution in the management of river otter populations.

73^F: Social organization and sexual segregation in American bison (*Bison bison*)

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Sexual segregation occurs commonly in sexually dimorphic ruminants. Factors underpinning this phenomenon, however, continue to be debated. We conducted research on spatial and social organization of American bison (*Bison bison*) on Antelope Island State Park, Utah, USA, to provide further insights into causes of sexual segregation. We focused our analyses on the two leading hypotheses associated with ecological segregation—the gastrocentric and predation hypotheses—but we also examined aspects of the social factors hypotheses. Results from MRPP (multi-response permutation procedure) and overlap analyses illustrated significant spatial and elevational separation between male and female groups throughout the year, which increased substantially during parturition (a period of sexual segregation), compared with the mating season (sexual aggregation). Male-only groups commonly used habitat on the northern end of the island, which is at lower elevation and received heavy human activity. Females used areas low in tourist activity and high in elevation. Those outcomes provide evidence for both the predation and the gastrocentric hypothesis. Our results did not support the social segregation hypotheses because spatial separation and social organization occurred simultaneously. This research can aid management of and habitat restoration for bison and other wild ruminants by providing new insights into spatial use and social organization during two critical periods—parturition and rut (mating season).

74: Breeding and growth in a new mammalian suicidal reproducer under threat from fire and ferals
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The Silver-headed Antechinus, *A. argentus*, is a recently-discovered, threatened carnivorous marsupial known from two small, isolated montane populations within central-eastern Queensland, Australia. Here, we present the first study of the species' life-history characteristics. Antechinuses are well-known for their spectacular annual male die-off at the close of a one- to three-week mating period. The genus also displays sexual dimorphism for size – with males up to three times heavier than females. The *A. argentus* population we studied at Kroombit Tops over two years fitted the norm for the genus, with strong evidence of both a synchronised male die-off (in June/July) and significantly larger males than females. We surveyed two proximate sites: one had been completely burnt by a wildfire six months before the study commenced and the other site only partially burnt. The burnt areas yielded very few captures over the two years, suggesting that the species does not respond well to fire in the short term. Unexpectedly, there was a marked difference in *A. argentus* numbers between years, and we propose this may be at least in part linked to the timing of rainfall and effects of fire on vegetation. The marked fluctuation in capture numbers between years, coupled with annual male die-off, climate change and feral animal pressures raises concerns over the future of the Kroombit Tops population of this threatened mammal.

75: Shaping small mammal trapping grids for multi-species occupancy modeling

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Square or circular patterns are traditionally used for small mammal trapping grids. However, long transects are thought to be superior for species detection. We trapped small mammals in south Texas on 50 grids in 2015 using 22 square grids and 28 rectangles in an effort to develop a long-term monitoring program for the East Foundation. Square grids contained over 3 times as many traps and occupied 2.7 times the area of rectangle grids. Detection probabilities were significantly greater for 6 of 8 species we captured on the square grids and not significantly different for the other 2. The increased detection probably for most species can easily be explained by the nearly 3-fold increase in area covered and traps used by square grids. However, square grids required 3 times the equipment and time to check.

Increasing the duration of trapping from 2 to 3 days requires an increase in effort of 50%; however, in our study, brought detection probabilities on rectangular grids to equivalent levels observed with 2 days of trapping with square grids for most species. Furthermore, since 3 of our species showed an increasing detection probability with time, we strongly recommend trapping smaller areas with elongated grids for longer durations than using traditional square grids when the objective is species detection or modeling occupancy.

769^{E,TA}: A weasely perspective on hybridization using phylogenomics**

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Secondary contact zones that formed in the Holocene provide an opportunity to investigate the evolutionary process of introgression, reinforcement, and divergence. We have initiated a phylogenomic approach to take a fine-scale look at the complex history of secondary contact in North American ermine (*Mustela erminea*). Ermine, the most widespread terrestrial carnivores in the arctic, are represented by four genetically distinct clades. Extended isolation in glacial refugia, followed by subsequent range expansion in the last 10,000 years has led to secondary contact and hybridization at multiple contact zones in North America. We use mitochondrial genomes and nuclear amplicons to generate robust phylogenies, resolve species limits, refine distributional boundaries, and begin to assess the consequences of secondary contact. Preliminary analysis of whole-genome sequences (N=10) corroborate our historical understanding of demography and provide a more detailed perspective on the timing and extend of divergence and history of hybridization. This research was supported by a Grants-In-Aid of Research awarded to Jocelyn Colella.

77^{TA}: A complete species-level phylogeny of Mammalia using a supermatrix of 31 genes

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Understanding the evolution of Mammalia is of unparalleled relevance to humans for a variety of ecological, medical, and cultural reasons—a fact that belies our relative lack of broad-scale phylogenetic knowledge about this group. Now nearly 10 years old, the supertree-based analyses of Bininda-Emonds et al. (2007, plus subsequent taxonomic updates in 2009 and 2011) still represents the most complete species-level phylogeny of mammals. However, the prevalence of poorly resolved nodes in that supertree reduces its utility for analyses of rate-based evolutionary questions, and highlights the need for the co-estimation of branch lengths and topology using a DNA matrix. Here we seek to reconstruct the phylogeny of global Mammalia by maximizing species-level sampling from all available DNA sequences of 31 genes. The resulting supermatrix analysis includes a sampling of at least one of the targeted genes for 4103 of 5910 species recognized in our revised taxonomy (updated from MSW3). We use taxonomic constraints and a birth-death model to impute the placement of unsampled (missing) species throughout the Bayesian posterior sample of trees, and join this with a backbone analysis of all families and 76 fossils tips to form a complete set of dated phylogenies for all mammal species. Our results provide a novel and newly rigorous perspective on the tempo and mode of species diversification across Mammalia.

78^{E}: The molecular basis of high-elevation adaptation in wild cavies**

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Organisms living at high-elevations experience physiological stresses due to reduced oxygen availability, low temperatures, and increased UV exposure. Despite these extreme conditions, many species have adapted to life at high altitudes. Recent advances in sequencing technologies now permit robust molecular-level investigations of convergent adaptive evolution to shared environmental conditions. Comparative genomic sequencing of three sister species of wild cavies (*Cavia tschudii* and *Cavia aperea*, *Microcavia niata* and *Microcavia australis*, *Galea comes* and *Galea leucoblephara*), each with a low- and high-elevation member (essentially three evolutionary replicates), is being used to identify signatures of positive selection in shared and unique genes and pathways between these genera. Genomic sequencing was chosen over transcriptomic sequencing to leverage existing samples from our natural history collections in the Museum of Southwestern Biology. Whole genome sequencing (Illumina HiSeq 125bp paired-end) to greater than 30-fold coverage for each of the six species is currently underway. These data will be quality filtered, assembled by mapping to the domestic guinea pig reference genome, orthologous genes identified, maximum likelihood and Bayesian phylogenies generated, and branch-site statistical tests for positive selection will be completed. Preliminary analyses showed high-altitude adaptations in the domestic guinea pig, and using genomic sequencing to compare the reproducibility and timing of molecular high-altitude adaptations across these three pairs of closely related mammals will greatly improve our overall understanding of the adaptive genetic response. This research was supported by a Grants-in-Aid of Research awarded to Jessica Weber in 2015.

79: Ecology, genetics, and conservation units despite gene flow in highly-vagile terrestrial mammals (caribou and wolves)

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Conservation Units (CUs) are groups of organisms distinguishable ecologically and genetically, and defining CUs is instrumental in conserving biodiversity within species. Recently, the use of both genomics and ecological information has been advocated for delineating CUs that better reflect local adaptations – i.e. the traits that in theory allow for population viability in the long-term. However, CUs are difficult to detect in highly-vagile terrestrial mammals characterized by long-range dispersal and, potentially, high levels of gene flow (e.g. caribou and wolves). My lab's work helped defining caribou CUs based on concordant distributions of traits of adaptive significance including behavioural (migratory, partially migratory or sedentary CUs), ecological (foraging specialization of CUs), and genetic variation at varied temporal scales. Preliminary data also highlight important morphological differences between migratory and sedentary populations. Wolf CUs could also be characterized based upon traits including behavioural (migratory vs. not), morphological (coat coloration), ecological (prey specialization), and genetic and genomic variation. Our findings also confirmed long-range dispersal (for wolves) and high levels of gene flow among populations (for both wolves and caribou). Thus, CUs are recognizable even in highly-vagile terrestrial mammals with long-range dispersal and high gene flow, and integration of genetic and ecological data allows for understanding the patterns of differentiation that could be maintained in nature.

80: Thousands of loci and hundreds of species: phylogenomics of crocidurine and myosoricine shrews

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Crocidurine and myosoricine shrews comprise a morphologically conserved but species-rich (230+ recognized species) clade distributed across the Old World. Relationships among the 12 recognized genera are not well established, and the monophyly of most genera has not been rigorously tested. Here we present the most comprehensive phylogenetic framework for the subfamilies Crocidurinae and Myosoricinae based on DNA sequences from over 4,000 ultraconserved elements sequenced from more than 300 specimens. We present results from both concatenated and species-tree analyses and discuss

parts of the tree that remain unresolved despite the substantial increase in data. We also discuss the methodological challenges of working with such a large dataset and chart a path forward in revising the taxonomy of Old World shrews.

81^E: Systematic and species delimitation in the genus *Calomys* (Rodentia: Sigmodontinae)

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Rodents of the genus *Calomys* are small granivorous rodents broadly distributed in South America. Approximately half of the currently recognized 13 species in the genus serve as reservoir hosts to rodent-borne viruses and other zoonotic agents, therefore, modern systematic appraisal is imperative to a) understand the evolution and systematic relationships of the species in the genus, as well as to b) identify the potential distribution of the pathogenic agents they carry. This project specifically aims to delimit species and revise the systematics and taxonomy of the constitutive species in *Calomys* using an integrative approach. We analyzed single and multilocus data for species delimitation using General mixed Yule-coalescent (GMYC), Poisson Tree Process (PTP), and Bayesian MCMC algorithms (BPP). In addition, we generated phylogenies based on Bayesian and maximum likelihood methods using individual and concatenated data. Results from different delimitation methods indicated a contrasting number of species (including the possibility of cryptic species) depending on the method of analysis and the data set used. However, analyses of single and multilocus datasets, in combination with genome-wide restriction enzyme digested sequence (RADseq) and morphometric data indicate a growing consensus on the number and distribution of the species in the genus.

82: Phylogenomics and Sigmodontinae: using big data approaches to examine a big taxonomic lineage

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Sigmodontinae is the largest and most diverse group of rodents in the new world. The inter- and intra-tribal relationships have been examined with small data sets (1-5 genes) using mitochondrial sequences, nuclear sequences, and combinations both. As sequencing cost has decreased and availability of high throughput solutions has increased the capability to generate full genomic sequences or reduced genomic sequences has significantly changed the potentially available data. This in turn has opened the doors to much larger datasets for examining old questions. We present here an examination of the tribe Sigmodontinae using mitochondrial genomes and Ultra Conserved Elements (UCE's) and compare the results to previous established phylogenies.

83^E: Ultraconserved elements reveal higher-level relationships among marsupials

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The phylogenetic position of the Monito del Monte (*Dromiciops gliroides*) relative to South American (Ameridelphia) and Australian metatherians (Australidelphia) has been controversial. A suite of morphological characters led Hershkovitz to place *Dromiciops* sister to all extant metatherians. In contrast, molecular analyses placed *Dromiciops* within Australidelphia or sister to it, and have uniformly rejected a placement within Ameridelphia. In order to resolve the relationships of the Monito del Monte relative to Australidelphia and Ameridelphia, we sequenced hundreds of ultraconserved elements from members of all three groups and inferred a tree using concatenation and coalescent-based methods. We will discuss our phylogenetic results and their implications for metatherian biogeography.

84^{}: Hung out to dry? Arid adaptation in hibernating big brown bats**

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Hibernation is typically a period of water deficit and humidity strongly influences hibernation patterns of small mammals. Drier conditions reduce torpor bout length, stimulate arousals, and can decrease overwinter survival. To mitigate these effects, many small mammals hibernate in near saturated (100% RH) conditions. However, big brown bats (*Eptesicus fuscus*) hibernate in a wider variety of conditions and tolerate lower humidity than most other bat hibernators. To assess arid adaptation in this species, we compared torpid metabolic rate (TMR) and total evaporative water loss (EWL) between two populations of *E. fuscus* with differing winter ecologies: one that hibernates in a humid (>98% RH) karst cave in Wood Buffalo National Park (WBNP), Alberta, and one that hibernates in dry (ca. 65% RH) rock-crevices in Dinosaur Provincial park, AB. We used flow-through respirometry to measure TMR and total EWL of bats in relatively dry (<10% RH) and humid (ca. 85% RH) conditions. Torpid metabolic rate did not differ between populations or with humidity. However, total EWL was lower in bats from DPP than those from WBNP. Our results suggest that *E. fuscus* hibernating in arid environments have adaptations to decrease cutaneous EWL that are not evident in bats from humid areas. Such adaptation complements the sedentary nature of *E. fuscus*, allowing them to tolerate more variable microclimate during hibernation and increasing the availability of overwintering habitat. This research was supported by a Grant-in-Aid of Research awarded to Brandon Klüg-Baerwald in 2015.

85: Do behavioral adaptations correlate with individual responses to white-nose syndrome in hibernating little brown bats?

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Host-pathogen interactions are central to the long-term dynamics of wildlife diseases. Variation in the behavior of mammalian hosts can engender differences in pathogen exposure, host tolerance, and host resistance, which together may affect host survival and evolution. However, emerging infectious diseases (EIDs) of wildlife are often caused by recent introductions of pathogens into naïve host populations. Thus, shared evolutionary histories of hosts and pathogens can be short, reducing the likelihood of host behavioral adaptations. We aimed to assess the adaptive value of EID-induced behavioral changes in mammals by examining the effects of behavioral differences on host fitness and inheritance via selection. Our study model was captive hibernating little brown bats (*Myotis lucifugus*) inoculated with the fungal pathogen causing the EID white-nose syndrome (WNS). Using infrared video, we systematically compared differences in behavioral responses to WNS in bats of different age classes and durations of colony experience with WNS. Preliminary analysis suggests all groups of infected bats, and adult bats from colonies with long WNS experience in particular, exhibited reduced locomotion and increased grooming relative to controls. These behavioral differences may represent adaptive changes by infected bats to maximize energy conservation and reduce infection loads, respectively. Investigating how these variables relate to infection severity, WNS mortality, and physiological variables influencing host susceptibility will clarify the influence of behavior on host responses to EIDs and host-pathogen co-evolution.

86: Activity and movements of habituated and supplemented wild black bears compared to of non-habituated bears

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Wild black bears that are habituated to the presence of humans and have their diets supplemented are often assumed to behave differently from “normal” wild bears. We studied wild black bears that avoided people in the southern Appalachian Mountains and wild black bears that were habituated to people and had supplemented diets in northeastern Minnesota. Although the southern Appalachian study area supported spruce-fir habitat at high elevations, similar to the habitat in the Minnesota study area, low elevations at the southern Appalachian site were considerably different. For female bears in the 2 populations, we compared 3 metrics of activity and movement (percent time active, distance move when

active, circuitous movement) during breeding and lactating summers and compared responses to variations in summer and autumn food supplies. Behaviors of breeding females differed from lactating females in similar ways at the 2 study sites. Analyses of more comparisons will be presented.

87: Experience breeds competitors: parity positively affects litter sizes, boldness, and hormones in coyote pups

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Environmental perturbations occasionally incite parental phenotype changes that later affect offspring, but such changes are not immutable across successive reproductive opportunities nor are the associated environmental factors. Consideration of temporal variation in parental effects is thus warranted, as both parents and selection pressures vary with time. We observed coyote (*Canis latrans*) offspring from parents exposed to novel conspecific odors mid-gestation, as well as offspring from first-time and experienced parents to determine how environment and time affect parental effects. Pup boldness was examined via feeding and novel object tests, whereas pup hormones were quantified using shaved hair collected monthly. Within the first reproductive effort, odor litters foraged independent of their parents (i.e. were bolder) and had higher cortisol concentrations at 5 weeks of age. However, experienced parents produced bolder litters with higher cortisol and testosterone concentrations at 15 weeks of age, regardless of whether those parents previously experienced odor. Further, experienced parents had larger litters that were bolder with greater hormone concentrations. Our results suggest the significance of environmental input for parental effects varies with both parity and litter sizes, as temporal plasticity may disproportionately structure the maternal environment (e.g. litter sizes), altering developmental conditions for siblings across reproductive events.

88: Factors influencing moose behavior in Voyageurs National Park

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The population abundance of moose (*Alces alces*) in Minnesota has recently declined sharply despite what appears to be adequate habitat. Rebounding wolf populations (*Canis lupus*), warming temperatures, and parasites have been hypothesized as factors contributing to the decline. Here, we evaluated fine-scale factors associated with moose behavior for a protected population in Voyageurs National Park that face the same suite of risks as other populations. We collected GPS collar data from 20 moose over 3 years (32 moose-years) and classified their behavioral state as resting, foraging, or traveling using state-space models. We differentiated the three states based on activity levels recorded on the collars and characteristics of the movement path (e.g., distributions of step lengths and turn angles). We used general additive models with a multinomial distribution to associate the probability of being in a given state with habitat type, ambient weather conditions, human factors, and location within a wolf pack's home range (based on GPS-collared wolves in the same area). Moose behavior differed significantly among habitat types. Moose were more likely to be foraging when located in deciduous forests and resting in coniferous forests. Moose rested much more frequently when ambient temperature increased. Wolves affected moose behavior significantly but individual responses of moose were not consistent among moose. These results provide information on how moose may respond to future alterations in their environment.

89: Cardiac response of American black bears to roadways

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Roadways produce negative impacts on most wildlife species through vehicular-related mortality and fitness-related opportunity costs due to road avoidance. These impacts are typically quantified by measuring changes in movement rates near roads or by quantifying selection for areas far away from roads. Many studies have attempted to link stress to fragmented or urban areas, but few have measured the physiological stress responses during discrete behaviors. We deployed GPS-collars in combination with cardiac biologgers on eight American black bears (*Ursus americanus*; 10 bear-years) throughout Minnesota. We tested whether bears exhibited acute stress responses, as defined by significant changes in heart rate, during road crossings. We quantified distance from roadways at which bear heart rates were no longer elevated. Road crossings resulted in higher maximum heart rates (9 of 10 bear-years), higher mean heart rates (9 of 10 bear years), and more mean heart rate variation (8 of 10 bears) relative to movements without a crossing. Bear heart rates became elevated at a mean distance of 118 meters from roadways (range 0-391 meters). Female bears with cubs showed the strongest responses to road crossings, whereas, bears living in areas with lower road densities exhibited stronger cardiac responses. Our findings suggest that roads are an acute stressor for bears and differences among study areas suggest a potential habituation toward roadways by bears that cross them with regularity.

90: California coyotes develop a taste for seafood in the absence of competitors

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Coyotes (*Canis latrans*) are known to consume marine foods, but it remains unclear how important marine subsidies are to modern coyotes and for how long they have persisted. We used stable isotope analyses to investigate modern coyote reliance on marine foods in the central coast region of California and compared present-day coyote diets to that of Holocene (~3000 – 750 BP) and historical (~1890 – 1990 AD) coyotes. We measured $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values in modern coyote scats sourced from three coastal sites, in coyote bone collagen from seven Holocene archaeological sites, and in historical coyote hair from museum collections. We found evidence for marine resource use by modern coastal California coyotes at only one site, Año Nuevo, which hosts a mainland northern elephant seal (*Mirounga angustirostris*) breeding colony. Seals and sea lions account for ~30% of Año Nuevo coyote diets throughout the year and this subsidy appears to have a positive impact on coyote population size. Our sub-fossil isotope data suggest that neither Holocene nor historical coyotes consumed marine-derived foods, even at a site adjacent to a past mainland northern fur seal (*Callorhinus ursinus*) rookery. Marine resource use by contemporary California coyotes is a new behavior relative to their recent ancestors. This change in behavior is likely enabled by reduced competition with humans or other, now-absent consumers (e.g. grizzly bears, *Ursus arctos californicus*).

91: Are migratory behaviours of bats socially transmitted?

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To migrate, animals rely on endogenous, genetically inherited programs, or socially transmitted information about routes and behaviours, or a combination of the two. In long-lived animals with extended parental care, as in bats, migration tends to be socially transmitted rather than endogenous. For a young bat to learn migration via social transmission, they would need to follow an experienced individual, most likely one roosting nearby. Therefore, we predicted that bats travelling together originate from the same place. It is also likely that young bats would follow their mothers or other kin, so we predicted that bats travelling together are more closely related to each other than bats not travelling together. To test our predictions, we used microsatellite genotypes and stable isotope values of $\delta^{13}\text{C}$, $\delta^{15}\text{N}$, and $\delta^2\text{H}$ to analyse

the relatedness and geographic origins of migrating hoary bats (*Lasiurus cinereus/Aeorestes cinereus*; n = 133) and silver-haired bats (*Lasionycteris noctivagans*; n = 87) killed at wind turbines over two consecutive autumn migrations. Contrary to our predictions, there was no evidence that related dyads of hoary bats or silver-haired bats were killed on the same night more frequently than expected by chance, or that the number of days between the fatalities of dyad members was influenced by relatedness or latitude of origin. Our data suggest that these bats do not socially transmit migratory behaviours among close kin.

92^E: Exploring the dietary variation of pikas (*Ochotona princeps*) across space and time

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Climate change is driving shifts in the range boundaries of taxa globally, but it may also alter the life history traits or ecology of many animals. The American pika (*Ochotona princeps*) is a threatened alpine mammal and is generally considered to be highly sensitive to climate changes. However, recent work has implicated shifts in forage availability and quality, rather than temperature, as the primary driver influencing *O. princeps* abundance, persistence, and body size evolution. Given the importance of *O. princeps* as bell-weather species for other alpine mammals and that they are also of conservation concern, understanding how diet may link climate with ecology is vitally important. Here, we utilize bulk Carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) stable isotope analysis (SIA) to characterize the dietary niche and nutritional quality of food consumed by *O. princeps* from six Rocky Mountain populations over the past ~125 years. Specifically we address the following questions: 1) How much do individual *O. princeps* and population dietary niches vary across their range in the Rocky Mountains? 2) Have *O. princeps* responded to climate change through dietary shifts? Our results allow us to characterize the isotopic dietary niche over both space and time. We compare results across this geographic gradient and across the last century to investigate the response of animals to past climatic shifts.

93^{E,TA}: Transberingian arvicoline colonization history and the biogeography of a Holarctic tapeworm species complex

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The Bering land bridge connected Eurasia and North America during glacial maxima in the Quaternary and facilitated the exchange of species between these continents. Phylogeographic investigations of mammalian histories are revealing the direction and timing of faunal movements. For example, studies investigating arvicoline rodents (e.g., *Myodes*, *Microtus*, *Lemmus*) have revealed deep and shallow colonization events across Beringia, with complex histories of expansion, contraction, and diversification. These northern rodents are parasitized by a tapeworm species complex (genus *Arostrilepis*) that has tracked its hosts throughout the Quaternary and provides a window on the ecological dynamics of shifting host distributions. Using a molecular phylogenetic approach we examine the biogeographic history of *Arostrilepis* in light of hypotheses for transberingian dispersal by its rodent hosts. Our data reveal unexpected levels of new *Arostrilepis* diversity (as many as 15 previously unrecognized genetic lineages) across the Holarctic, but especially in the northwestern United States. Phylogenies based on multi-locus datasets suggest multiple Nearctic colonizations by *Arostrilepis* species, with patterns indicating that *Arostrilepis* colonized the Nearctic both simultaneously with multiple host genera, and sequentially in association with distinct waves of host dispersal. These results highlight the complex history of faunal assembly associated with Beringian mammal-parasite assemblages.

94^{E,TA}: Using ancient DNA to uncover occupancy patterns of woodrats (*Neotoma*) and co-occurring species through time

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One of the most pressing challenges in ecology and evolution is to understand how species and ecosystems react to major environmental changes. While contemporary biological collections offer insight into biotic change through the recent past, paleoecological collections offer crucial physical evidence of these processes on far longer timescales. North American woodrats (*Neotoma*) provide extensive physical evidence of past processes by building paleomiddens, which contain environmental debris and copious fecal pellets from the woodrats themselves. Using a 33,000-year series of paleomiddens from Death Valley, CA/NV, we isolated ancient DNA from fecal pellets, prepared and enriched libraries for *Neotoma* mitochondrial DNA, and sequenced nearly 40 million reads across 41 samples. By focusing on regions with power to discriminate between species and clades, we reconstruct the Pleistocene-Holocene replacement of the montane-adapted *N. cinerea* by the relatively desert-adapted *N. lepida*. Because enrichment for *Neotoma* DNA was imperfect, we also opportunistically sequenced complex community-level (metagenomic) information from the *Neotoma* fecal pellets, uncovering sequences from groups including plants, invertebrates, and endoparasites. This opens the door for an enormous amount of future work focusing on the dynamics of *Neotoma* species through time, as well as analysis of communities and co-occurring species from the woodrats' perspective.

95^{E,TA}: Comparative phylogeography of a Beringian host-parasite assemblage

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Historical episodes of climate change caused distinct patterns of dispersal and differentiation in mammals across the Holarctic. Understanding of these patterns can be strengthened by examining histories of associated parasites, which were influenced by host population events. For example, northern red-backed voles (*Myodes rutilus*) and the tapeworm *Arostrilepis macrocirrosa* share a complex history of dispersal and differentiation across Beringia, the land bridge that periodically connected Eurasia and North America. Previous work has demonstrated that populations of *M. rutilus* were isolated in separate Beringian and central Asian refugia during past glacial periods. Subsequently, vole lineages underwent geographic range shifts due to vicariance, as some populations retracted while others expanded. This study investigates patterns of intraspecific diversity within *A. macrocirrosa* to quantify the consequences of climate-mediated host history for parasite populations. We used a multi-locus phylogeographic approach to resolve geographic patterns of genetic structure. As detected for the host, we show support for refugial isolation between parasite populations in Beringia and central Asia. However, we did not detect evidence of historical geographic shifts by *A. macrocirrosa* that were congruent with those inferred for the host. These partially incongruent histories suggest that though major vicariant events associated with refugial isolation may have structured host and parasite populations similarly, additional factors caused host and parasite populations to follow semi-independent trajectories when environmental barriers were released.

96: Testing for body size divergence in Neotropical frugivorous bats

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Closely related species are usually similar in morphology and ecological preferences because they share a recent common ancestor. When close relatives live in the same area, they must differ in at least one ecologically-relevant trait to avoid competition. Body size can be such trait, because it relates to reproduction, physiology, and ecology. Divergence in body size might allow closely related species to partition space or resources. Two species of yellow-shouldered bats (*Sturnira hondurensis* and *S. parvidens*) occur in Mexico, with diets, geographic ranges, and diagnostic physical measurements that almost completely overlap. On average, *S. hondurensis* is slightly larger-bodied. Anecdotal field data suggests that the interspecific difference in body size is greater when both species occur in the same area than the overall size difference between both species. To test this, representative body size measurements and occurrence data for both species have been collected from museum specimens. Identifying areas where only one of the species occurs is challenging, and the number of localities where only one of the two species occurs is too small for any meaningful comparisons. This study explores

alternative approaches to test for body size divergence in a framework that unifies spatial patterns of intra and interspecific variation.

97: Dynamics of cougar recolonization in the Midwest: investigating trends in confirmations over 25 years

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Since the early 1990s, cougar presence in the midwestern portion of North America has steadily increased despite harvest pressure in the Dakotas since 2005. We were interested in the potential effects of harvest on the spatial and temporal trends in confirmations of cougars during 1990-2015, and determined: 1) if the number and location of confirmations differed between pre-harvest and post-harvest pressure in the Dakotas; 2) if confirmation type disproportionately affected the total number of confirmations in the Midwest; and 3) for cougars for which genetic data were available, determined the source location for 37 individuals to identify spatial patterns. We mapped >810 confirmations of cougars east of their established range in North America in ArcGIS 10.3 and conducted a hotspot analysis and further conducted t-tests to compare the number of pre- and post-harvest confirmations. The total number of cougar confirmations increased during 1990-2015 and we found significantly more confirmations ($P < 0.005$) after 2005. Confirmations occurred in more counties in the post-harvest timeframe than prior to 2005 and the longest-known dispersal distance occurred during the post-harvest time frame. Despite harvest in the Dakotas, it appears that cougars continue disperse from populations farther to the west (Wyoming and Colorado), further supporting the notion that the Midwest will eventually be recolonized.

98: Habitat suitability and population viability of recolonizing cougars in the midwestern U.S.

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Cougars (*Puma concolor*) are attempting to recolonize the midwestern U.S. following extirpation more than a century ago. Increased cougar presence presents challenges to wildlife conservation agencies and raises many questions, such as (1) where may cougar populations become established? and (2) which factors may affect cougar population viability? We describe efforts to address these questions, following a decade of research by our team. We first created a model of potential cougar habitat in 3.2 million km² of western and midwestern U.S. About 10% of the study area comprised highly-suitable habitat for cougars with 8 large, contiguous patches of highly-suitable habitat. These patches were generally connected along riparian corridors and represent potential dispersal routes for subadult cougars. We then built a stage-based demographic model for cougars and modeled population viability given potential harvest in the Midwest for 25 years (mean $\lambda = 1.083$). Our no-harvest model indicated all 8 large patches of habitat in the Midwest occupied after 25 years; the harvest scenario found 7 of 8 large patches occupied. Both models were most sensitive to changes in dispersal rates and distances. We suggest that cougars are likely to recolonize habitat patches in the Midwest in the next 25 years, regardless of current harvest pressure. These studies represent the first assessments of cougar recolonization potential in the Midwest and have proven valuable for wildlife conservation planning.

99: A trait-based model of dynamic insular biogeography: applying hysteresis to community biogeography

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Major challenges exist for considering historical and regional processes in determining local communities, including the identification of candidate species pools relevant for local assembly. To address these obstacles, we propose a model that uses species traits to predict candidate species pools for continental

and habitat islands that are dynamic through time (e.g., “sky islands” over glacial-interglacial cycles). Colonization probability is influenced by the species’ ability to cross the matrix between the “mainland” source and an island. Extinction probability is influenced by the species’ spatial requirements for sustaining a population. As islands cycle between periods of increasing and decreasing connectivity and size, the dominant process driving community composition switches between colonization and extinction. For a given taxon, different suites of organismal traits mediate these two processes. Therefore, the model predicts that similar environmental conditions (connectivity and size) can result in distinct candidate species pools, depending on the trajectory within the cycle. Such a dependence on historical conditions (termed “hysteresis”) exists in other fields, and the model predicts its importance in biogeography. The model applies to many taxa and to islands whose size and connectivity cycle on timescales of decades (anthropogenic fragmentation and succession) or thousands of years (vegetational changes over glacial-interglacial cycles). We outline our ideas for future research testing the model in a classic system of non-volant mammals in “sky islands” of western North America.

100: Linear mix modeling for understanding diversity along a distance to edge gradient

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Habitat fragmentation results in partitioning of continuous areas into fragments, reducing area, increasing isolation, changing connectivity, and increasing edge effects. The aim of this study is to improve the understanding of biodiversity on forest patch edges, by analyzing small mammal diversity patterns based on distance to edge (DTE), in four eastern Paraguay forest remnants. Biodiversity was quantified via Hill numbers for Shannon diversity and Pielou evenness. Principal Components Analysis was conducted on small mammal abundances as a proxy to decipher the gradient along DTE. A mix model framework was implemented with aims to explain the effect of external variables, which directly/indirectly explain small mammal patterns, testing theoretical mechanisms for biodiversity along edges; including the presence of megafauna and top predators; illegal logging; presence of indigenous groups; and the ownership and management of reserves. Using a nested framework, with reserves as factors, models were compared via Akaike Information Criterion. Each diversity metric showed influences by different mechanism, for example, species richness and abundances were best explained by land ownership; biodiversity by presence of indigenous people; evenness by none of these mechanisms; PC1 and PC2 by extent of logging in reserve. With continued fragmentation, understanding the mechanisms that effect biodiversity can be very valuable to maximizing conservations efforts and minimizing extinction risks on the planet.

101^E. Testing the efficacy of an acoustic lure on bat mist netting success in North America

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Severe population declines in numerous North American bat species makes population monitoring increasingly difficult. We tested the effectiveness of an acoustic lure at increasing capture success of bats in mist nets. We conducted our study at 3 properties in southern Indiana during summer 2014. We set up 7 mist netting sites at each property, netting 2 times at each site, with and without the use of an UltraSoundGate Player BL acoustic lure. The lure played recordings of various social calls from *Myotis*, *Eptesicus*, and *Lasiurus* spp. on a loop throughout the net night. We ran a series of zero-inflated Poisson generalized linear models on number of bats captured per trapping night to test whether the lure produced a difference in bat captures overall and for each genus while accounting for additional sources of variability. For bats in the genera *Myotis* and *Eptesicus*, the top performing models contained an effect for use of the lure. This effect was positive and significant ($P = 0.007$) for our *Myotis* model, indicating that use of the acoustic lure had a positive effect on capture of individuals. This effect was negative and marginally significant in the *Eptesicus* model ($P = 0.10$). Use of an acoustic lure can be a valuable tool to increase capture success of some bat species, but may act as a deterrent to other species.

102^E: How picky is the Great Basin pocket mouse?

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Understanding species' responses to environmental change is critical to protect and maintain biodiversity. Small-mammal responses have been studied in terms of abundances, community structure, and range dynamics. Less well understood is the interaction between species and changing land-cover. Yet anthropogenically driven alterations to the resource base challenges the persistence of small mammals, especially specialist rodents. *Perognathus mollipilosus*, a granivore and xeric specialist, is widely distributed throughout the Great Basin. In the Toiyabe mountain range *P. mollipilosus* demonstrated a range contraction with its lower elevation limit shifting upslope slightly and peak abundance moving downslope over an 80-year interval. Understanding the relationship between *P. mollipilosus* and its resource base, past and present, is critical for determining the role of resources vs. climate change in shaping the elevational distribution of this species. Analysis of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ stable isotopes in hair shows variable resource use by *P. mollipilosus* along its modern day elevation range. Under resource tracking, we expect both $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ signals to increase with increasing temperature and aridity downslope and through time. However, we find a mid-elevation peak in both $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ today corresponding to variation in the resource base after accounting for climate. Isotope analysis of historical hair samples now enables us to evaluate the impact of 80 years of intensifying human land-use on the relationship between this rodent and its resources.

103^E: Dealing with spatial dependency in occupancy studies: a 20-year track-station survey of carnivores in Minnesota

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In the last decade, species distribution patterns have often been estimated through occupancy models that take into account imperfect detection and, thus, false absences (i.e., surveys where the species goes undetected even though it is present). These models are based on the critical assumption of independency in detection among replicate surveys. Nevertheless, occupancy models have been applied to data collected through spatial sampling designs that clearly violate this assumption (e.g. carnivore tracks along adjacent trail segments), resulting in biased estimators of presence probability and their standard errors. Here we explore the spatial dependency in detection probability for 8 carnivore species (*Canis lupus*, *C. latrans*, *Martes pennant*, *M. americana*, *Lynx rufus*, *Vulpes vulpes*, *Procyon lotor*, *Mephitis mephitis*) using data collected between 1983 and 2013 by the Minnesota Department of Natural Resources during annual scent station surveys conducted at a state wide level. Presence/absence data were collected through a 1-night scent station survey along, on average, 240 transect routes (4.5 km long) consisting of 10 stations, regularly spaced. Preliminary results for each species demonstrate spatial correlation in the detection of individuals within a transect, despite the large difference in home range size among the listed species. We will discuss the relevance of these findings to current work exploring optimal spacing of trail cameras in future carnivore surveys in Minnesota.

104: Resurvey of historical localities reveal decline in the broad-toothed rat (*Mastacomys fuscus*) across Victoria, Australia

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Resurveys of historical distributions help document range shifts and predict future changes. The once widely distributed broad-toothed rat (*Mastacomys fuscus*) is now found in isolated populations across south-eastern Australia. Recent changes in distribution have not been well documented and there is limited knowledge about its current occupancy and population size. Surveys to better define its distribution are of high priority as further declines are predicted with climate change. This study aimed to determine if there has been a significant decline in the persistence of *M. fuscus* at historical localities across Victoria and test if these changes are correlated with elevation and climate. We geo-referenced all documented records for

M. fuscus in Victoria prior to 1990 using field notes and verbal descriptions. We resurveyed these localities using a repeated sampling design, conducting six timed searches for scats, reporting detection or non-detection. This study design resulted in high detectability (>0.99), providing statistical confidence in the absence of *M. fuscus* from 36 of the 68 sites. Generalised linear models revealed that absences were more likely to occur at sites with low elevation, low annual precipitation, high mean temperatures and high minimum temperatures. The best predictor for site persistence was minimum temperature. This study reveals a significant decline in the persistence of *M. fuscus* at historical localities across Victoria, providing a benchmark for future monitoring and management efforts.

105^F: Differential effects of prescribed fire vs. herbicide induced longleaf pine restoration on fox squirrel occurrence

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Restoration of the longleaf pine (*Pinus palustris*; LLP) ecosystem in the southeastern U.S. is a principal goal of many land management agencies. Frequent prescribed fire and herbicide application are two common methods of LLP restoration. We employed a multi-scale approach to investigate the effects of prescribed fire frequency and herbicide application on fox squirrel (*Sciurus niger*) occurrence in LLP sandhill communities of north Florida. To determine the influence of prescribed fire and herbicide on fox squirrels we sampled 106 and 50 nine-point camera trapping grids (0.84 ha), respectively. We evaluated *a priori* grid-level candidate models using an occupancy modeling framework. At a finer point scale (0.09 ha) we evaluated fox squirrel occurrence using a Bayesian occupancy framework to account for spatial auto correlation. We found that reduced shrub density linked to frequent prescribed fire provided the best explanation of fox squirrel occurrence on prescribed fire grids. On herbicide grids the application of herbicides significantly decreased turkey oak (*Quercus laevis*) densities, which were positively correlated with grid-level fox squirrel occurrence. Point-level analysis revealed that frequent fires and elevated turkey oak densities were positively correlated with fox squirrel occurrence. Fox squirrel occurrence declined with increased time since the last prescribed fire. We found no point-level effects of herbicide on fox squirrel occurrence. These findings reveal the importance of prescribed fire for fox squirrel conservation.

106^F: Detection of American martens as a function of season and habitat in northern Wisconsin

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In order to conserve the state-endangered American marten (*Martes americana*) in Wisconsin, it is invaluable to develop effective monitoring methods and to understand marten habitat requirements. Previous studies of Wisconsin martens indicate that patches of hemlock and white cedar within northern hardwood stands provide important habitat during the winter, but little research exists on summer use of hemlock-cedar patches. We investigated the seasonality of marten space use by comparing the frequency of marten detection as a function of distance to hemlock-cedar patches. We predicted that the likelihood of detection would decrease with distance from hemlock-cedar habitat in the winter and would increase with distance in the summer. Martens were detected using remote cameras and baited hair snares placed 0 m, 50 m, 150 m, and 300 m sites away hemlock-cedar patches. Martens were detected within 150 m of hemlock-cedar in the winter and within 50 m in the summer. We detected martens at more sites across the landscape and with higher overall detection in the winter compared to the summer. These preliminary results suggest that hemlock-cedar use is more frequent during the winter and that martens are less reliant on this habitat in the summer. Monitoring marten populations with these techniques is most applicable in the winter but there is still a need to develop effective techniques for the summer.

107: Effects of range contraction on genetic variation in the woodland deer mouse (*Peromyscus maniculatus gracilis*)

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The range of the woodland deer mouse (*Peromyscus maniculatus gracilis*) in Michigan's Lower Peninsula (LP) has contracted over the last 40 years at the same time that regional temperatures have risen and the abundance of the white-footed mouse (*P. leucopus*) has increased. Recent trapping shows that the LP range of *P. m. gracilis* has shrunk to two areas: a larger one in parts of Cheboygan, Otsego and Montmorency Counties, and a much smaller one in western Alpena County. We used a Geographic Information System (GIS) habitat analysis to predict where *P. m. gracilis* might be found between those areas, trapped at numerous locations, and analyzed 11 microsatellite loci for all trapped individuals. Genetic diversity within populations was high and differentiation between populations was low, as is typical for *Peromyscus* species. The genetic diversity and bottleneck analyses agree with the historical trapping information in indicating that LP populations of *P. m. gracilis* once were continuous across the entire region and had extensive gene flow; however, the recent trapping data and the assignment tests indicate that the Alpena population is becoming geographically and genetically isolated from all other populations. This research suggests that early genetic effects of range contractions might be detectable in small mammal populations before they become seriously endangered.

108: Big data meets mammalogy: small mammal, vector, and pathogen data collection in the National Ecological Observatory Network

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The National Ecological Observatory Network (NEON) is a long-term, large-scale research program that is designed to enable ecological discovery by providing open-access data generated by standardized sampling of a diversity of taxa and ecosystem variables. A key component of the Observatory is terrestrial organismal sampling, which is intended, in large part, to increase our understanding of climatic forcing of and land use impacts on phenology, demography, diversity, community dynamics, pathogen presence, and ecosystem function. This includes the long-term community dynamics of small mammals and their pathogens at 47 sites distributed throughout the United States. Standardized sampling at this combination of spatial and temporal scales for small mammals is unprecedented. Here we outline the current small mammal sampling designs for NEON, including vector and pathogen data, and the rationale for these designs, and demonstrate how these and other NEON data can be accessed by the larger community (<http://data.neonscience.org/>) to support individual research and education programs (<http://neondatakills.org/>).

109^F: Scientific reproducibility and the role of data archiving

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Reproducibility is a fundamental aspect of scientific research. The ability to independently generate the same results allows validation of findings and ensures a sound understanding of biology. Because science is a field that builds upon existing knowledge, it is essential that there is no lack of reproducibility in published studies. We tested the reproducibility of results from a common method used in evolutionary biology for clustering populations, Structure. Starting from published studies containing archived data, we attempted to recreate the same qualitative results presented by authors. We found that 30% of studies were not reproducible (Gilbert et al. 2012). However, this percentage was only out of studies for which we were able to obtain data, and the lack of reproducibility is much greater when including the absence of data and details needed to attempt reproduction of an analysis. We thus further investigated the role of data archiving and the factors contributing to the presence of data with published studies. We found that journal policies encouraging or requiring data archiving at the time of publication improve the availability of data (Vines et al. 2013), and that when not publicly archived, the probability of a dataset being lost increases by 17% each year (Vines et al 2014). I present a summary of these results as well as broad recommendations for improving future storage and reuse of data.

110: VertNet and beyond: advances in biodiversity discovery and data quality improvement

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Over the past 17 years, data on reptiles and amphibians have been increasingly accessible through distributed-data networks such as HerpNet, GBIF and iDigBio. VertNet is an NSF-funded project to create a cloud-based platform for vertebrate biodiversity records, building on HerpNet, FishNet2, ORNIS and MaNIS. VertNet works with a global museum community to mobilize data online. Since its inception, VertNet has grown to include 201 institutions with 639 collections of vertebrate and non-vertebrate, and has published more than 230 million species occurrence records that are made also available to other aggregators (e.g., GBIF, iDigBio). In addition to data publishing, VertNet strives to catalyze critical innovations in biodiversity data standards, cloud-based data publishing, data reporting, and—most needed for research use of records—data quality. We will present an update on VertNet and its services, including data cleaning and issue tracking, and the future of the organization. We will discuss the challenges of maximizing data quality from diverse data sources, and will highlight the importance of high standards during data capture in the field or from museum records. We will stress the value of high quality data for maximizing the scientific impact of VertNet on the study and conservation of biodiversity.

111: VertNet traits: biocollections as a critical source for mammal trait data

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For vast areas of the globe and large parts of the tree of life, our knowledge of trait diversity is incomplete. However, it is exactly these trait data that form the link between the evolutionary history of organisms, their assembly into communities, and the nature and dynamic functioning of ecosystems. Recent efforts to close those gaps have typically focused on collating species-by-trait databases using primary or secondary literature, but such aggregated data lose the direct observations on which those values are based and ignore individual variation. Perhaps under-appreciated is that a vast trove of trait data directly assessed from individuals is already in digitized and available from VertNet. However, this content is highly heterogeneous along multiple dimensions, making discoverability and full use challenging. Here we provide a detailed description of the creation of VertNet Traits, a new resource that provides over a million

fully normalized measurements on vertebrate body mass and body length, linked directly to specimen records. We demonstrate new search functions via VertNet for discovering trait content, document the process by which these data were unlocked and re-provisioned, and show how this work can be extended to other communities. Further, we discuss how to continue to grow this resource, especially how to work with the VertNet provider network to improve trait data publication, and thus assure the greatest sustainability of these crucial data.

112: Geometric morphometric studies of rodent disparity: influences of climate, diet and topography

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Quantitative analysis is crucial to understanding an important aspect of the diversity of life – its disparity. Until recently, quantitative studies of morphology could only analyze proportions of sizes and were unable to directly analyze differences in shape. The key advance of geometric morphometrics is agreement on a definition of shape; that definition is central to the quantification of the magnitudes and directions of shape differences. It is also the touchstone for evaluating methods proposed to test hypotheses of mechanisms of shape evolution. In the first part of this talk, I briefly review Kendall's definition of shape and its implications for the study of shape evolution. In the second part, I illustrate the utility and power of geometric morphometrics with examples from our own studies testing hypotheses about the evolution of disparity using data on mandible shape in rodents.

113: Why the long face? Evidence for (or against?) a new 'rule' in mammalian evolution

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The search for common trends in morphological evolution has a long history in mammalogy. Often the focus is on easily measurable traits, such as body mass and the relative proportions of the limbs. For instance, in closely related populations, body mass tends to increase with latitude (Bergmann's rule) while the relative length of appendages decreases in colder climates (Allen's rule). If the generalizability of these 'rules' is not always as obvious as the term 'rule' implies, the study of evolutionary trends has not lost its popularity. The most recently proposed 'rule' is a propensity, in closely related species, for small ones to be relatively short-faced, and somewhat paedomorphic, and for large species to be long-faced. While causal explanations are elusive, comparative analyses strongly support this trend of Cranial Evolutionary Allometry (CREA) in antelopes, fruit-bats, mongooses, squirrels and kangaroos. Whether this is really a 'rule', which may join the list of well established evolutionary trends, however, is still largely an open question. By more than doubling the number of study lineages being analysed, I will thus try to move a fundamental step forward to assess the validity of the CREA 'rule' and its potential contribution to the origin of the exceptional disparity of mammals.

114: Macroevolution of the mammalian mandible: primates, ungulates and carnivorans compared

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The mandible by definition (from the latin *mandere* = 'to chew') is a highly functional morphological structure. In mammalian species, evolutionary changes in size and shape of this bone have been often interpreted in relation to dietary adaptations. Recent evidence from different taxonomic groups provides equivocal support to the link between mandible shape and diet at the interspecific scale. Here, I provide a comparison of interspecific shape variation in mandibles of extant primates, ungulates and carnivorans by means of geometric morphometric method. The mandibular morphospace indicates presence of a significant phylogenetic signal in the shape data. Procrustes ANOVA models also support association between diet (simplified into three categories: carnivore, omnivore and herbivore) and mandible shape.

Models that take phylogenetic covariance matrix into account do not validate such association. Comparison of evolutionary rates also indicates that carnivorans' mandible shape differentiate between species at a faster rate than ungulates and primates. Differences in the tempo and mode of evolution of mandible shape between taxonomic groups might explain the equivocal link between shape and diet. The time is ripe to merge datasets and finally address fundamental questions in mammalian evolution.

115: Climate-linked morphotypes identify populations vulnerable to changing climate

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Understanding a species' potential evolvability with respect to changing climate is critical to understanding how they will respond to impending climate change. Some species live under a broad swath of environments, and have an apparently broad niche, but individual populations are quite vulnerable to small fluctuations, making and therefore to extirpation. Here I borrow a powerful method from neurosciences and other fields with high signal-to-noise ratios to analyze the high-dimensionality data produced by geometric morphometrics. I use an asymmetrical partial least squares analysis to perform a dimensionality reduction analysis that identifies the component of tooth shape that maximally correlates with climate variables of interest. Using this method, I identify the dental morphotypes that correlate with precipitation in *Microtus californicus* (the California vole). I demonstrate that as California climate has changed throughout the Holocene, these climate-linked morphotypes have shifted across the landscape. As precipitation levels have decreased, morphotype variation has decreased. By examining the distributions of these morphotypes in conjunction with projected climate change, we can hypothesize what populations are vulnerable to or robust to extirpation in the near future. Broadly integrating this method into intraspecific shape analyses will allow for many more analyses of these sorts, allowing us to identify species and populations that will be most vulnerable to impending climate change.

116: Does bite force matter on shaping the head of strepsirrhine primates

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The cranial system in mammals is highly constrained. Feeding forces, phylogeny, and the need to protect the brain and sensory organs are all important factors driving the evolution of the shape of the skull. In primates it has been shown that parts of the face are likely not constrained by feeding forces. Here, we explore relationships between bite force and craniomandibular shape by combining data on molar and incisor bite forces and analyses of cranial and mandible shape using 3D geometric morphometric approaches for 18 species of strepsirrhines that differ in feeding ecology. Our results show that bite forces vary across species with dietary specialists that gnaw showing relatively high bite forces at the incisors for their size. In non-gnawing species, molar bites are generally stronger than incisor bites. Bite force influences the shape of the mandible more strongly than the shape of the cranium. Finally, a significant phylogenetic signal was observed in the data suggesting that ecology and phylogeny both play an important role in driving variation in form-function relationships.

117^{TA}: Black and white rhino space use and resource selection in the lowveld of South Africa

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How animals utilize resources and partition space are key factors necessary to understand species coexistence, and improve conservation efforts of threatened and endangered species. South Africa harbors 82% of Africa's rhino population, and is disproportionately impacted by poaching. In 2011, nineteen black rhinos (*Diceros bicornis*) and several resident white rhinos (*Ceratotherium simum*) in

Balule Nature Reserve (BNR), part of the Kruger Associated Private Nature Reserves, were fitted with VHF transmitters and tracked weekly. After 4 years of spatial data collection, reserve-wide vegetation data to inform rhino space use remain a priority. Our goals are to 1) develop a classified vegetation land cover model for BNR and 2) model rhino space use and resource selection as functions of conspecific and heterospecific density, vegetation, and physical landscape. We developed a vegetation model via unsupervised classification of Landsat 8 imagery surrounding BNR and visited a stratified random subset of Landsat pixel centroids to validate our model. We examined species-specific associations with vegetation and physical landscape variables and quantified kernel density home range estimates and home range overlap within and between species. Preliminary results suggest black and white rhino in BNR associate with distinct vegetation types and exhibit considerable spatial segregation with little heterospecific overlap. Improved understanding of rhino resource selection and space use will aid species-specific management plans and anti-poaching efforts within BNR and the Greater Kruger area.

118^F: Anthropogenic impacts on forest duiker occupancy within a mixed land use forest mosaic, South Africa

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KwaZulu-Natal (KZN) province contains 16% of South Africa's remaining indigenous forests, including the Endangered Indian Ocean Coastal Belt Forest. Coastal development has resulted in a land-use mosaic including agriculture, forestry and urban landscapes. The effects of changing land use on forest mammals remain largely untested in KZN; thus, determining factors influencing wildlife presence across different land-use types is crucial, as remaining forest patches are highly fragmented, reducing habitats for forest specialists such as Vulnerable blue duiker, *Philantomba monticola*. Therefore, we surveyed 276 sites using camera traps to estimate occupancy (Ψ) of duiker in forest patches of various sizes across a gradient of different land-use types in southern KZN. Within the occupancy models we incorporated habitat characteristics, disturbance factors and surrounding land-use classifications to compare sites, and thus highlight factors responsible for duiker distribution across the habitat mosaic. Preliminary results indicated that occupancy was significantly higher, with a positive detection probability in semi-urban areas ($\Psi = 0.97$, $SE = 0.02$; $\beta = 0.7 \pm 0.05$), than in Protected Areas (PAs; $\Psi = 0.45$, $SE = 0.06$) and that PAs influenced occupancy negatively ($\beta = -2.01 \pm 0.52$). There is an increasing realization that conservation objectives require approaches for managing landscapes holistically, focusing on PAs but also including urban settings and agricultural landscapes. These findings highlight the value of non-PAs and their potential for aiding biodiversity persistence.

119: Solving inequalities: high reproductive skew in a social African ground squirrel with no dominance hierarchies

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In complex animal societies, females usually live with their close kin but these close kin are also their closest competitors. Reproduction in such groups is not equally distributed and success is often determined by dominance or aggression. Less is known about the factors influencing reproductive distribution in what appear to be egalitarian societies that do not use aggressive means of competing for resources, even when we observe unequal reproductive success. Female Cape ground squirrels (*Xerus inauris*) are plural breeders that live in kin groups of 1-6 adult females and up to 9 related sub-adults of either sex. Their social system appears to be egalitarian (all adult females mate and there is no dominance hierarchy), yet not all females are successful in breeding (70% of estruses fail to produce young to emergence). I examined the distribution of reproductive success (skew) in amongst females in a South African population to test if reproduction in these groups is truly egalitarian. The genetic data revealed that only 45% of breeding females weaned offspring and only 8 females produced 41% of all weaned offspring over 5 years. Factors such as experience (parity) and parasite loads affected reproductive success but reproduction was still skewed towards only a few individuals in multiparous or parasite-free females. Why reproduction is so highly skewed in what superficially appears to be an egalitarian species is unclear.

120: Small-mammal community responses to ungulate exclusion and prescribed fire on the East African savanna

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Whether suppression of small mammals by abundant wild and domestic ungulates in savanna ecosystems of Kenya is driven by depletion of nutrients and food resources; or depletion of cover by grazing, browsing and trampling; is poorly understood. We used two replicated large-herbivore enclosure experiments, one each on red sandy loam and black-cotton clay soils; a multiple-scale burn experiment on black-cotton clay soils; and non-adjacent controls on both soil types to examine the abundance, diversity, and biomass of small mammals across sites varying in vegetation cover, forage quantity, and forage quality. Small-mammal density: 1) responded strongly to grass height, which was tallest on nutrient-rich glades (former cattle night pens) where all large herbivores were excluded by electric fencing; 2) was similar between burn areas as a whole (each site's burned plots and adjacent, unburned controls as one sample) and non-adjacent, black-cotton matrix habitat; and 3) within burn sites, was significantly higher on unburned patches than adjacent burned patches; the latter had shorter grass and lower dead-stem density up to 55 months post-burn, although vegetation differences were less following significant rains. Small-mammal density and species diversity on red sand were double that of black cotton; small-mammal abundance was 20-fold greater on fenced glades than matrix habitat on both soils. Results suggest that loss of cover is a primary driver of large-herbivore suppression of certain small savanna mammals.

121^F: Consistent individual differences and long-term cortisol levels in an African ground squirrel

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Personality traits, or consistent individual differences in behavior across time and/or context, have been identified in an increasing number of species. The Hypothalamus-Pituitary-Adrenal (HPA) axis, which culminates in the release of cortisol into the bloodstream, is an important mechanism through which vertebrates respond to changes in their environment and may be a system through which personality traits are mediated. Previous studies have found varying support for the role of blood and fecal cortisol levels in personality differences leading some researchers to suggest that the cortisol response may be responsible for differences in some traits but not others. However, few studies have examined long-term cortisol accumulation in hair, which is not necessarily affected by collection methods and may better represent long-term stress levels that individuals experience under natural conditions. We compared cortisol levels obtained from hair samples to scores of boldness, exploration and docility in a free-living population of female Cape ground squirrels (*Xerus inauris*). Preliminary results have found no significant relationships between cortisol and personality assays suggesting that long-term stress may not play a significant role in consistent behavioral differences observed among individuals.

122: Don't forget about the little ones: assessing continent-wide knowledge gaps for Africa's small carnivores

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African small carnivores - species with adult body mass < 15 kg - represent about 35% of extant small carnivores worldwide. Eight of the world's nine terrestrial carnivore families have representative species meeting this criteria in Africa (Canidae: 14% of African small carnivores; Eupleridae: 8%; Felidae: 9%; Herpestidae: 32%; Hyaenidae: 1%; Mustelidae: 12%; Nandiniidae: 1%; and Viverridae: 21%). In spite of

this diversity, studies on Africa's larger species seem to dominate carnivore research in this region. In order to both quantify research bias and highlight knowledge gaps for small, African carnivores, we undertook a thorough literature review of all published works on African carnivores, both large and small. We identified 8,867 published records for all carnivore species including duplicates. Of these, a total of 6,177 papers or more than 69% of all papers focused on at least one of the 10 large carnivore species, compared to 30% or 2,690 for the remaining 81 small species. Utilizing titles and abstracts we scored papers across 21 categories to identify particular areas of research lacking for individual species. For African small carnivores, a majority of research to date has focused on peripheral inclusion of species in broader studies (e.g. carnivoran phylogenies, morphological evolution), evolution of sociality in mongooses, and distributional records/observations. For a majority of Africa's small carnivores, little to no research exists on the fundamental ecology or conservation status.

123: Identification of genomic regions of divergence across a mammalian hybrid zone

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The availability of genomic data has increased substantially over the past few years. As a result, the opportunities for hybrid zone research and the ability to work with non-model organisms have expanded. *I. parvidens* and *tridecemlineatus* hybridize in isolated populations within southeastern New Mexico and West Texas as a result of secondary contact due to recent changes in climate. Identifying rapidly diverging regions in *I. parvidens* and *tridecemlineatus* genomes will provide insights into genes under selection, factors limiting introgression, and genetic components responsible for reproductive isolation. We used double digestion restriction-site associated DNA sequencing (ddRADseq) to identify SNPs in hundreds of individuals of both taxa and known hybrids to identify regions of low heterozygosity (high F_{ST}) genetic components associated with species. Genome annotations and gene ontologies for low heterozygosity regions were used to build a list of phenotypic and genetic traits that have undergone divergent selection in each species. This hybrid zone provides an excellent opportunity to address evolutionary questions in a non-model system.

124^E: Movement patterns of *Peromyscus leucopus* across the Upper Peninsula of Michigan during a 30-year expansion

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Climate change is one of the largest drivers of biodiversity loss, but not all organisms are negatively affected by environmental change—some species are expanding into new territory. The presence of ecological corridors can facilitate the establishment of novel populations, while poor connectivity between patches of high-quality habitat can lead to founder effects. The white-footed mouse, *Peromyscus leucopus*, has established new populations across Michigan's Upper Peninsula over the past thirty years. This expansion presents the opportunity to understand movement patterns of a small rodent into novel territory. We hypothesize that the recent expansion of *P. leucopus* occurred as animals moved through short, direct, and heterogeneous ecological corridors. Five populations from across the Upper Peninsula were sampled, mice from each population were genotyped across 10 microsatellite loci, and population genetic structure was analyzed using GenAIEx and STRUCTURE. These genetic measures were used as correlates in an analysis of geographic data, which were collected from the USGS and used in a path analysis in ArcGIS software. The path that is most relevant to the genetic structure of the populations is determined by Akaike's information criterion. This study shows how rodents can use ecological corridors to rapidly expand their ranges into new territory, and may provide insight as to how other small mammal taxa may be expected to respond to climate change.

125^E: Population genomics of the mountain treeshrew (*Tupaia montana*) in the sky islands of Borneo

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The mountain treeshrew (*Tupaia montana*) is a small mammal endemic to the mountains of Borneo. It has a disjunct range over several isolated “sky islands” including Mount Kinabalu and Mount Tambuyukon. On both mountains, *T. montana* occurs at high densities from approximately 900m to 3200m above sea level. The two mountain treeshrew populations are separated by ca. 18 km of lowland forest habitat that is occupied by several congeners. We tested the hypothesis that this lowland habitat poses a barrier to dispersal and gene flow between the two sky island populations, leading to genetic subdivision. We densely sampled treeshrews along elevational gradients on both mountains and used DNA capture methods to sequence both mitochondrial genomes and a large number of unlinked ultraconserved element (UCE) loci. Our data show well-resolved but phylogeographically discordant patterns of population subdivision. Fine scale analysis of genetic structure reveals a signature of two genetic clusters in both the mitochondrial and nuclear data sets but these clusters do not correspond to the two mountains and are discordant between the two types of markers. The two sky island populations have high levels of genomic variation, low F_{st} values, and weak genetic structure. We explore several potential biogeographical scenarios, including intermittent habitat connectivity during Pleistocene interglacial periods, that may explain the complex patterns observed.

126: Source-sink dynamics and barriers to gene flow in Alaska red foxes

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Red foxes occur statewide in Alaska and are a spillover host for rabies, so their population structure and patterns of gene flow are important information for trying to understand the potential for rabies outbreaks to spread into Interior Alaska. We studied variation in 9 microsatellite loci in 257 red foxes collected across the entire state except southeastern Alaska. Spatial principal components analysis identified 5 regional populations (Southwest, Seward Peninsula, North Slope, Interior, and Southcentral), which were distinct when using discriminant analysis of principal components. We found that migration rates between tundra habitat (Southwest, Seward Peninsula, and North Slope) and boreal habitats (Interior, Southcentral) were much less than rates between populations within those regions. This suggests that tundra and boreal regions may harbor distinct units of foxes, which is borne out by F_{st} values. This also lends support to the idea of tundra and boreal ecotypes of red fox. Model selection using reversible-jump MCMC analysis selected a model with boreal/tundra as a variable 80% of the time versus a null model. Fifty percent of genetic variance was explained by the tundra/boreal model. With limited gene flow from tundra to boreal regions, red fox does not appear to be a great threat to be a rabies vector across regions. Finally and interestingly, Southcentral was a complete source for foxes, receiving no migration from any population.

127: Tracking translocations: interdisciplinary approaches to investigating the origins of the California Channel Island mammals

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As many recent genetic and archaeological studies have shown, humans have intentionally and unintentionally moved plants and animals around the world. The California Channel Islands provide a unique environment to explore ancient translocations due to their close proximity to the California mainland, long human occupation (~13,000 years) and limited terrestrial diversity. Here we present our interdisciplinary approach to investigating the origins of California Channel Island terrestrial mammals integrating archaeological, isotopic, genomic and radiometric datasets to explore the role of human agency in island biogeography. Additionally we propose a number of possibilities for why ancient peoples might have introduced these taxa.

128: Tiger conservation through a genetic lens

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Tigers are emblematic of conservation, and India harbors around 60% of the world's wild tigers. We used genetic data from wild populations to understand their relatively recent past and current connectivity in a hope to predict future trajectories. Modern and historical data support a recent, anthropogenic population bottleneck. Genome-wide SNP data help identify tiger landscapes. While the total numbers of tigers in India have increased due to focused conservation efforts, the median population size is 19. Future survival is critically dependent on exchange between these fragmented populations. Is such connectivity possible in a developing India? In recent analyses, we used genetic data from 116 individuals from the Central Indian tiger landscape to infer how human footprints, agriculture and forests impact connectivity. We modeled landscapes 100 years into the future, and assessed impacts of different development scenarios on connectivity and extinction using spatially explicit landscape genetics simulations. Our results suggest that connectivity between populations will decrease with high risk of local extinction in many small and/ or isolated populations. Decreasing extinction will require stepping-stone populations that act as corridors between larger populations. Our results can prioritize mitigation efforts associated with development activities, providing a link between science and policy.

129^E: Linking climate and habitat to nutritional condition and recruitment in moose

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A major goal in population ecology is to understand factors underlying density-dependent and density-independent shifts in demography. Life-history theory predicts that nutritional reserves of long-lived mammals should be allocated to reproductive effort in a state-dependent manner because survival is highly conserved. Consequently, the effects of climate and density on reproductive success are often mediated through nutrition. Recruitment rates in many moose (*Alces alces*) populations across the Intermountain West are declining, even in areas lacking large carnivores, which suggests bottom-up limitation. From 2011–2014, we measured habitat condition via an index of willow (*Salix spp.*) condition, autumn nutritional condition of harvested animals using a kidney fat index, recruitment of young from aerial surveys, and climate using remotely sensed data across eight moose populations. We evaluated models describing both temporal trend in recruitment and annual recruitment rates. Willow condition and kidney fat predicted trend in recruitment, but prediction of annual recruitment required additional climatic data, suggesting that increased habitat quality and nutritional condition buffer against unfavorable climatic conditions. Our work indicates that life-history theory provides a useful conceptual framework through which reproductive effort of long-lived large herbivores can be linked to shifts in nutritional condition stemming from habitat and climatic conditions. Thus, monitoring habitat and nutritional condition of large herbivores should allow managers to preempt prolonged declines in recruitment.

130^E: Understanding the past, present, and future of a rare species: modeling distribution shifts

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In light of evidence of global climate change, it is becoming increasingly important to understand past and present-day distributions of species to better predict future distribution shifts. However, obtaining this fundamental information for rare taxa is often difficult, and represents a challenge for identifying effective conservation strategies. The Texas kangaroo rat (*Dipodomys elator*) is a rare and potentially threatened species that has historically occurred at two localities in Oklahoma and within 10 counties in north-central Texas. Due to its small geographic distribution and potential population decline this species is currently under consideration for heightened conservation efforts. We surveyed 454 sites across the historical distribution of *D. elator*. Using historical museum records and occurrence records from these surveys, we developed distribution models with land cover, soil, and climate data to identify the probability of *D. elator* occurrence under past, present, and future conditions. Model results indicate a reduction in the number of areas with high probabilities of *D. elator* presence, as well as the importance of temperature and seasonality to the distribution of *D. elator*. Results from this work should improve the understanding of factors contributing to the apparent rarity of this kangaroo rat species and its vulnerability to future climate change, along with implications for improving conservation and management strategies for threatened and endangered species.

131^F: Bat cravings: dietary variation during reproductive periods of Seba's short-tailed fruit bat

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Optimal foraging theory is based on the premise that an individual will efficiently collect and handle food while maintaining a diet that maximizes fitness. Dietary choices are influenced by extrinsic and intrinsic factors such as reproductive status. Pregnancy and lactation in females can be energetically expensive. Whereas energy availability may be one of the main precursors to reproductive success, nutrients such as calcium and nitrogen can also limit reproduction. Since energy and nutrient costs are high during reproduction, choices of foraging strategies or diet may be critical for survival of both mother and young. Our research analyzed diet of Seba's short-tailed fruit bat (*Carollia perspicillata*) during reproduction. Dietary analysis was done on fecal samples from males and non-pregnant, pregnant, and lactating females at the Macaregua Cave in Santander, Colombia. We predicted three outcomes. Firstly, with pregnancy and lactation being energetically expensive and reproductive periods occurring during high fruiting periods, we predicted that reproductive females will have a more generalist diet compared to males and non-reproductive females. Secondly, to fulfill calcium demand associated with skeletal growth, we predicted that lactating females will consume fruits that are calcium-rich than non-reproductive females and males. Thirdly, due to the importance of nitrogen in the development of tissues, we predicted that pregnant bats will consume a greater amount of fruits that are nitrogen-rich compared to males and non-reproductive females.

132: Understanding ecological, phenotypic, and genetic effects on the movement and spatial configuration of *Peromyscus leucopus*

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One of the most influential mechanisms affecting a species' evolutionary trajectory is gene flow via dispersal. Factors that can influence an individual's propensity to disperse may be biotic or abiotic, including sex, physical condition, and landscape heterogeneity. Understanding factors significantly affecting movement patterns may give insight to the species' evolutionary trajectory. Due to their abundance and often-widespread distribution, many rodent species represent ideal model organisms to investigate the relationship between biotic and abiotic factors and individual movement patterns. Across

North America, one such species is the white-footed mouse, *Peromyscus leucopus*; a species considered to be a habitat and food generalist. Here, we investigate the effects of sex, morphology, relatedness, and habitat type on *P. leucopus* movement and spatial organization. A grid of 152 traps, covering an area of approximately 60,800 m² and spanning both prairie and woodland habitat, was monitored from June-December 2015. Upon initial capture, basic information was recorded, individuals were implanted with a unique PIT tag for ease of identification during subsequent captures, and a biopsy tail sample was collected for genetic analysis. Samples were genotyped at 8 microsatellite loci in addition to mitochondrial gene sequencing. Results will be discussed.

133: Survival of black-footed ferrets before and after a plague epizootic in South Dakota

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Endangered black-footed ferrets (*Mustela nigripes*) were reintroduced to Conata Basin, South Dakota from 1996-1999, resulting in a self-sustaining wild population. Sylvatic plague, caused by the bacterium *Yersinia pestis*, partially caused the near extinction of ferrets in North America during the 20th Century and remains a challenge for recovery of the species. The Conata Basin population thrived without plague but an epizootic began in 2008. Our objective was to estimate survival rates of ferrets before and after a plague epizootic to better understand population vital rates needed to sustain this species in the wild. We used spotlight surveys to locate and identify tagged black-footed ferrets from 1998-2012. Program MARK was used to estimate survival rates. We built capture histories for 1,589 black-footed ferrets and estimated annual survival before and after plague for both sexes. Annual male survival was 0.37 for juveniles and 0.36 for adults before plague and decreased to 0.15 for all age classes after plague. Annual female survival was 0.61 for juveniles and 0.52 for adults before plague and decreased to a low of 0.18 for all age classes after plague but increased again to 0.40 by 2012. Our results indicate female black-footed ferret survival may rebound after a plague epizootic. Survival of males remained low after a plague epizootic indicating that male survival may be critical to sustain ferret populations in plague-impacted ecosystems.

134^F: Factors influencing mule deer neonate survival

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Population dynamics of large herbivores are especially influenced by juvenile survival and recruitment relative to other demographic parameters. Many factors have the ability to affect juvenile survival during the first months of life when mortality is the highest. We used program MARK to determine the effect of a variety of parameters on the survival of mule deer neonates at Starkey Experimental Forest and Range during 2014 and 2015. Parameters included the mothers ingesta free body fat, over winter supplemental feeding, neonate birth dates, weights, and body condition, normalized difference vegetation index values, instantaneous rate of green-up values, mean daily precipitation and temperature, and the amount of overstory cover, woody debris, and aspect at birth sites. Additionally we determined how survival probabilities changed with the age of a neonate. Our results indicate that survival is most variable during the first month of life in our population, after which it begins to stabilize at a survival rate of 99%. South facing slopes at an individual's birth site were also significant in our best model for neonate survival. South facing slopes tended to be warmer and drier than north facing slopes, creating a difference in vegetation among slopes. This difference in vegetation and climate at a birth site may increase the likelihood of a neonate surviving when it is the most vulnerable, following birth.

135: Habitat use of the San Bernardino flying squirrel in a post fire landscape

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Wildfires affect species worldwide and their occurrence is expected to increase with climate change. Species dependent on mature, intact forest are negatively affected by such fire events. The San Bernardino Mountains of Southern California have experienced a number of these events recently, which has affected a high elevation forest obligate found in these mountains, the San Bernardino flying squirrel (*Glaucomys sabrinus californicus*). Extirpation from the nearby San Jacinto Mountains and the isolated nature of the remaining population has led to this subspecies being reviewed for protection under the Endangered Species Act. We focused on the 355 ha area affected by the 2007 Grass Valley Fire near Lake Arrowhead, CA, much of which was documented habitat for the San Bernardino flying squirrel. This fire resulted in a landscape containing patches ranging from heavily burned to intact forest. We used hair tubes and trail cameras to assess presence and occupancy of flying squirrels across burn severities and habitat types. Our analysis of photos shows flying squirrels occurring frequently in unburned to moderate burn severities that contain a high number of large, live trees. By using non-invasive methods to assess occupancy, we aim to safely and accurately estimate the presence of a sensitive species, determine to what extent its habitat use is affected by fire, and inform management practices in fire effected ecosystems.

136^{E,TA}: Effect of forest opening landscape characteristics, prey abundance, and vegetation structure on bat activity

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Over the past century, abundance of early successional habitat (ESH) in hardwood ecosystems of the eastern United States has decreased resulting in the decline of many ESH dependent species. In response to these declines, some land managers have initiated programs to restore ESH. However, the effect of ESH restoration on bats is not well understood. Our objective was to determine how forest opening size, presence of edge, vegetation structure, and prey abundance affects bat activity within forest openings. We placed Anabat SD2 acoustical detectors at the interior and edge of small (0.13 – 2.01 ha), medium (2.02 – 6.07 ha), and large (> 6.07 ha) openings in the Nantahala National Forest, North Carolina during summer 2014 and 2015. The insect community was sampled using modified Malaise traps and vegetation structure was quantified. Differences in mean insect abundance and bat activity between treatments was tested using mixed effects general linear models. We found that insect abundance and activity for all bat species detected did not differ significantly among opening sizes or interiors and edges. However, tree density and shrub cover negatively affected *Eptesicus fuscus* and *Lasiurus borealis* activity, although *Myotis spp.* responded positively to coverage of herbaceous plants >1 m. The results of our study suggest that when restoring ESH in the southern Appalachians, managers should strive to maintain open forest structures to foster bat foraging activity.

137^{TA}: Assessing calf survival and cause-specific mortality in the declining moose population in northeastern Minnesota

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Recruitment is an important driver of population dynamics. The northeastern Minnesota moose population has been declining since 2006. Our research was initiated because survival and specific causes of mortality of calves were largely unknown. We placed GPS collars on neonates during 2013 and 2014 to estimate survival, cause-specific mortality, and space use of calves and their mothers, but due to an executive order we were precluded from collaring in 2015. Using an alternate method involving behavioral cues from already collared moose and helicopter surveys, we continued the study. Survival of calves 2013–2015 dropped precipitously in the first 30 days of age (~40% mortality). Thirty-one of 40 collared calves (77.5%) died by 9 months of age in 2013–2014. Surveys indicated 56% mortality by 7 months of

age in 2015. In 2013–2014, 84% of mortalities were due to wolves or black bears. In 2015, we investigated 31 instances of cow behavior indicative of calf mortality, resulting in the discovery of 6 wolf-kills, 1 bear-kill, and 2 unknown predator-kills. Tracking cow movements was a reliable way to estimate calving in all years and to a lesser degree calf mortality in 2015. Identifying causes of calf mortality and understanding their relations to various landscape factors should yield insight into mechanisms contributing to the declining population and serve as a basis for an ecologically sound management response.

138: Up and down and all around: *Peromyscus* population responses in a long-term forest management experiment

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The Missouri Ozark Forest Ecosystem Experiment Project (MOFEP) assesses landscape-level ecological responses to alternative forest management strategies (even-aged vs. uneven-aged vs. no-harvest approaches) in Missouri oak-hickory-pine forests. The project uses mark-recapture sampling to assess small mammal populations each sampling year. We used hierarchical mark-recapture models to examine treatment effects on *Peromyscus* (*P. leucopus* and *P. maniculatus*) abundance pre-treatment (1994-1995), after the first (1996) forest harvest entry (1998-2001, 2008-2010), and after the second, 2011 harvest entry (2012-2014). Even-aged and uneven-aged forest management increased *Peromyscus* abundance compared to no-harvest management in the first 5 years after each harvest entry. In even-aged treatment sites, the positive treatment effect initially was localized near harvested patches, as only approximately 10% of each site was clearcut-harvested per entry. However, by years 4-5 after harvest, *Peromyscus* abundance in even-aged treatment sites had increased site-wide, and this response was no longer localized to harvested patches. Effects of harvest treatments on abundance had partly dissipated 13-14 years after the 1997 harvest entry. Our results indicate complex spatial-temporal patterns of change in *Peromyscus* abundance during the first two decades of this experiment. These patterns likely reflect the rapid re-establishment of tree and tall shrub cover in harvested areas within the first decade after harvest, supporting higher mouse abundance until harvest effects dissipate as the tree canopy cover and understory cover return to pre-treatment levels.

139: Spatial ecology of a mesocarnivore to inform about future disease management

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Space use is a fundamental characteristic of a species' ecology that informs our knowledge about habitat selection, movement across landscapes, and inter- and intraspecific interactions. The spatial ecology of gray foxes (*Urocyon cinereoargenteus*) is poorly known in the southwestern US. Gray foxes may be a substantial reservoir for rabies in the Southwest; knowledge of gray fox movements across an expansive geographic area can improve the success of any potential disease management plan where they are believed to be a vector. Understanding how foxes use the landscape is important for controlling the spread of rabies in case of an outbreak. We will use data from satellite collars on gray foxes in the White Mountains and Pinaleño Mountains, Arizona, to compare habitat selection, movement patterns, and home range requirements in a well-connected landscape and an isolated sky island. In addition, we will use a grid of remote wildlife camera traps to learn about density and co-occurrence with other carnivores. Through the application of occupancy modeling and resource selection functions, we will compare habitat use and resource selection between continuous and isolated forests. Our results on the spatial ecology of gray foxes can be used to inform Arizona-specific disease control plans, but also can be applied more broadly across the southwestern United States, and other areas where rabies continues to be a wildlife-management and public health challenge today.

140: Using drones and thermal imaging for night ungulate surveys in forests—opportunities and challenges

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The reliable assessment of population size is required for effective ungulate management and conservation. Yet, none of the several ungulate monitoring methods is satisfying in terms of cost-effectiveness and precision. A new method combining two modern technologies: unmanned aerial vehicles (drones) and thermal infrared (TIR) imaging may have great potential as a tool for ungulate monitoring. In addition to having all of the advantages of aerial surveys, it also enables operations at night, when ungulates are most active and easy to detect. To assess the feasibility of the proposed method we use a fixed-wing drone equipped with TIR camera to conduct test surveys in different forest types and at different times of the day. During tests in Drawieński National Park, Poland in April 2015 (covered areas ~100–200 ha) we detected animals both in leafless deciduous forests and in broken canopy coniferous forests. The time of day highly influenced the results—during the noon flight we discovered only 1 animal while during the flights conducted in the morning, evening and at night we recognized from 12 to 29 ungulates. Our preliminary results show that drones with TIR sensors are a suitable tool for ungulate surveys. The main challenges of the method are law regulations (drone operations limited to visual line of sight), high dependence on weather, and relatively low resolution of TIR cameras hindering species identification.

141: Fleas of kit foxes (*Vulpes macrotis*) at Dugway Proving Ground, Utah

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Fifty-five kit foxes (*Vulpes macrotis*), 25 females and 30 males, were collected at Dugway Proving Ground, Utah in 2012 and 2013. Foxes were examined, sexed, measured, fitted with radio collars, and combed for ectoparasites. Five hundred seventy-five fleas of 5 species were collected as well as approximately 100 ticks, not yet identified. Fleas identified included *Pulex irritans* (568), *Meringis parkeri* (4), *Aetheca wagneri* (1), *Foxella ignota utahensis* (1) and *Peromyscopsyllus hesperomys adelpha* (1). Mean intensity and prevalence of flea infestation were examined over three 4-month intervals of the year designated breeding, pup rearing, and dispersal. There was no difference in mean intensity of fleas on foxes over the year as determined by a χ^2 test.

142: Temporal and spatial comparison of the impacts of logging on white-footed mice

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Habitat fragmentation, such as logging, has multiple effects on small mammal populations. Because small mammals affect forest regeneration and serve as prey for many larger species, the effects of logging on small mammal populations could have large impacts on overall forest community structure. We used mark-recapture methods in live trapping grids in logged and unlogged sites in a small forest in Pennsylvania. We estimated population sizes of white-footed mice (*Peromyscus leucopus*) in a long-term grid across multiple years and sites to determine how logging impacted this species. We also assessed population densities in areas with different types of logging (select-cut, clear-cut, salvage logging, and undisturbed habitat) to determine the short-term effects of habitat fragmentation. Within year comparisons showed higher population densities in unlogged versus logged areas. The magnitude of this effect depended on the type of disturbance, however, with the clear-cut site having the lowest population density. Comparing the post-logging densities to pre-logging densities, we found significantly higher densities pre-logging, but this was likely due to an abnormally high density in 2004. We found significant differences in vegetation patterns between pre- and post-logging data including the appearance and dominance of an invasive grass species. Overall, we conclude that logging has some impact on small

mammal populations, but these impacts are likely due to microhabitat changes rather than changes at the larger spatial scale.

143^{E,TA}: Flesh off the bones: calculating late Quaternary canid body-sizes from fossil fragments for paleoecological study**

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Mass is a characteristic that imposes constraints; from metabolic rates to energy flow through food-webs, body-size is a widely studied character in ecology. While mass is easy to measure in living individuals, it is more challenging to measure in fossils. Relationships between skeletal structures and mass have been used to estimate body-size from remains, but has been limited to a few postcranial elements. To increase the utility of skeletal remains for studying body-size, modern collections were used to establish relationships between mass and 24 skeletal measurements across the Canidae. These included dental, cranial, as well as limb bone and partial ephiphyses typically found as fossils. Relationships had very high r-squared values, low average percent standard error of the estimate, and low percent prediction error. This study increases the potential number of elements that can be used to estimate mass in fossil canids. Body-size estimates were made for canids from seven Pleistocene and eleven Holocene faunas in west central Texas. Mass estimates for the extinct dire wolf were consistent with those previously published. Mean body-size of extant species did not change significantly over time; however, the Holocene community exhibited a reduction in the abundance of small canids and an increase in medium size canids, including domestic dogs. These changes altered the size profile of the canid community, and likely the ecological function of this guild. This research was supported by an A. Brazier Howell honorarium awarded to Melissa Pardi in 2015.

144: Morphometric divergence and functional similarity in *Sciurus vulgaris* and *Sciurus carolinensis*

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We used geometric morphometric techniques to explore and compare the shapes of dentaries and skulls in 4 species of tree squirrels: European red squirrel (*Sciurus vulgaris*), eastern gray squirrel (*S. carolinensis*), eastern fox squirrel (*S. niger*) and western gray squirrel (*S. griseus*). These species were chosen because of current competitive interactions amongst the species, and because of their phylogenetic affinities. A canonical variates analysis of Procrustes shape coordinates revealed significant shape differences between the skulls and dentaries of *S. carolinensis* and *S. vulgaris*. We compared biomechanical properties of the dentaries for the 4 species, and used discriminant functions analysis to discriminate between the species in a jaw-function space. There was extensive functional overlap between *S. carolinensis* and *S. vulgaris*, but not between *S. carolinensis* and *S. niger*. Although the skulls and dentaries of *S. carolinensis* and *S. vulgaris* differ morphologically, they are functionally similar.

145^E: Taxonomic revision of the *Dasyopus kappleri* and revalidation of *Dasyopus pastasae* and *Dasyopus beniensis* (Dasypodidae)

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Dasyopus kappleri is the largest species of the genus *Dasyopus* and is restricted to the Amazonian rainforest biome. Over the last century, related taxa have been described and synonymized without comprehensive analyses, and the current classification involving two subspecies, *Dasyopus k. kappleri* and *Dasyopus k. pastasae*, was never revised. The aim of this work is to clarify the taxonomy of *Dasyopus kappleri* through integrative morphological and morphometric analyses. We examined 70 specimens

housed in scientific collections as well as photographs of the type specimens of five taxa. Three methodologies (discrete characters, linear and geometric morphometric analyses) were employed. All results converge on the recognition of three groups with diagnosable autapomorphies, differences in size and shape of the skull and distinct distribution patterns that we consider as a full species. *Dasyopus kappleri* Krauss, 1862 occurs on the Guiana Shield, north of the lower Amazon; *Dasyopus pastasae* (Thomas, 1901) is distributed from eastern Andes of Peru, Ecuador, Colombia, and Venezuela south of the Orinoco river into the western Brazilian Amazon; and *Dasyopus beniensis* Lönnberg, 1942 occurs in the lowlands of Amazonian Brazil and Bolivia to the south of the Madre de Dios, Madeira, and Lower Amazon rivers. This new arrangement of the *Dasyopus kappleri* complex raises to nine the number of living species of *Dasyopus*.

146: Are coyotes contributing to the spread of Rocky Mountain spotted fever in Arizona?

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Rocky Mountain spotted fever (RMSF) is a tick-borne bacterial infection that can cause permanent disability or death in humans. In 2003, RMSF moved into Arizona and has become increasingly common since then. The vector and reservoir for RMSF has been narrowed down to the brown dog tick (*Rhipicephalus sanguineus*). Domesticated dogs are considered sentinels of RMSF and the brown dog tick's primary host. Large numbers of free-roaming dogs have been implicated in the spread of RMSF on American Indian reservations, where most of the infections occur, but evidence is absent to explain long-range dispersal of this tick species. Coyotes are genetically similar to dogs and have larger home ranges, so we hypothesize that coyotes are contributing to the long-range dispersal of infected ticks. We reviewed 35 publications dated from 1956 to 2015 to establish precedent for coyote-mediated dispersal of these ticks.

147^{TA}: Phylogeography of the Florida mouse (*Peromyscus floridanus*)

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In addition to anthropogenic fragmentation of habitat, historical biogeographic processes can strongly shape the amount and geographic distribution of diversity. We are using microsatellites, mtDNA sequences and genome-wide SNP markers to investigate how the late-Quaternary geological events have affected the intra-specific diversity of the Florida mouse (*Peromyscus floridanus*), a xeric habitat associated species that is currently undergoing status assessment in the State of Florida. Data from 530 samples genotyped at 17 microsatellite loci, and 200 sequenced for a partial mitochondrial gene (cyt b) indicate a high degree of geographic structuring. Samples as close as a few kms have moderately high levels of differentiation that can be due to a number of factors. Our data indicate structuring is shaped in part by the discontinuous distribution of Tertiary ridges where scrub and sandhill habitats predominate. Diversity is greatest at southern latitudes, in particular on the Lake Wales Ridge, which is a center of endemism for many scrub endemic species. In addition to biogeographic structuring, population divergence may be the result of ecological processes, including population dynamics that would lead to a relatively strong role for genetic drift that may overlay historical processes and lead to higher differentiation. These data provide useful insight into what may be a relatively complex biogeographic structure in Florida mice, and may influence conservation assessment decisions.

148^{TA}: Geographic variation in morphological characters in meadow jumping mice (*Zapus hudsonius*) follow Bergmann's Rule

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Organisms with wide geographic ranges often have morphological variation across populations with one explanation being Bergmann's Rule where body size correlates with latitude. The meadow jumping

mouse (*Zapus hudsonius*) is a wide ranging (>50° latitude) North American species with 12 described subspecies (Kruttsch 1954) and represents an ideal model to test patterns of geographic variation. However, some subspecies were originally described using a limited number of specimens and only adjacent subspecies were ever compared. Consequently, the described and often cited differences among subspecies may be the result of Bergmann's Rule and may partially account for much of the debate on subspecies validity. In this study, we used genetically informed morphological analyses and comprehensive taxon sampling to reassess the described morphological variation and test competing hypotheses of geographic variation. We show that northernmost subspecies are larger than southernmost subspecies, suggesting *Z. hudsonius* follows an expected pattern consistent with Bergmann's Rule. Furthermore, described differences fail to reflect significant morphological differences and therefore questions the validity of morphologically defined subspecies. Consequently, this study builds upon previous genetic tests that indicate Holocene expansion of jumping mice, and formalizes a reasonable process by which observed morphological variation evolved. Nevertheless, a more comprehensive approach is needed to thoroughly reassess the taxonomic classification of *Z. hudsonius*, more completely explore geographic variation in morphology, and better account for both spatial and ecogeographic correlates.

149^{E,TA}: Ecology of native mice in midwestern row-crop agriculture and implications for ecosystem services

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Facilitation of agricultural ecosystem services, such as weed seed predation and biological pest control, can improve farmland ecological integrity and reduce costs of chemical inputs to farmers. Native rodents are ubiquitous within midwestern row-crop agriculture and some species (e.g. prairie deer mice [*Peromyscus maniculatus bairdii*] and white-footed mice [*Peromyscus leucopus*]) are known to provide ecosystem services by regulating weed seed and waste grain populations. Few studies have investigated the ecology of native mice within corn/soybean agriculture and a greater understanding of their diets, seed predation, and crop damage behavior will help elucidate the functional role (positive or negative) of these animals within agro-ecosystems. We coupled demographic data with seed predation experiments and stable isotope diet analysis to investigate the ecology of native mice in row-crop agriculture. When presented with cafeteria-style feeding trials of waste grain (corn/soybean) and weed seed, prairie deer mice showed strong preferences for grain, presumably due to the high nutritional value of corn and soybean. However, despite a preference for grain mice were efficient predators of weed seed (~50% consumption) during seed removal experiments, with rates of seed removal varying as a function of crop stage and distance from field edge. Native mice appear well adapted to capitalize on super-abundant and high quality food resources afforded by crop fields, such that their populations reach robust densities (i.e. >20/ha) and have year-round reproduction.

150^F: Flea distribution across American pika (*Ochotona princeps*) populations in North America's Intermountain West

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American pikas (*Ochotona princeps*) are small mammals that are widely distributed across North America's Intermountain West. Previous investigations revealed five geographically distinct mitochondrial lineages within *O. princeps*. These lineages represent genetically distinct pika populations that have been evolving independently in association with different mountain systems of the Intermountain West. In contrast, diversity of endoparasitic helminths are not structured geographically in the same way. Instead there are two primary parasite assemblages, one distributed across southwestern pika populations and one found across the northeastern part of the host range. These contrasting patterns suggest that the shared history of pikas and their parasites had different consequences for the evolutionary trajectories of these organisms. Here we investigate whether or not patterns of ectoparasite diversity suggest a history that is similar to that of the endoparasites. Alternatively, were they more strongly influenced by the factors that isolated host lineages? Specifically, is the distribution of flea species similar to the distribution of the helminths, or is it concordant with the five host lineages? We acquired fleas from 227 pikas across 37

localities in the Intermountain West. These fleas were identified to the species level based on their morphological characteristics, and species distributions were mapped geographically. The distribution patterns of the fleas were then compared with the previously investigated diversity of the endoparasites and the pikas.

151: How black-tailed jackrabbit abundance affects golden eagles: an ongoing study

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Successful golden eagle reproduction relies on the availability of prey. The main prey species for Arizona's eagles is the black-tailed jackrabbit (*Lepus californicus*), which is also in decline. Black-tailed jackrabbits occur in grasslands, shrub-lands, and mixed woodlands, but relationships among their abundance, habitat use, and availability as prey items are not well understood. This study focuses on jackrabbit abundance and habitat selection to determine how these relate to golden eagle breeding success in Northern Arizona. Understanding these predator-prey dynamics will facilitate the management and recovery of golden eagle populations. Recovery experts can use data on jackrabbit abundance and distribution to model quality habitat for eagles. With such models, eagle population trajectories could be predicted, and prey could be actively managed to benefit at-risk populations.

152: Small mammal niche differentiation within the Alexander Archipelago of southeast Alaska

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Stable isotopes allow for investigation of dietary variation and niche space in individuals, populations, and species across time and across environments (i.e. localities). This study investigates dietary differentiation among six species of small mammals including 2 insectivorous shrews (*Sorex cinereus*, *Sorex monticolus*) and 4 herbivorous rodents (*Microtus longicaudus*, *Microtus oeconomus*, *Microtus pennsylvanicus*, and *Peromyscus keeni*). These species were sampled from multiple locations across the Alexander Archipelago of Southeast Alaska to assess the potential role of competition in niche variability. Island populations were selected that vary in the number of potentially competitive sympatric species and multiple mainland localities with diverse levels of species richness were also sampled for comparison. I expect that the isotopic signatures from mainland localities, where there are multiple competitors, will be indicative of niche partitioning. Whereas resource limitations on smaller islands as well as low mammalian richness will lead to isotopic signatures indicative of broader niches. Furthermore, it is expected that isotopic signatures of individuals from medium and large islands with intermediate numbers of competitors will fall between these two extremes. This study sheds light on the role competition plays within this island system and also has the potential to influence future conservation efforts within this area.

153^{TA}: Ecological causes of intraspecific variation in aposematism: a study of the striped skunk *Mephitis mephitis*

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Aposematic signals - bold warning colors and patterns paired with unpleasant defenses in prey species - are predicted to take on similar forms both across and within species facing the same predators to enhance predator memory. Yet some species show considerable individual variation in aposematic signaling, an occurrence that is widely recognized but poorly understood. My research explored the roles of different selective forces and relaxation in selection in shaping aposematic variation within the striped skunk, which shows immense variation in degree of striping both within and between populations. Specifically, I investigated whether coloration patterns are (H1) no longer under intense selection due to fewer contemporary predators, and are (H2) shaped by different predatory threats. For this study, morphometric data was gathered for stripes from 618 selected *M. mephitis* museum skin specimens representative of their North American range, and resulting specimen stripe whiteness indices together

with individual capture locales were compared to predation risk maps. Results supported both hypotheses (H1) and (H2). Specimens from regions of low predator risk showed high stripe variation while specimens from high predator risk areas showed reduced variation, indicating that increased variation reflects a reduction in overall predator risk (H1). Additionally, stripe variation appeared more prevalent in regions of predominantly raptor risk and reduced in regions of mostly mammalian predator risk, suggesting that variation reflects differences in predator type (H2).

154^{E,TA}: Geometric-morphometric analysis of *Dipodomys ordii* dentition: shape change along environmental and climatic gradients

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As the primary interface between a mammal and its diet, teeth and their specialized morphologies reflect the outcome of evolutionary adaptation and ecological processes occurring over both geologic and recent timescales. Geographic variation in dental morphology can be related to several factors, including structured gene flow among populations across complex landscapes and differences in diet, phenotypic plasticity, or tooth wear in relation to climatic conditions, properties of the local vegetation and substrate, and microhabitat use. The kangaroo rat, *Dipodomys ordii*, is a small granivore whose geographic range spans several biomes and strong environmental gradients in western North America. In order to evaluate geographic variation among *D. ordii* populations across the species distribution, we utilized landmark and semi-landmark geometric morphometrics to: 1) quantify shape variation in the occlusal surface of their tooth rows, 2) analyze and correct for the role of ontogenetic wear on tooth shape, and 3) quantify geographic variation in tooth shape in relation to environmental variables. Tooth morphology differs significantly among *D. ordii* populations, and geographic variation in shape is significantly correlated with climate variables, including mean annual temperature and temperature range. Results from this study highlight the utility of this species and its abundant fossil relatives as sensitive paleoclimate proxies for recovering environmental conditions and ecological responses of small mammals to climate change in the past.

155^E: New records and two possible local extinctions from a sky island in the Great Basin

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Understanding the geographic distribution of species is a key requirement for accurate implementation of programs targeting conservation and management of biodiversity. Unfortunately, we still know far too little about the regional distribution of many species, and less of long-term changes in community composition and population dynamics. Fortunately, monitoring programs based on specimen collection can document geographic distributions and allow monitoring of change. During the summer of 2015 we conducted small mammal trapping along an elevational transect (>6000 trap nights) of a sky island in the western Great Basin (Mt. Grant, Mineral Co. Nevada). From these new collections, we report the first vouchers for the mountain and the county including the short-tailed weasel (*Mustela ermine*), mountain cottontail (*Sylvilagus nuttallii*), house mouse (*Mus musculus*), yellow-bellied marmot (*Marmota flaviventris*), western gray squirrel (*Sciurus griseus*), montane shrew (*Sorex monticolus*), and Inyo shrew (*Sorex tenellus*). We also provide the first specimen verification for two species, and visually document three others not previously known from the range but that still require vouchers. Finally, we document possible local extinctions, perhaps due to land use changes, of the American water shrew (*Sorex palustris*) and white-tailed jackrabbit (*Lepus townsendii*). When combined, these new records underscore the value of specimen-based research including monitoring programs targeting new vouchers to measure changes in biodiversity, but also, highlights how little we know of too many wild places.

156: Small mammal population dynamics in habitats associated with northern Michigan old growth white pine forest

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A small mammal population dynamics study was conducted each year from 2002 to 2013 for five weeks during June and July at a research site in Kalkaska County, Michigan. These studies surveyed four microhabitats, an old growth white pine (*Pinus strobus*) forest, a secondary growth pine forest, a kettle bog, and an aspen forest. The study site is located 4.39 km SE of Big Twin Lake (44° 47.147' N, 84° 55.659'W). Sherman traps and pitfalls were the primary tools used to trap small mammals. An assessment and comparison of approximate population size, and species richness were calculated for each year. A Shannon-Weaver diversity index and Peterson-Lincoln index were used to estimate species richness and population size. Throughout the entirety of the surveys, *Sorex cinereus*, *Tamias striatus*, and *Microtus pennsylvanicus* were the most numerous species respectively. The highest species diversity was seen in 2004, whereas the highest number of individuals caught was observed in 2012. During the course of the study northern Michigan was gripped by a protracted drought that had an impacted on the vegetation and the mammalian diversity.

157^E: Cranial and mandibular morphological variation in African *Scotophilus*: examining species limits using a morphometric approach

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Kenya supports more than 110 species of bats, including 40 species of vesper bats (Vespertilionidae), many of which are only weakly distinguished from one another. In too many cases, scientific names cannot be certainly applied to bats in the hand. Clear understanding of variation due to age, sex, and geographic variation is needed to accurately apply currently available names and hence to determine when the proposal of new names is necessary. It goes without saying that accurate nomenclature is needed to understand the ecology, evolution, and agricultural and public health impact of these bats. Cranial and mandibular morphological variation was examined amongst African species of the house bat genus *Scotophilus* Leach, 1821 (Vespertilionidae). Geometric morphometric analyses were used to assess 147 African specimens of *Scotophilus*, based on 17 dorsal, seven lateral, 17 ventral, and ten mandibular landmarks. This analytical framework was used to examine species limits and morphological overlap among populations of *Scotophilus* species in Africa. The analyses identify diagnostic characters and range boundaries for these species and help to clarify the application of existing names to Kenyan bats.

158^E: Geometric morphometric investigation of marten (*Martes* spp.) in northwestern North America

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The number of extant species of marten in North America is controversial, with some authorities suggesting the existence of a single species, *Martes americana* (American pine marten) and others suggesting the presence of a second species, *Martes caurina* (Pacific marten) based on genetic, parasitological, and ecological evidence. The latter species is a potential relict that persisted in a Quaternary North Pacific refugium near the Alexander Archipelago of southeast Alaska. Hybrid zones between these two forms have been identified on Kuiu Island and along the northern Rocky Mountains. This complex history of divergence and contact requires further investigation to better understand contemporary geographic variation and species limits, refine diagnostic characteristics, and ultimately guide management of this economically important furbearer. Geometric morphometrics enables quantification of morphological distinctiveness and characterization of incipient species and hybrid phenotypes. We employ high resolution landmarked images of >300 marten crania from the collections of

the Museum of Southwestern Biology, the University of Alaska Museum of the North, and the National Museum of Natural History. We focus on populations in the Pacific Northwest and test for significant species-level differences and explore patterns of shape evolution across this complex landscape. The morphologic data are compared to genetic investigations and support the existence of two species of marten in North America. *M. caurina* has limited geographic distribution and may require federal protection to ensure persistence.

159: Factors affecting detectability of small mammals in roadkill surveys

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Roadkill surveys are a common method used to determine the vulnerability of species to roads. Surveys are typically done by patrolling roads via vehicles or walking, and noting data associated with any wildlife mortality. Knowing what factors can affect the detectability of small mammals in roadkill surveys is thus important to understand the benefits and limitations of using this methodology. The purpose of this study was to test if speed limit, traffic level, cover level (open agricultural fields vs. closed forested areas), placement on road (shoulder vs. middle of road), and season affect the detectability of small mammal roadkill. I used a variety of roads in southeastern Wisconsin that differed in the aforementioned factors to drop dead feeder rats (purchased commercially), in various seasons, to simulate roadkill of small mammals. I conducted surveys every 12 hours to check the detectability of the feeder rats. My results show that the majority of simulated roadkill specimens disappeared within the first 24 hours. In addition, cover level also affected the detectability of small mammal roadkill. Anecdotal evidence suggests that many of the specimens were removed by crows (*Corvus brachyrhynchos*). My results suggest that the mortality of small mammals may be underestimated in roadkill surveys.

160^F: Opposing seed dispersal and seed predation by mammals for an invasive cactus in East Africa

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The invasive prickly-pear cactus (*Opuntia stricta*) has reduced rangeland quality and altered understory-plant communities throughout much of the globe. In the Lakipia Highlands of central Kenya, olive baboons (*Papio anubis*) frequently consume *O. stricta* fruits and disperse the seeds via defecation. This animal-mediated dispersal can increase germination and subsequent survival of plants, which is of concern to both ranchers and conservationists due to *O. stricta*'s ability to outcompete native plants consumed by livestock and wildlife. However, consumption of seeds by rodents (seed predation) may offset the potential benefits of seed dispersal for cactus establishment. We investigated whether seed predation by an abundant rodent—the fringe-tailed gerbil (*Gerbilliscus robustus*)—could reduce or altogether offset the benefits of seed dispersal for *O. stricta* establishment. We tested if foraging by gerbils was biased towards seeds in baboon feces. Using remotely-triggered cameras, we monitored paired sites, each consisting of a control pile of seeds and a pile of baboon feces containing seeds. We then used a Cox regression model to determine that seed predation was higher for seeds embedded within baboon feces than for control seed piles. These data suggest that high abundances of rodents may disrupt the process of seed dispersal and reduce rates of cactus establishment. Future research should focus on if and how seed predation by gerbils ultimately affects the spread of this invasive plant.

161^F: Using acoustic detectors to document arrival of gray bats (*Myotis grisescens*) at maternity colonies

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Migration is a critically important and understudied aspect of life histories of many bats, and it impacts conservation decisions with respect to distance traveled, disease susceptibility and spread, and seasonal habitat requirements. The federally endangered gray bat (*Myotis grisescens*) is a migratory species with documented infections by *Pseudogymnoascus destructans*, the fungus that causes white-nose syndrome. Gray bats are cave-obligate, and migrate between discrete hibernacula and maternity caves. We

documented gray bat seasonal movements in Missouri at 4 maternity sites from January to May 2015 using acoustic detectors and analyzed patterns of arrival using the R package PVAClone. We generated estimates of r and K as measures of arrival rate and an index of population, with and without observation error. These values were plotted against that cave's distance from a major hibernacula to examine whether distance had an effect on the arrival of gray bats at a site. Values of r varied between ~ 0.3 and ~ 0.9 and K varied between 981 and 3020 among maternity roosts, and estimates were consistent between models with and without observation error. While bats arrived at the closest maternity colony quicker and in greater numbers, the remaining rates and indices were equivocal with distance. This method could be useful for wildlife management officials who want to monitor phenology of bat migrations and changes in population size at sites with seasonal aggregations.

162^F: Habitat use and species composition of bats in a northeastern coastal plain ecosystem

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Cape Cod National Seashore (CACO) is on a coastal plain peninsula where our understanding of bat assemblages, habitat associations, and other ecological information is limited to historic work from the early 1900's. We deployed acoustic detectors at 61 sampling points from 1 June to 21 July 2015 for 4 visits per sample point to investigate species assemblage and habitat use. We conducted vegetation surveys to quantify canopy cover, forest clutter, and ground cover type, and used remote sensing data to quantify distance to road and water around sample points. We will discuss local and landscape conditions associated with habitat use and species assemblage on CACO and show detection data to model co-occurrence probabilities in an effort to learn more about species niche partitioning with a focus on the recently listed northern long-eared bat (*Myotis septentrionalis*). Our preliminary results show eight of the nine bats expected in Massachusetts, including the northern-long eared bat that was detected in all sampled habitat types. This study will be useful to wildlife managers in the northeast as they evaluate management tools in response to the listing of the northern long-eared bat and declines in many other bat species.

163: Evidence for a relationship between class experience handling wildlife and interest in wildlife careers

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Instructors of organismal courses (e.g., mammalogy) often encounter challenges gaining approval from Institutional Animal Care and Use Committees (IACUC) to conduct class activities including live vertebrates. While many instructors believe class activities allowing interaction with wildlife (e.g., live-trapping) encourage students to pursue wildlife careers in a less biased, more time- and cost-effective manner than individual research internships, evidence is lacking. We developed a 52-question survey to examine the relationship between class experiences with wildlife and interest in wildlife careers. Exploratory factor analysis of 36 responses resulted in 6 internally consistent scales (alpha range = 0.768 - 0.961) measuring aspects of attitude towards wildlife and wildlife careers. Students with prior class experience handling wildlife had greater values for scales representing confidence in attaining a wildlife career ($B = 5.460$, $SD = 1.125$) and desire for a wildlife career ($B = 6.000$, $SD = 0.997$) than students without such experience (Confidence-in-Career: $B = 4.242$, $SD = 1.163$; Desire-for-Career: $B = 4.473$, $SD = 1.5470$); differences were significant (Confidence-in-Career: $t_{34} = 2.963$, $P = 0.006$; Desire-for-Career: $t_{34} = 3.010$, $P = 0.009$). Results suggest class experiences handling wildlife play a role in encouraging students to pursue wildlife careers. Refining survey questions and increasing sample size may yield further evidence for the value of class experiences handling wildlife that instructors can present when seeking IACUC approval of such activities.

164:** **Congressional Visits Day: communicating the importance of biological research to policymakers in Washington, D.C.**

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The Student Science Policy Award (SSPA) of the American Society of Mammalogists is an opportunity for graduate students to visit Washington, D.C., receive public policy training, and participate in the Biological and Ecological Sciences Coalition Congressional Visits Day (CVD). During this two-day event, participants meet with members of Congress and their staffs on Capitol Hill to discuss the importance of federal investment in biological research. We describe our experiences taking part in two different visitation teams during CVD. We also discuss interactions among mammalian research, the legislative process, and policy. CVD is important because it contributes to policymakers' understanding of biological and mammalian research. We believe this increased knowledge will positively affect the decisions of policymakers on Congressional bills that impact the country's natural resources. In addition, federal investment in basic biological research provides the United States with data necessary to make informed decisions about our country's ecological future. Without consideration of biological information, non-scientific factors may dictate our biological research and natural resource legislation and policy. We advocate for greater involvement of natural scientists in the national policy conversation through events such as CVD and Congressional District Visits. The SSPA offers an extraordinary opportunity to become more engaged in the interface between biological science and public policy. This research was supported by a Student Science Policy Award awarded to Elizabeth Flesch in 2016.

165: Amphibious and terrestrial adaptations in the nose of a carnivorous murid: evidence from the turbinates

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Major functional shifts in organisms trigger exceptional adaptations and convergences of phenotypes. The nasal chambers of placentals have three sets of plate-like thin bones: ethmoturbinates, maxilloturbinates, and nasoturbinates, each of which, has a distinct function. The maxilloturbinates are located anteriorly on the skull within the nasal fossa, and are covered in non-sensory respiratory epithelium, with a small amount of squamous epithelium anteriorly. They function to moisten and warm air during respiration, as well as to recover water and heat on exhalation. Upon the maxilloturbinates lie the nasoturbinates, which likely function in orienting air to the posterior part in the ethmoturbinates. Ethmoturbinates and nasoturbinates are covered by a mix of non-sensory and sensory epithelia. The largest sensory area is found on the ethmoturbinates. Mechanisms underlying the adaptations that form the foundations of how these adaptive processes emerge are understudied. Recent advances in X-ray microtomography and functional anatomy gives us the opportunity to examine all the aspects of how organisms adapt to their environments. We propose to integratively study the processes and mechanisms underlying exceptional adaptive changes in island carnivorous shrew-rats. Here we used turbinate surface area as a proxy for olfactory epithelial surface area and compare this parameter across a large sample of murine rodents to document patterns of allometry and to test whether olfactory surface area negatively correlated with degree of carnivoran and amphibious adaptation.

166: Paleobiology of ground sloths and other Pleistocene South American mammals: evidences from 3D humerus geometry

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Long bones can provide useful ecomorphological inferences of mammalian lifestyle. In particular, humerus size and shape are good indicators of locomotory behaviour and manual dexterity in mammals. In order to provide inferences on the paleobiology of Quaternary South American extinct mammals, we started investigating three dimensional humerus size and shape of a broad range of extant species by means of geometric morphometrics. 3D models were first generated using photogrammetry and then 27 three dimensional landmarks were recorded using the software LANDMARK. Preliminary analyses confirm the morphological differentiation of South American prehistoric ground sloths (*Megatherium* and *Scelidotherium*) from the extant arboreal two-toed sloth whose humerus shape appears more similar to that of arboreal primates and flying mammals than to the other Xenarthrans (e.g., giant ant-eaters). Also the extinct Litopternan *Macraeuchenia* and the sabretooth cat *Smilodon* clearly show unique humerus shape that are distinct from that of their extant counterparts (i.e., large ungulates and felids). A strong allometric signal (15% of shape variance) is detected in mammalian humerus shape confirming that the shape of this structure is primarily influenced by load bearing function. Although phylogenetic signal is generally present in humerus size and shape data, a broader taxonomic perspective is needed to interpret extinct mammalian morphologies such as the one exhibited by the unique Quaternary fauna of South America.

167: Intraspecific variation in western subspecies of *Peromyscus maniculatus*

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Approximately 3500 museum specimens of *Peromyscus maniculatus* were studied in an attempt to understand intraspecific variation in body size. As expected body weight was the best predictor of body size. In addition, island mice are larger. However, latitude, altitude, and year trapped (~"climate change") were poorer than expected predictors.

168: Training citizen scientists in the analysis of bat acoustic data

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Citizen scientists are volunteers who collect and or process data as part of a scientific inquiry. Wisconsin's bat monitoring program allows citizens to collect and upload bat calls. The ability to both collect and analyze bat acoustic data provides a better educational opportunity by allowing people to engage with local bat communities. The goal of this project is to determine the best crowdsourcing model to accurately describe bat communities. We wanted to know if the consensus of five citizen scientists working independently performed as well as a single expert. Fifteen teams of 5 mammalogy students each were divided into three treatments. All students received the same level of training. We compared student data to expert and Kaleidoscope Pro Auto ID software by calculating Percent Similarity and Morisita's Community Similarity Index. There was no difference between students working independently and students working together on the same data set. However, the consensus of 5 students working independently performed the same as one expert working on the same dataset. The best crowdsourcing model involves multiple users engaging the same data file at least 5 times.

169^F: Parasite mediated competition between the New England (*Sylvilagus transitionalis*) and eastern (*Sylvilagus floridanus*) cottontail

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Historically common throughout the northeastern United States, the New England cottontail (*Sylvilagus transitionalis*) has experienced declines throughout its range. Loss of early successional habitat and competition with the eastern cottontail (*Sylvilagus floridanus*), introduced in the early 1900s, limit the New England cottontail population. Parasitism and disease may also play a role in limiting New England cottontails, as high numbers of ectoparasites and endoparasites occur at certain times of the year. Moreover, parasite mediated competition may be occurring between the two cottontail species. To

investigate this, we compared endoparasite species of New England cottontails among sites with different proportions of eastern cottontails. We evaluated the proportion of tick species and tick abundance found on New England cottontails and those found on eastern cottontails and compared it to the proportion found in the environment. Protozoan endoparasites of the genus *Eimeria* were examined from both host species comparing morphological characteristics and DNA sequence data. Results from this study will provide insight into the parasite mediated competition between the two cottontail species as well as provide insight on the parasites of the declining species.

170: Comparing identification using salivary amylase and morphology to identify *Peromyscus leucopus* and *P. maniculatus*

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White-footed (*Peromyscus leucopus*) and deer mice (*P. maniculatus*) are two of the most abundant small mammals in North America and are identified as significant seed dispersers, predators of pest insects, prey items of avian and mammalian predators, and disease vectors and reservoirs. These two species are extremely difficult to tell apart in the field. Morphological measurements, typically used for identification, are inconsistent. Reliable identification is possible through different allozymes for salivary amylase. We collected saliva and used cellulose acetate electrophoresis for identification from a variety of sites throughout northwestern Minnesota between 2004 and 2015. We tested over 900 *Peromyscus* saliva samples from a variety of habitats and compared the amylase results with morphological data. Our objective was to definitively identify *Peromyscus* species in a region with high habitat overlap and to examine how well morphological predictors compared to the amylase identification. We found that 33% of the captured mice could not be identified by measurements because of extensive overlap. Additionally, we found 15-25% of identifications based on morphology were incorrect. In sum, the cumulative error when trapping *Peromyscus* results in up to 48% of the mice we captured being unidentifiable or incorrectly assigned to species based on the body identifiers.

171: Interactions between American red and eastern gray squirrels on a college campus

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Tree squirrels (Order Rodentia, Family Sciuridae) are one of few groups to thrive in an urban setting such as on the Concordia College campus in Moorhead, MN. Our campus has a mix of deciduous and coniferous trees and supports populations of both American red (*Tamiasciurus hudsonicus*) and eastern gray squirrel (*Sciurus carolinensis*). These two squirrels are typically found in different habitats, with red squirrels found associated with conifers and gray squirrels found associated with deciduous forest. Over the past year and six months we have collared 47 squirrels and documented over 495 locations. Recently we have observed some shifts in habitat use. During 2014 we observed gray squirrels almost exclusively using deciduous trees and red squirrels using coniferous trees. Over the summer of 2015, we saw a decrease in the number of gray squirrels (high mortality coupled with apparent dispersal) and have seen more red squirrels using deciduous trees. Our hypothesis is that the two species will partition the campus in such a way that gray squirrels will occupy deciduous trees and red squirrels will move back into predominantly coniferous trees. We further predict red squirrels and gray squirrels will have low overlap of locations determined through telemetry.

172^F: Variation in dental morphology among heteromyid rodents in present-day and fossil communities

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Small mammals, such as heteromyid rodents (kangaroo rats and pocket mice), are abundant and diverse in the fossil record and modern assemblages, and are thus useful for understanding the ecological

processes that promote high species richness in relation to biotic interactions and environmental conditions. Present-day communities of heteromyids partition microhabitats and dietary resources; however, the extent of niche partitioning within extinct heteromyid communities is unknown. We used dental morphology as an indicator of dietary ecology among six modern heteromyid communities in the US and Mexico and one fossil community from the middle Miocene (~17 Ma) Crowder Formation of the Mojave Desert. Using linear measurements and geometric morphometrics, we analyzed crown height and occlusal surface area and shape of heteromyid tooth rows. Significant differences in all three measures were found in the upper first molar and lower fourth premolar among co-occurring modern species, although the degree of differentiation varies across sites. These results contrast with species from the fossil assemblage, which do not vary significantly in these dental traits. Our findings suggest that partitioning of dietary resources was less pronounced among diverse heteromyids (six species) in the Crowder ecosystem. Increased productivity and greater resource availability during the warmer, mesic conditions of the middle Miocene Climatic Optimum may have reduced competition and niche partitioning among fossil species, whereas present-day communities comprise fewer species in relatively harsher environments.

173^E: Are tree bats actively foraging at wind turbines in the southern Great Plains?

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Although the ultimate causes of high tree bat fatalities at wind farms are not well understood, several lines of evidence suggest that bats are attracted to wind turbines. One such hypothesis is that bats could be attracted to turbines as a foraging resource if invertebrates that bats prey upon are commonly present on and around turbines. If wind turbines provide a valuable and consistent foraging resource, we may be able to devise targeted strategies to deter bats from foraging at wind turbines. To investigate the foraging attraction hypothesis, we conducted a series of surveys at a wind farm in north-central Texas from 2011-2015 to determine if eastern red (*Lasiurus borealis*) and hoary (*Lasiurus cinereus*) bats forage on invertebrates near wind turbines. First, we conducted light trapping surveys to characterize the invertebrate community. Second, we assessed diet composition using DNA barcoding of the stomach contents of 45 eastern red and 24 hoary bat carcasses collected in fatality searches. Third, we compared the turbine invertebrate assemblage to the diet analysis results. Finally, we compared seasonal peaks in bat fatality with seasonal peaks in invertebrate abundance. We found that the invertebrate assemblage at wind turbines was similar to the invertebrates in the bats' diets, and that those same invertebrates were abundant throughout the survey period. Together these results provide support for the foraging attraction hypothesis.

174^E: The influence of urbanization on boldness and aggression in Merriam's kangaroo rats (*Dipodomys merriami*)

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Urban development can fragment and degrade habitat. Such habitat alterations can have profound impacts on the behavior of wildlife. In urban areas, individuals may occur in close proximity to each other and experience high levels of disturbance, which may increase boldness and aggression in urban-dwelling wildlife. We investigated the influence of urbanization on boldness and aggression in Merriam's kangaroo rat (*Dipodomys merriami*). We predicted that urban development would result in increased boldness and aggression in kangaroo rats in urban versus wild land areas. We live trapped kangaroo rats at 8 sites in and around Las Cruces, NM: 4 urban and 4 wildland sites, from June to September 2014 and May to October 2015, and captured 59 kangaroo rats, 31 from urban and 28 from wildland sites. We placed kangaroo rats into 2 behavioral trials, Mirror Image Stimulation to elicit aggressive behaviors and predator scent to elicit bold behaviors. We found no difference between urban and wildland for either aggression or boldness. However, we found a stronger correlation between aggression and boldness in urban areas. These results indicate that kangaroo rat behavioral correlations may be influenced by urban development even when no difference is found in individually measured behaviors.

175: Do you hear what I hear? Integrating acoustic monitoring into a pika citizen science project

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Detecting recent changes in species distributions is key to mammalian conservation, and enlisting the help of citizen scientists has recently become an effective means of increasing sensitive species detections. American pikas (*Ochotona princeps*) are small, climate-sensitive lagomorphs that are ideal for volunteer monitoring projects because they are charismatic and generally easy to identify. However, because pikas behave differently in marginal habitats and at range edges than they do in typical habitat, citizen scientists may be less accurate at assessing occupancy precisely where declines are most likely to occur. To address this challenge, Cascades Pika Watch is working to integrate “microphone traps” into a citizen monitoring effort in an atypical habitat. We have developed an algorithm that identifies the harmonic structure of pika vocalizations in the spectrogram of ambient sound collected by citizen scientists. Preliminary results suggest that our method has high sensitivity and that true pika calls can be easily distinguished from false positives by a trained volunteer. The algorithm is also efficient and constructed with simple, open source building blocks that can run on any personal computer. Together, our results suggest that acoustic monitoring may be an inexpensive and engaging way for citizen scientists to collect accurate occupancy data at range edges. In addition, this platform could also be leveraged to address questions about pika distribution, behavior and activity levels in other habitats.

176: Niche overlap between sympatric coyotes and bobcats in highland zones of Olympic Mountains, Washington

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The 20th century's extensive range expansion of coyote *Canis latrans* throughout North America may impose negative effects on native carnivores. We investigated the interspecific niche relationships to assess potential for competition between sympatric coyote and a similar-sized felid—bobcat *Lynx rufus*—throughout the highland zones (elevation >1000 m) of Olympic National Park, Washington. Through systematic collection and analyses of scats for both carnivores, we determined food habits and habitat use patterns. To ensure correct determination of carnivore species, we used mtDNA analysis of scats. Scat analysis indicated extensive dietary overlap between coyote and bobcat (Pianka's overlap index=0.97). For both carnivores mountain beaver (*Aplodontia rufa*) and snowshoe hare (*Lepus americanus*) comprised the predominant prey. High dietary similarity indicated the potential for interspecific exploitative competition for mammalian prey, especially in harsh climatic conditions of high mountains. However, observed patterns of habitat selection inferred from scat distribution showed differences between coyotes and bobcats, implying some degree of habitat partitioning. Bobcats preferred relatively dense montane forests (canopy cover >40%) at lower elevations, and avoided the alpine zone, while coyotes inhabited mainly alpine and subalpine zones and mostly avoided forest. We conclude that observed habitat separation may alleviate foraging competition between coyote and bobcat. Whether this habitat separation will decrease potential negative effects of coyote colonization on bobcat abundance, or whether it indicates ongoing displacement of bobcats by coyotes, remains an open question.

177^F: Habitat usage in proximity to wind farms by local bat species in northwest Missouri

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Wind farms are becoming increasingly abundant as development of green energy in the United States becomes a priority. This rapid expansion has come at a cost to local bat populations. Wind farms have been credited for hundreds of thousands of bat kills nationwide and as such has become a priority of research in mitigation measures and understanding bat behavior. This is of increasing concern as bats

are key predators for insects and a prey item for raptors. Our study found that habitat usage varied at the species level *Lasiurus borealis* and *Nycticeius humeralis*, were more active at wind farms while *Eptesicus fuscus* and *Lasionycteris noctivagans* had higher activity in non-wind farm sites. Wind farms were also found to have more diverse bat populations than non-wind farms. There was no difference found in agricultural versus wooded areas, suggesting that the wind farms do attract more diverse populations. A comprehensive understanding of habitat usage in bats will allow the expanding wind farms to have a reduced impact and help conserve the bat population.

178: The University of Alaska Museum's rapidly growing and increasingly utilized marine mammal collection

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With over 125,000 catalogued specimens, the University of Alaska Museum (UAM) houses the 8th-largest mammal collection in North America and is the foremost repository of marine mammal specimens in the U.S., with material from over 21,000 cetaceans, pinnipeds, sea otters, and polar bears. Most of these are represented by frozen tissue samples in the museum's state-of-the-art Genomic Resources facility. In addition to granting regular physical access to specimens, UAM's Department of Mammalogy provides samples from over 1,000 specimens to researchers around the world each year. Recent grants from the North Pacific Research Board and the National Science Foundation are supporting the archival and digitization of over 20,000 marine mammal specimens that remain uncatalogued and therefore unavailable to researchers. Upon completion of these projects, the marine mammal collection at UAM will nearly double in size. We will provide an overview of the current marine mammal specimen holdings, recent research using UAM's marine mammal specimens, and future directions.

179^{E}: Understanding habitat selection by endangered Himalayan musk deer and impacts of livestock grazing in Nepal Himalaya**

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In an effort to understand the habitat selection by Himalayan musk deer (*Moschus chrysogaster*) and explore any potential impacts of livestock grazing, we conducted the present study in a conservation area of central Nepal Himalaya. We recorded data on musk deer and livestock presence and absence (based on signs of fecal pellet, footprint, and resting site) along the elevational transect with associated topographic features (elevation, slope, aspect, distance to water, and vantage-point distance) and vegetation features (tree sp., shrub sp., herb sp., and canopy-cover). Using logistic regression model we found that elevation, aspect, canopy-cover, and tree sp. in the area significantly affect the likelihood of habitat selection by musk deer. In particular, they selected the southern aspect of the area with elevation ≥ 3529 m, canopy-cover $\geq 42\%$, and with stands of *Pinus* sp. and *Abies* sp. Slope and canopy-cover significantly affected the foraging area selection by livestock. They selected the gentler slopes in the northern aspect of the area with altitude < 3529 m and canopy-cover $< 42\%$. Also, presence of one group of herbivore (i.e. musk deer and livestock) was not found to affect the likelihood of habitat selection by the other group. These independent habitat selections are possibly the responses to morphological and behavioral adaptations than to impacts and interactions between these two groups of herbivores. This research was supported by Grants-In-Aid of Research awarded to Kapil Khadka.

180^F: Relationship of masseter volume to diet in different cebids

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Primates exhibit a wide range of diets and feeding habits, including insectivory, exudativory, frugivory, folivory and omnivory. Therefore, changes in muscle anatomy should be visible and indicative of dietary composition and mechanism. Such variation in function should be useful in understanding the evolutionary history of primates and the role of diet in muscle architecture. In this study we analyzed the

muscle architecture of three primates (*Saimiri boliviensis*, *Callithrix jacchus*, and *Cebuella pygmaea*), using iodine stained CT. *S. boliviensis* is primarily an insectivore-frugivore, *C. jacchus*, an exudativore-insectivore, and *C. pygmaea*, an exudativore. We hypothesized that these species would show different masseter volumes due to their varied diets and how much chewing each diet required. The use of iodine stained computed tomography (CT) reduces the risk of damage and allows for the study of muscles with minimal disturbance to them and their associated tissues. Heads from the three cebid species were soaked in an I₂KI (Lugol's solution) in multiple stages and then CT scanned. The masseters were digitally segmented and measured using Amira 5.6. In order to prevent body size from unduly influencing the results, ratios of masseter volume to other cranial features were used to give the data proper context. Preliminary results suggest that larger relative masseter volumes are associated with diets reliant on increased bite force.

181: Evolution on a complex adaptive landscape: diet and jaw shape in Sciuridae

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Convergence is widely regarded as compelling evidence for adaptation, but convergence is strongly contingent on ecological and morphological constraints; absent them, convergence may be rare. Convergence may be especially rare in adaptive landscapes with many-to-many mappings between ecological classes and functions, many-to-one mapping of form onto function, or trade-offs having several possible resolutions. Even in these complex adaptive landscapes, the main explanation for infrequent convergence and for a weak signal of ecomorphological adaptation, may be historical—after an early burst of divergence, lineages neither diverge nor converge. We analyzed mandibular shape in 145 sciurid species and found that convergence is indeed rare but there is a strong signal of ecomorphological adaptation. Aside from the well-recognized case of bark-gouging miniatures, most cases of convergence were not ecomorphological; species with different diets converged on jaw shape. Nevertheless, dietary niche explains 42% of the variation in jaw size and 45% of the variation in jaw shape, even more when lineages are separated by habitat type. That diet explains so much variation results from treating size as part of the ecological explanation for shape and from including an interaction between size and diet. Size is clearly important to feeding performance because bite-force scales with body size; shape compensates for size-dependent functional constraints and the impact of size depends on diet, just as the impact of diet depends on size.

182^F: Species limits in the neotropical nectar bat genus *Anoura*

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The nectar bat genus *Anoura* is one of the most diverse genera within the subfamily Glossophaginae, however species limits and phylogenetic relationships within the genus are unclear. We present a morphological study using 16 cranial and 11 external measurements. Our sampling represents all ten species hypothesis in the genus, including the type series of *A. carishina* and *A. cadenai* as well as specimens used to elevate *A. peruana* and *A. aequatoris* to species level. After conducting the same analyses used in previous research to justify the descriptions of *A. cadenai* and *A. carishina* (PCA and Discriminant functions) we find little support for elevating *A. peruana* and *A. aequatoris* to the species level. When analyzed independently, *A. cadenai*, *A. luismanueli* and *A. aequatoris* seem to be distinct and discrete morphological clusters, however when specimens of *A. caudifer* are included the apparent gaps disappear. The same is true for *A. carishina*, *A. geoffroyi*, and *A. peruana*, suggesting that their species hypothesis should be revised. Growing evidence suggests that diversity in the genus *Anoura* is currently over estimated. We propose the use of Mixture Gaussian Models instead of the usual PCA and Discriminant functions analysis to assess this problem. Our results suggest that in order to clearly understand the diversity of this genus further genetic work is needed.

183^E: Perfect timing: the coevolution of the sensory brain and temporal niche in rodents

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Temporal niche is a key determinant of the biotic and abiotic factors to which an animal is regularly exposed, resulting in discrete sensory environments for diurnal and nocturnal animals.

Although the earliest mammals were probably nocturnal, evolutionary transitions to diurnality, and sometimes back again to nocturnality, have occurred numerous times across mammals.

Here, we examine sensory adaptations in the brain that accompany evolutionary shifts in temporal niche, focusing in particular on visual and auditory investments. We tested the hypothesis that diurnal species, when compared to nocturnal species, invest more heavily in visual brain centers than in auditory brain centers. Brain tissue was collected from 32 individuals, representing four nocturnal and four diurnal species, from the largest extant order, Rodentia. For each brain, we measured the volumes of two visual processing structures (Lateral Geniculate Nucleus, Superior Colliculus) and two auditory processing structures (Medial Geniculate Nucleus, Inferior Colliculus). Preliminary data suggest that evolutionary transitions in temporal niche prompt changes in the utilization of sensory information, as well as tradeoffs in the allocation of visual and auditory processing tissues. This research was supported by Beacon: An NSF Center for the Study of Evolution in Action.

184: Seasonal shifts in foraging strategies of eastern gray squirrels (*Sciurus carolinensis*): time-minimization to energy-maximization

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Many mammals rely on one of either two strategies to optimize their feeding efficiency: time minimization or energy maximization. Here we argue that Eastern gray squirrels rely on both strategies by shifting from a strategy of time minimization early in the fall to one of energy maximization later in the season. We followed the feeding and scatter-hoarding behavior of individual, free-ranging gray squirrels over two years from early autumn to mid-winter while feeding on acorns two species of oak (*Quercus rubra* and *Q. palustris*). We measured time invested in eating and caching each item, and the distance each acorn was dispersed before caching. Eating times, caching times, and the distance acorns were moved increased steadily through autumn. When possible we recovered all remaining fragments of acorns when eaten, and recalculated feeding efficiencies. These results suggested that while squirrels invested more time per acorn later in the season, they were eating more carefully. Hence actual feeding efficiencies were nearly similar across the season suggesting that squirrels were minimizing time invested per acorn in the fall while maximizing energy gain later in the season. A supplemental feeding experiment late in the season reduced caching frequencies but did not modify feeding strategies. We discuss the potential implications for these shifting strategies for both foraging efficiency and seed dispersal by the squirrels.

185: Oak dispersal by rodents across a rural-urban gradient

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The effects of urbanization on species richness is well established, yet we understand very little of the impact of urbanization on plant-animal interactions and related ecological processes. Oaks and their seed dispersers are an ideal system to study the effects of plant-animal interactions in anthropogenic-dominated landscapes. Our study monitored the feeding and caching decisions of small mammals and their dispersal of acorns of pin oak (*Quercus palustris*) and red oak (*Q. rubra*) across a rural, urban and suburban gradient in northeastern Pennsylvania. We presented 75 acorns of each species in 30 different exclosures that prevented access by larger acorn consumers, such as deer, but allowed access by rodents. In urban sites, seed removal occurred at a slower rate compared to rural

sites. As urbanization increased, we also observed an increase in dispersal distance, along with a higher directionality of dispersal patterns. This result is likely due to the lower availability of suitable cache sites in urban areas. We observed little variation in caching frequency, which is likely to vary more with seasonality and seed abundance. We conclude that increasing urbanization influences spatial patterns but not frequency of acorn dispersal.

186^E: Rates and patterns of morphological diversification in two clades of Philippine murine rodents

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A key question in evolutionary biology is how the increase in morphological diversity among species (“disparification”) occurs. This question is typically explored through inference of rates and/or patterns of disparification, which are then interpreted in terms of the broader evolutionary and biogeographic histories of the focal taxa. We argue that analyzing both rates and patterns of evolution will yield the best understanding of how disparification occurs. The members of the two morphologically-diverse “Old Endemic” clades of endemic Philippine rodents, the Phloeomyini and Chrotomyini, provide an ideal system to examine this process in the context of independently-colonizing, potentially competing lineages. We combine mandibular geometric morphometrics with phylogenetic information obtained from 49 species of Philippine murines to estimate the patterns of disparity, morphospace occupancy, and rates of morphological evolution. Our analysis of patterns of disparity suggests that interspecific interactions play a strong role in influencing disparification, with most disparity originating early in the evolution of each clade and no morphospace overlap occurring between clades along the first two principal component (PC) axes. Estimates of rates of disparification reveal no consistent pattern when examining standard or phylogenetically-corrected PC data. Our results indicate that both rates and patterns of disparification are important to consider not only because they provide different and complementary contexts for understanding how disparification occurs, but they also provide a more comprehensive assessment of evolutionary history.

187^E: Associations between otter (Mustelidae: Lutrinae) diet and craniodental morphology

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Members of Family Mustelidae range widely in body size and have highly variable diets reminiscent of the larger Order Carnivora. Subfamily Lutrinae displays unique adaptations for a semi-aquatic life not seen in other carnivorans with exception of more specialized pinnipeds. Although craniodental specializations of terrestrial carnivorans are well known, functional analyses of feeding structure in semi-aquatic otters are lacking. Otters exhibit a variety of diets. Some species specialize on snails, clams, or other hard-bodied invertebrates (e.g., *Enhydra lutris*), others have diets comprised entirely of fish (e.g., *Pteronura brasiliensis*), or nearly equal quantities of vertebrates and invertebrates (e.g., *Aonyx capensis*). We examined 32 craniodental features in 13 extant otter species to reveal how morphology is related to diet. All species were separated into diet categories from extensive review of available literature. Principal Components (PCA) and Discriminant Function Analyses (DFA) were used to reveal relationships between diet and morphology. Results indicate that otters feeding on hard-bodied invertebrates are characterized by larger size, extensive grinding areas on molariform teeth, and a tall P3 crown that may mirror the P3 “hammer” in borophagous hyenas. Piscivorous otters have longer tooth rows and longer jaws, likely to produce a faster bite and create widely distributed points of contact between teeth and quick-moving fish prey. We applied our findings to reveal the most likely diets of well preserved fossil otter species.

188^{E}: Not all claws are the same: form and function of unguis morphology in Family Felidae**

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Morphologies of manual and pedal claws in cats are generally considered to differ due to differences in function when subduing prey. Generally, fore claws are believed to be used for grasping struggling prey and are strongly curved and pointed. Hind claws tend to be straighter and sickle-shaped and are generally believed to be used for climbing or raking at large prey to potentially bring them down quicker from blood loss or disembowelment. These generalizations, however, are based on observations of a very limited sample of species and extension to the entire family (41 species) may be erroneous. For example, cheetahs have sheathless claws that have a less tightly curved morphology associated with their unique cursorial hunting behavior. Our research is focused on examining morphological variation of manual and pedal claws in a larger survey of felids in order to better understand and characterize how claws may vary in shape according to hunting habits, ability to climb, or differences in preferred prey size. Measurements taken include dorsal and ventral lengths and radii of curvature, claw dorsoventral thickness measured at the base and midlength, and claw sharpness (apical angle). Preliminary results indicate that felids with scansorial habits have more robust (thick) claws that are more tightly curved than cursorial species. Cats that do not regularly hunt large prey have shorter and less robust pedal claws. This research was supported by Grants-In-Aid of Research awarded to Cammie McCann.

189: Morphological variation of *Gerbillurus* in southern Africa

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The genus *Gerbillurus* is restricted to arid regions in southern Africa, and is composed of four species. Although these species are sympatric in several areas, they are clearly phenotypically divergent from one another, with the widest ranging species, *Gerbillurus paeba*, also showing intriguing intraspecific variation. Despite this, few studies have examined this genus comprehensively across its full distribution. We took 21 craniodental measurements from over 500 specimens of *G. paeba*, 50 of *Gerbillurus setzeri*, 59 of *Gerbillurus tytonis*, and 43 of *Gerbillurus vallinus*. These specimens represent the majority of the distribution of each of these species and together represent one of the most comprehensively sampled morphological datasets for this genus to date. We used these data to examine morphological variation within *Gerbillurus* to test current species and subspecies designations. To visualize and diagnose distinct groups, we used a variety of ordination and clustering methods. Analyses focused on differences among species, subspecies, and unique localities. *Gerbillurus paeba* is shown to be morphologically divergent from the other three species. Additionally, morphological variation exists within *G. paeba*, but not all current subspecies consistently exhibit this variation. Elucidating a more complete view of the morphological variation seen in *Gerbillurus* will help inform future biogeographic and systematic studies of this genus.

190: From fossils to mitochondrial genomes: analyzing size variation in caviid rodents

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The New World representatives of Hystricognathi, the Caviomorpha rodents, present a great evolutionary history with relevant fossil records in South America since the Eocene. Many questions have been debated within the last decades concerning their arrival time and pathways since lineage split from African relatives. This is also true for some contentious relationships within superfamilies and genera. Besides still controversial aspects on the biogeography and evolution of Caviomorpha, some other questions remain unclear. One of these is the intriguing relationship within Caviioidea with the uncertain arrangement among *Hydrochoerus* and *Kerodon*, specifically considering their discrepant body size. Although the close relationship is well supported by both morphological and molecular characters, many interesting issues remain unanswered, for instance: what could be the ecological explanation to the size disparity between *Hydrochoerus* and *Kerodon*. In an attempt to determine this, we are performing new phylogenetic analyses based on a larger molecular dataset, composed by nuclear and mitochondrial genes. Besides the ethanol and nitrogen preserved samples, we additionally gathered some from muscle “crusties”. The vouchers accessed to obtain such material were dated from 1905 to 1979. “Ancient” DNA

retrieved from such samples after library-prep were submitted to Illumina MiSeq (NGS). The assemblage of mitochondrial genomes, as well as gene capture procedures, are being carried on to increase taxon and gene sampling; leading to a new panorama to solve this puzzle.

191^E: The twisted tale of zygapophyses: intervertebral joint morphology and locomotor strategies in terrestrial carnivorans

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The mammalian Order Carnivora includes almost 300 species that range greatly in body size, dietary specialization, habitat preference, and other aspects of their ecology. Many examples of independent convergence within the clade make carnivores an ideal taxon with which to examine relationships between form and function. We examined the relationship between zygapophyseal shape and locomotor strategies in 44 species of terrestrial carnivores. Species selected for analysis included congener or closely related pairs of taxa that differed in locomotor strategies in order to assess convergence among distantly related lineages. Locomotor categories included highly cursorial (e.g., cheetah), moderately cursorial (e.g., wolf), weakly cursorial (e.g., bears), scansorial (e.g., leopard), and semi-fossorial (e.g., badger) species. Angles of inclination, curvatures, and transverse widths of pre- and postzygapophyses were measured from posterior thoracic and lumbar vertebrae. Data were explored using Discriminant Function Analysis (DFA), using locomotor categories as a priori groups. Scansorial and highly and moderately cursorial species tend to have vertebrae that transition from nearly horizontal zygapophyseal angles to highly angled (60-70°) zygapophyses at a position more anterior to other locomotor groups. This transition is likely due to increased demands for spinal mobility needed to climb trees and run. More cursorial species also have zygapophyses positioned closer to the midline. Semi-fossorial and weakly cursorial species tend to have zygapophyses that are less inclined relative to horizontal.

192: Comparative forelimb morphology and function in hippopotamids, peccaries and suoids: ecomorphy trumps phylogeny

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Hippopotamus forelimb bones and girdles were compared with suoids. No longer considered closely related, these remain ecomorphs, sharing body shapes and partially overlapping ecological niches. Despite differing habits (semiaquatic hippos; terrestrial pigs and peccaries) similar selective forces accommodate large, robust canines for combat and defense. *H. amphibius* has an especially large head. Forelimb proportions also differ between hippos, and among suids and tayassuids. *H. amphibius* has the relatively shortest legs. Pigs and peccaries weigh from less than 1/10th of *H. amphibius* to approximate pygmy hippo mass. Hippo scapular glenoid fossae are rounded, with rounded, convex humeral heads. Suoid glenoids are more elongate, although all show humeral circumduction. Hippopotamid supraspinous fossae are relatively larger than in suoids; the latter show more gracile scapulae with prominent spines. The hippo large, sharp lateral projection recurves distally, with a greatly ventrally expanded acromion. Peccary scapular spines arise anteriorly; originating increasingly posteriorly in progressively larger-bodied taxa (*P. porcus*, *S. scrofa*, *P. aethiopicus*) until halfway anteroposteriorly in *H. meinerzhageni*. Suoid scapular spines slope gently, projecting laterally, without an acromion, except in *H. meinerzhageni*, wherein it projects slightly farther laterally halfway distally. Hippos show a wide, thickened midspinal bulge, not reaching the posterior border, as would a metacromion process. Suoids have prominent, triangular, rounded, thickened, rugose posteriorly pointing metacromions. These features emphasize that different muscle groups perform forelimb anteroposterior and circumduction movements.

193: Reynolds Number (Re) and the evolution of endothermy

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Endothermy has arisen at least twice among vertebrates, separately in mammals and birds. Advantages of a high, constant body temperature include toleration of temperature fluctuations in the environment, and an accelerated rate of enzyme function maintained at optimal levels that allow higher levels of

mobility in animals. This paper will examine the role played by fluid mechanics in the circulatory systems of mammals and other endotherms. Reynolds number (Re) is a dimensionless quantity that can be used to predict similar flow patterns in different fluid realms, such as the circulatory system. It is defined as the ratio of inertial forces to viscous forces in fluids. Viscosity of water is sensitive to temperature changes, and there an exponential drop in viscosity going from 0°C to 40°C, at which point endotherms function. Prerequisites had to be available for endothermy to arise, including a closed circulatory system to distribute nutrients and oxygen to cells, a minimal body mass for the production of heat, and a layer of insulation to reduce heat loss. This convergence of factors was enhanced by the reduction in blood viscosity that was triggered by rising temperatures in the ancestors of endotherms. This reduction in energy required for circulation could have been a major trigger that allowed endothermy to arise.

194^{E}: Post-introduction shift in sexual selection causes evolutionary change in the small Indian mongoose (*Herpestes auropunctatus*)**

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Little is known about how ecological changes affect sexually selected traits. Theory indicates that population density is positively related to the strength of sexual selection. The small Indian mongoose (*Herpestes auropunctatus*) is a carnivore native to South Asia that was introduced to many tropical islands, where, due to a lack of predation and interspecific competition, densities average 30 times higher than the ancestral range. I hypothesized that the high densities on these islands have relaxed sexual selection on male chemical advertisement and the condition-dependent advertisement tool, the anal pad, predicting a reduced frequency of advertising and a reduction in size and condition dependence of the anal pad. Further, the high densities likely allow for a greater number of mating partners in this promiscuous species. Thus, males may have become less mate-limited but more sperm-limited, selecting for greater sperm volume. I test these hypotheses and predictions by comparing mongooses from their native range to four islands of introduction. These predictions were supported, providing an example of rapid trait evolution, and suggesting that ecological features can play a key role in the evolution and maintenance of sexually selected traits. This research was supported by Grants in Aid of Research awarded to M. Aaron Owen in 2015.

195: Concurrent evolutionary changes in lower jaws, molars, and chewing cycles in early crown mammals

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The lower jaws of Mesozoic mammals possess disparate morphologies, and it is expected that such major differences correlate with modifications in biomechanical functions. To examine this issue I use fossil data to analyze evolutionary changes in lower jaws of early mammals. I focus on the evolutionary origin of cladotherians (i.e., eutherian-placentals, metatherian-marsupials, and eupantotherians), which include all but three genera of living mammals. Morphometric analyses are used to establish macroevolutionary trends, demonstrating the appearance of a prominent mandibular angular process and elevated jaw joint in early cladotherians. Morphometric results are used as the framework for three-dimensional jaw models that mimic evolutionary changes. The models are used to estimate muscle vectors and calculate mechanical advantages for various skeletomuscular configurations. Results indicate that the posterior extension of the cladotherian angular process has little effect on mechanical advantage for rotation of the jaw around a mediolaterally oriented axis (i.e., pitch). However, molar morphologies of early cladotherians suggest that the chewing cycle includes significant transverse movement. When the jaw model is restricted to transverse movement produced by rotation around a dorsoventrally oriented axis (i.e., yaw), the presence of a posterior angular process results in muscle force vectors with considerably greater mechanical advantage. This suggests that the molar and jaw morphologies of cladotherians evolved in concert, permitting a more complex chewing cycle with significantly increased transverse movement.

196: Insights into the evolutionary history of Mesoamerican gray foxes revealed by mitogenomes from museum specimens

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The gray fox (*Urocyon cinereoargenteus*) is the only extant non-domestic canid with a widespread natural range that spans from the southern edge of central and eastern Canada to the northern part of Venezuela and Colombia. Because of the relatively high abundance and low economic value of the gray fox, surprisingly little research has been conducted on this species. Most taxonomic studies are based on morphology and only a few phylogeographic studies have been recently conducted to characterize the geographic patterns of genetic diversity in the United States. Sixteen subspecies have been described, ten of which are distributed in Mesoamerica. While subdivision into subspecies based on patterns of morphological variation has served as a convenient starting point for studying intraspecific diversification, in order to achieve a more comprehensive understanding of the evolutionary history of this species, it is necessary to conduct a robust phylogeographic analysis including representatives from Mexico and Central America. In this study, we extracted DNA from 30 museum specimens that represent the ten subspecies of Mesoamerican gray foxes. We combined in-solution capture enrichment and high throughput sequencing protocols to obtain whole mitochondrial genomes. The results of our phylogenetic analyses based on Maximum Likelihood and Bayesian Inference are discordant with taxonomic groupings based on morphology and suggest that the southern part of Mexico could be the center of diversification of *U. cinereoargenteus*.

197^E: Whole genome sequencing of procyonids: insights into adaptation and alternative *de novo* assembly methods

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Here we present the initial comparison of the complete nuclear genomes of the North American raccoon (*Procyon lotor*) and the kinkajou (*Potos flavus*), the first procyonid genomes to be sequenced to date. These two species encompass almost 21 million years of evolutionary history within Procyonidae, and fill a gap of about 30 million years to the next closest relative for which a genome has been generated. For this project, three paired-end and two mate-pair libraries were generated and sequenced on an Illumina HiSeq 2000 system. Our initial assemblies suffered from low N50 contig and scaffold sizes, even though coverage was fairly high, likely due to high genome heterozygosity. Since assemblies greatly impact downstream results such as gene prediction and annotation, we tested a number of *de novo* assembly strategies (implemented in ALLPATHS-LG, Platanus and MaSurCA) some of which are optimized for highly heterozygous genomes. We discovered significant improvements in contig and scaffold N50 and L50 statistics, also genome completeness, and number of successfully recovered genes, depending on the *de novo* assembler used. We compared the performance of several assembly algorithms in hopes that this study will aid others looking to improve the quality of existing draft genome assemblies even without additional sequence data.

198: Species sorting of endemic mice along replicated elevational gradients of Luzon Island, Philippines

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A variety of factors may influence the co-occurrence patterns observed among closely related species. Luzon Island, in the northern Philippines, is home to a compact but rapid radiation of eleven species in the subgenus *Megapomys*. Each species is endemic to a single mountain or mountain range, and most montane areas are home to two species of *Megapomys* that occur along mostly exclusive elevational bands, with narrow zones of overlap. External morphology of these species is correlated with local habitat; high elevation species tend to be smaller, with proportionally shorter tails. We tested for evidence of non-random patterns of co-occurrence, including over-dispersion among co-occurring species in terms of phylogenetic relatedness and external morphology. We also tested whether a random dispersal process without ecological influences could generate the observed evenness of local species richness. Our analyses indicate that co-occurring species are more distantly related than in randomized simulations, suggesting that a sympatry threshold and local limits on species richness govern co-occurrence.

199^{E}: The utility of zonadhesin in examining a potential reproductive isolation mechanism in rodents**

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Species-specificity in mammals is crucial to maintain reproductive isolation boundaries and prevent interbreeding and dilution of the gene pool. It has been hypothesized that gamete recognition (sperm/egg compatibility) is one of the first steps in establishing post-mating isolating mechanisms. Gamete recognition is a known prezygotic isolation mechanism in certain invertebrates, but its significance in vertebrates, such as mammals, is not well established. One of the proteins crucial in this process is zonadhesin (ZAN), a rapidly evolving, sperm protein that mediates species-specific adhesion to the egg. It has been suggested that ZAN evolution correlates with reproductive isolation in mammals and is an adaptive gene found only in certain internally fertilizing mammals. In addition, it has been concluded that intra-species differences exist in human and pig ZAN and might be under strong selective pressures, and thus, evolution of those alternative transcripts of the gene might contribute to the process of speciation. Therefore, by examining the protein-coding sequence of ZAN between and within species, we can determine the level of variability and conservation of the gene. To address this, we examined genetic variability in multiple species of *Peromyscus* to assess the extent of sequence variation across a 400 bp region of the gene. Currently, we are sequencing 4 species of *Peromyscus* to establish baseline variation of ZAN. This research was supported by Grants-In-Aid of Research awarded to Emma Roberts.

200^{}: Quaternary diversification of Mesoamerican montane Neotropical Cricetid rodents**

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Mesoamerica is recognized for its high levels of mammalian species richness and endemism and it is documented as a global biodiversity hotspot. Some datasets suggest that the Isthmus of Tehuantepec (IT) may act as a vicariant barrier allowing regional diversification. However, climatic fluctuations associated with cycles in the Pleistocene also affected the vertebrate distributions and consequently promote diversification. To understand processes responsible for current biodiversity in Mesoamerica, the mitochondrial Cytochrome-*b* gene was used to infer phylogeographic relationships and divergence times for 12 species of cricetid rodents. Analyses indicated that cricetid taxa have responded similarly to the

past climate changes during the Pleistocene with no genetic differentiation, but the response have not been entirely coupled due to different or simultaneous speciation events. The combined results depict a rapid expansion of the populations of cricetid rodents across the IT during glaciation times, and indicated unstructured populations along their current range with low genetic diversity. The only pattern that indicated that the IT was an effective barrier to gene flow was found in *Reithrodontomys sumichrasti*. Estimated divergence times between populations NW and SE of the IT indicated that isolation occurred mostly during the Pleistocene. The results indicated that the speciation process of these rodents is a result of climatic changes and that the IT did not form an effective vicariance barrier during their diversification. This research was supported by the 2014 Albert and Alma Shadle Fellowship, 2012 Latin American Student Field Research Award, and the 2010 Grants-In-Aid of Research awarded to Nicté Ordóñez-Garza.

201^{E,TA}: Patterns and timing of diversification among major lineages of mountain voles, Genus *Neodon***

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Recent molecular systematic studies of arvicoline voles of the genera *Neodon*, *Lasiopodomys*, *Phaiomys*, and *Microtus* from Central Asia suggest the inclusion of *Phaiomys leucurus*, *Microtus clarkei*, and *Lasiopodomys fuscus* in *Neodon* while moving *Neodon juldashi* to *Blanfordimys*. In addition three new species of *Neodon* (*N. linzhiensis* and 2 additional species in press) have been described from China. *N. sikimensis* occurs on both sides of the Himalayas and currently, sequences in GenBank only represent *N. sikimensis* from north of the Himalayas. Analysis of concatenated mitochondrial (Cytb, COI) and nuclear (GHR, IRBP) genes showed *N. sikimensis* from Nepal, southern portion of range, did not form a monophyletic clade with the Tibetan specimens of *N. sikimensis*, but rather formed a sister clade to all *Neodon* species from Tibet and China. Principal component analysis conducted on 12 skull measurements from 175 *Neodon sikimensis* specimens at the Field Museum suggest that northern and southern *N. sikimensis* are distinct morphospecies. Divergence times using BEAST analysis seem to represent Pleistocene divergences supporting the suggestion that *Neodon* were Pleistocene relicts. The first split separated the *Neodon* from north and south of the Himalayas (1.34 ± 0.3 Mya) followed by the divergence of the *Neodon* in Tibet and China (1.19 ± 0.3 Mya). Since the type specimen of *N. sikimensis* was taken from Sikkim, India, the Tibetan specimens currently identified as *N. sikimensis* likely represent an unnamed species. This research was supported by a Grant-in-Aid of Research awarded to Nelish Pradhan in 2013.

202^F: Phylogenetic relationships within the leaf-eared mouse *Phyllotis xanthopygus* (Rodentia: Sigmodontinae)

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Phyllotis xanthopygus has a wide distributional range, from the south of Peru to the Patagonian region of Argentina and Chile, and from sea level up to 5000 meters also. The variety of habitats across this geographic range includes environments such as grasslands, steppes, mountains and deserts. Due to its distribution, the glaciations cycles of the Plio-Pleistocene should have affected the distribution of this species on southern South America and over the Andes. It can be inferred that *P. xanthopygus* has been brought under different selection pressures across its distributional range. In fact, six subspecies have been recognized along the range of this species using morphological characters: *P. x. chilensis*, *P. x. rupestris*, *P. x. posticalis*, *P. x. vaccarum*, *P. x. xanthopygus* y *P. x. ricardulus*. This project focus on to evaluate the systematics relationships and the biogeography of *P. xanthopygus*. To those goals, we used the Cytochrome B gene and the control region from the mitochondrial DNA, and the seventh intron of the β -Fibrinogen gene (β Fgb-I7) of the Nuclear DNA. We used tissue samples of liver and kidney stored at different museums and collections, collected from most of the distributional

range of the species. All data were phylogenetically analyzed, contrasting results from previous studies, and proposing new systematic rearrangements within the species.

203: Dynamics of genetic and morphological diversification in an incipient intra-island radiation of Philippine rodents

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The Philippine archipelago is exceptional for its high concentration of endemic terrestrial biodiversity. Although the dynamics of inter-island speciation responsible for producing much of this diversity are generally well understood, the factors driving diversification within islands have received less attention. Murid rodents, which comprise approximately two-thirds of the native non-volant mammalian diversity in the Philippines, are especially well suited for understanding speciation dynamics across the archipelago. On Luzon, the largest island in the Philippines where murid rodent diversity is highest, numerous 'Old Endemic' lineages diversified at high elevation on the island's numerous isolated mountain ranges after colonizing ca. 7-15 Ma. By contrast, no evidence currently exists for diversification in the several 'New Endemic' murid rodent lineages on Luzon, which typically occur at lower elevations. In this study, we used multi-locus genetic data and craniodental morphometrics to examine patterns of inter- and intra-island diversification in a New Endemic lineage, the genus *Bullimus*. We demonstrate that substantial diversification has occurred on Luzon during the last ca. 250,000 years, producing seven distinct genetic lineages, at least one of which constitutes a previously unrecognized species. Lowland habitat is implicated as an important driver of diversification, despite *B. luzonicus* having a wide elevational range. Our results add to a body of literature suggesting that Luzon is truly an exceptional setting for murid rodent diversification.

204: Taxonomy, systematics, biogeography, and evolution of the South American cottontail rabbits (Lagomorpha, Leporidae: *Sylvilagus*)

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The South American cottontail, *Sylvilagus brasiliensis*, was described by Linnaeus with "South America" for type locality. As a result, *S. brasiliensis* acquired a vast distribution in the Americas, over an area ca. 1.09×10^7 Km², and containing upwards of 37 subspecies. Here, we restrict the type locality of *S. brasiliensis* to coastal Pernambuco State, Brazil. Morphological and molecular analyses suggest that *S. brasiliensis* has a more restricted range in South America. We also find sufficient distinction in characters and measurements between *S. brasiliensis*, *S. andinus*, and *S. tapetillus*, to retain the latter two as valid species. Molecular analyses of 12S rRNA and cytochrome-*b* genes support the distinction between *S. andinus* and *S. brasiliensis*: distances calculated from cytochrome-*b* between these species reached ca. 15 %, the largest interspecific distance among *Sylvilagus*. Lineages Through Time analysis suggests the diversity among *Sylvilagus* is based on high speciation rates combined with low extinction rates. Episodes of explosive speciation in *Sylvilagus* have been coeval with cooling events; warm periods have in contrast slowed down speciation rates. The status of described subspecies of *S. brasiliensis* will require careful scrutiny. There is a lack of specimens of Neotropical *Sylvilagus* in museum collections; however, our approach from first principles—examination of holotypes—not only serves to establish a more stable

taxonomic framework for Neotropical *Sylvilagus*, but also further suggests that many of the existing taxa currently subsumed as subspecies within *Sylvilagus brasiliensis* likely are valid species.

205: Phylogeny and species limits in Olympic, Vancouver Island, and hoary marmots revisited: a 21-gene salute

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Alpine-adapted species face multiple threats from climate change, including habitat loss due to tree and shrub encroachment, phenological mismatch, and increased isolation on shrinking 'sky islands'. Three closely related allopatric species of alpine marmots occur in the Pacific Northwest of North America and include the broadly distributed hoary marmot (*Marmota caligata*); the Olympic marmot (*M. olympus*), found only in the Olympic Mountains of Washington's Olympic Peninsula; and the endemic Vancouver Island marmot (*M. vancouverensis*). Olympic marmots have recently experienced significant population declines, and *M. vancouverensis* is considered Canada's most endangered mammal and has been the subject of an intense captive breeding and relocation project. Although these species have long been considered distinct and well circumscribed phylogenetically, a recent study suggests a complicated history of divergence, isolation, and subsequent gene flow, as well as indistinct and overlapping phenotypic boundaries. These findings are directly relevant for conservation, especially if genetic rescue proves necessary to maintain viability of *M. olympus*, *M. vancouverensis*, or both. To better understand the evolutionary history of this complex, we generated and analyzed DNA sequence data from two mitochondrial and 19 nuclear loci in multiple representatives of the three target species and multiple outgroups. Using recently developed methods that simultaneously estimate gene flow and phylogeny, we recovered novel and better-supported relationships compared to previous studies and traditional approaches that do not parameterize migration.

206^E: Phylogeography and the origin of free-ranging elk (*Cervus canadensis*) in Texas

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The historic range of elk (*Cervus canadensis*) included much of the western United States. Natural distributions of this species decreased substantially in the early twentieth century, presumably eliminating the Texas population. In the past 40 years, several herds of free-ranging elk have reappeared in the Trans-Pecos region of Texas. It is not known if these herds were the result of introduction from captive herds, or if they represent natural migrants from New Mexico or Colorado that re-established a Texas population. The objective of this study is to determine the origin and genetic affinities of free-ranging *C. canadensis* in Texas. DNA sequences from the mitochondrial cytochrome-*b* locus and the D-Loop gene was used to generate an concatenated dataset to compare samples of *C. canadensis* from Texas with samples from New Mexico, and South Dakota. In addition, 9 microsatellite loci were used to examine the phylogeography and genetic divergence of the various aforementioned populations and to determine the origin and the relatedness of the elk herds in Texas. Findings depict high degree of relatedness among individuals throughout the population range. Correlation of origin between Texas and New Mexico populations is supported with the high degree of relatedness between the populations. Expression of unique alleles in the South Dakota samples depict separate evolutionary history and effectively eliminate them from being a source of introduction for Texas populations.

207: Using ecological niche modeling to reevaluate the status of formerly recognized small-eared shrews (*Soricidae: Cryptotis*)

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Estimating the geographic distributions of species through time can be useful to study the role of geographic barriers on current patterns of morphological variation. Here we inferred the current and past potential distributions of three previously recognized species of Mexican small-eared shrews (genus *Cryptotis*) during the last glacial period using Ecological Niche Modeling. We also assessed their taxonomic status based on morphology and a comprehensive sampling. The status of *C. nelsoni* is strongly supported by morphological differentiation and geographic isolation. On the other hand, patterns of morphological variation are not in agreement with the current taxonomy, suggesting that *C. mexicanus* and *C. obscurus* cannot tell apart with the evidence at hand. In addition, no environmental barriers were detected within the ranges of *C. mexicanus* and *C. obscurus* west of the Isthmus of Tehuantepec at either current or glacial times, suggesting that a constant possibility for interpopulation connectivity has facilitated gene flow. We found that the population previously identified as *C. mexicanus* located east of the Isthmus of Tehuantepec has been isolated through time, resulting in clear morphological differentiation from conspecifics. This population deserves further analyzes to determine whether it represents a new species. We strongly encourage combining morphological and genetic data within this clade, and the integration of species delimitation methods to resolve the taxonomic issues highlighted by our findings.

208: Choosing the shape of Bayesian priors when calibrating a molecular clock, an example in caviomorphs

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Systematic studies increasingly rely on combining molecular sequences and fossil dates to infer time-calibrated phylogenetic trees. Calibrating by using the oldest known fossil in a clade as an absolute age estimate yields known underestimates of clade ages. An older fossil can always be discovered. Nevertheless, constraining minimum ages only without setting “soft maxima” demonstrably overestimates clade age. Available calibration software provides many options for the shape of the prior probability distribution of ages at a node to be calibrated, but limited data exist to aid researchers in selecting the appropriate prior shape. We present information on the recently developed penultimate gap (PenG) and ghost lineage length (GLin) methods, which apply information gleaned from multiple oldest fossils in a clade to create a well-defined calibrating prior shape. We evaluate how these methods estimate when the Caviomorpha arrived and subsequently diversified in South America and how PenG and GLin approaches compare with previous studies that have generating prior shapes through “phylogenetic bracketing” techniques.

209: Factors influencing estimates of river otter abundance following reintroduction: pre- and post-harvest assessment

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By the early 1900s, river otters (*Lontra canadensis*) were extirpated across large parts of their range in North America. River otters were reintroduced to Ohio from 1986-1993 and harvesting of this population began in 2005. While circumstantial evidence points to rapid population growth and a sustainable harvesting regime following the reintroduction, actual changes in population size over time is unknown. We used empirical and literature-based data on river otter demographics in Ohio to generate multiple Leslie matrix models of the population from 1986-2005. We then used statistical population reconstruction methods to generate otter population estimates in Ohio from 2006-2008 using age-at-harvest data, supplementary survival data, and multiple scenarios of trapper effort and initial (2005) abundance. Our Ohio-based Leslie matrix model predicted that there were 4,116 (SD = 1071) river otters in Ohio in 2005

with an exponential growth rate of 0.21. Trapper effort and initial population abundance both influenced our population estimates from 2006-2008. Assuming otter pelt price was a good index of trapper effort and if the initial population was between 2000-4000 individuals, then we estimated the exponential population growth rate to be 0.17-0.20. The river otter population in Ohio appears to have grown very rapidly, although our estimates could be over-estimated as we did not account for carrying capacity. Nonetheless, the current harvesting regime of river otters in Ohio is likely sustainable.

210^E: Impacts of insecticide plague treatment on populations of deer mice on prairie dog colonies

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Plague (*Yersinia pestis*) is a major threat to populations of prairie dogs (*Cynomys spp.*) and black-footed ferrets (*Mustela nigripes*) in western North America. In many black-footed ferret reintroduction sites, deltamethrin is sprayed inside prairie dog burrows to remove plague-carrying fleas (Siphonaptera), increasing survival of prairie dogs and potentially reducing plague epizootics. We investigated the effects of deltamethrin dusting on populations and fleas of non-target deer mice (*Peromyscus maniculatus*) in black-tailed prairie dog colonies (*C. ludovicianus*) at Wind Cave National Park and Custer State Park, South Dakota from 2013 to 2015. Captured deer mice were individually combed resulting in the collection of 167 fleas from 144 mice in 2013, 67 fleas from 273 mice in 2014 and 649 fleas from 310 mice in 2015. Significantly fewer mice were infested on treated grids during the first (odds ratios of infestation=0.050, 0.005-0.471 95% CI) and second (odds ratio=0.028, 0.003-0.261 95% CI) trap sessions after dusting in 2013 and 2015. Based on Cormack-Jolly-Seber models, deer mouse populations showed no change in survival between treated grids (2013=0.496, 0.363-0.628 95% CI, 2014=0.905, 0.861-0.936 95%CI, 2015=0.367, 0.303-0.437 95% CI) and untreated grids (2013=0.483, 0.388-0.579 95% CI, 2014=0.816, 0.748-0.869 95% CI, 2015=0.353, 0.282-0.431 95% CI). Results from flea infestation data and mouse capture data indicate that deltamethrin treatment reduces flea loads on non-target deer mice with little evidence of negative population effects.

211: Potentially suitable environments for westward expansion of black bears in Oklahoma

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Black bears (*Ursus americanus*) have recolonized eastern Oklahoma from Arkansas. In recent years, bears have been sighted moving farther westward than the Ouachita Mountains and the public is starting to wonder how far westward bears might expand their range. The goal of this research was to identify potentially suitable areas for bears if they expand their range westward. I used MaxEnt to produce a species distribution model for black bears in Oklahoma based on occurrences of satellite collared bears in the Ozark and Ouachita Mountains. While some areas in western Oklahoma were identified as good habitat for bears, the degree of fragmentation was much higher in western Oklahoma. I used Fragstats to determine the average amount of "good habitat" fragmentation within collared bear home ranges and identified novel areas in Oklahoma that would be large enough and contain acceptable amounts of fragmentation and connectivity to support black bears. As large generalists, bears are capable of moving long distances and living in many different environments, so it is possible they will continue expanding breeding populations westward. The results of this research will be transferred to the Oklahoma Department of Wildlife Conservation and used to educate the public about possible range expansion of black bears in Oklahoma.

212: Transmitter performance and effects on fitness of American beavers (*Castor canadensis*)

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One key assumption that is often inferred with using radio-equipped individuals is that the transmitter itself has no effect on the metric of interest. To evaluate this assumption, we 1) used a known fate model in Program MARK to assess the effect of transmitter type (i.e., tail-mounted or peritoneal implant) on short-term (1 y) survival and 2) used a joint live-dead recovery model and results from a mark-recapture study to compare long-term (8 y) survival, body condition, and reproductive performance of ear-tagged only American beavers (*Castor canadensis*) to those equipped with radio-transmitters in Voyageurs National Park, Minnesota, USA. Results of survival analysis indicated survival was not influenced by transmitter type or whether an animal was fitted with a transmitter (annual survival = 0.76) vs ear tagged only (annual survival = 0.78). Additionally, we found no difference in weight gain or tail area from spring to summer between the two groups. In contrast, we found winter weight loss and tail area decreased significantly between transmitter-equipped and ear-tagged only animals. We also will report on the retention and performance of tail-mounted transmitters on beavers in a northern climate. Our results tend to support the continued use of transmitters on beavers for estimating demographic parameters, although we encourage other researchers to test the effect of transmitter type under different environmental conditions.

213: Determining population density estimates for Florida panthers using trail camera photos and spatial data

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Accurate estimates of the size of endangered mammal populations are often imperative due to criteria established by agencies monitoring recovery. The standard for deriving population estimates using trail camera photos has been variations of traditional capture-recapture methods, which have been effectively applied to mammals with unique pelage patterns that permit individual identification. Challenges arise when dealing with a wide-ranging, elusive large carnivore without natural identifiers. The endangered Florida panther (*Puma concolor coryi*) is comprised of a single breeding population restricted to South Florida and current recovery criteria set specific numeric goals for the population. We applied a spatial capture-recapture (SCR) model to trail camera and telemetry data collected on panthers using two parcels of public land in South Florida: Florida Panther National Wildlife Refuge and adjacent state-owned lands (FPNWR); the northern Addition Lands of Big Cypress National Preserve (ADD). A portion of the population was radiocollared and ear-tagged prior to deployment of 50 cameras within each 162km² study area. We incorporated data from 15,050 camera trap days and 2461 telemetry locations into an SCR model to derive density estimates. Panther density for FPNWR (3.5 panthers/100km², 1.85-5.62 [95% CI]) was greater than ADD (1.4 panthers/100km², 0.49-2.42). Further development of our SCR model may permit a range-wide population estimate for panthers and is the focus of ongoing research that should prove important to monitoring recovery.

214^F: Effects of three land management regimes on small mammals at Grand Forks Air Force Base

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Grassland management at Grand Forks Air Force Base in North Dakota includes tallgrass prairie restoration, old field succession, and hayfield maintenance. To determine which management regime promotes the highest biodiversity of small mammals, we determined species diversity and relative abundance of small mammals within each area, measured each area's herbaceous vegetation height and

density, and related vegetation data to small mammal diversity and abundance. During the summers of 2014 and 2015, 463 individuals were captured from the genera *Microtus*, *Peromyscus*, *Zapus*, *Sorex*, and *Mustela*. Relative density of small mammals (number of individuals captured per 100 trap nights) was highest in the restored prairie (2.1-3.4) and lowest in the hayfield (0-0.4). Vegetation height and density was determined using Robel measurements. The restored prairie had the most variable Robel means (2-17.75 dm), whereas the hayfield had the least variable means (0-3.75 dm). Robel measurements were assigned to the surrounding study area through Kriging interpolation in ArcGIS. Preference of vegetation height and density was determined through chi-square tests. Small mammals selected for vegetation height and density between 4.1-6 dm and 10.1-18 dm. Determining small mammal abundance in a variety of managed habitats at Grand Forks Air Force Base will allow for better management of biodiversity and provide baseline data for future small mammal studies on the base.

215: A novel management strategy for controlling eastern gray squirrel (*Sciurus carolinensis*) populations in urban areas

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The eastern gray squirrel (*Sciurus carolinensis*) is a common wildlife species in urban and suburban communities within the eastern United States. Human-squirrel conflicts are on the rise due to increasing gray squirrel populations. The objectives of this project were to determine peak breeding seasons for gray squirrels on the campus of Clemson University, evaluate the effectiveness of the contraceptive DiazaCon™ in reducing gray squirrel reproduction, and to determine the best management strategy suited to optimize gray squirrel reproductive control without creating a source-sink dynamic. The first year of the study, gray squirrels were trapped monthly and blood samples were collected to determine their breeding periods. In years 2 and 3 of the study, DiazaCon™ coated sunflower seeds were placed in 4 treatment sites across campus. DiazaCon™ can persist in the liver for up to 4 months; therefore, following each administration, up to 100 gray squirrels, per month for 4 months, were trapped in the treatment and control sites. Serum samples were analyzed for progesterone or testosterone levels, and both desmosterol and cholesterol levels. Results from this study showed gray squirrels treated with DiazaCon™ had a significant enough decrease in cholesterol levels to reduce reproduction. DiazaCon™ shows promise as a cost-effective and humane management tool for reducing gray squirrel reproduction, but further population level studies are needed.

216^F: The ecology of coyotes (*Canis latrans*) in a shifting heterogeneous landscape

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Due to the extirpation of many large, native carnivores the coyote has become one of the most widespread and successful predators in North America. For this reason, it is important to understand how they respond to both natural and anthropogenic disturbances. Ten coyotes were captured within the Tallgrass Prairie Preserve (TPP), fitted with GPS collars, and monitored for 18 months. Tallgrass prairie is a highly endangered and fragmented habitat types with less than 2% remaining; the TPP is one of the largest, contiguous remnants of this native ecosystem. By combining GIS data with GPS data from the collars we assessed how coyote movements and use of habitat are affected by energy development and prescribed fires. Preliminary results indicate coyotes select prairie over woodland vegetation types, and have significantly smaller home ranges in the TPP compared to similar studies conducted elsewhere. They also appear to alter their temporal and spatial activity patterns based on anthropogenic pressures. Knowledge of how anthropogenic and natural disturbances impact coyotes could provide insight into prey vulnerability. Coyotes regulate other species in many ecosystems throughout North America. It is important to assess the current apex predator in the tallgrass ecosystem in order to have a more complete picture of various faunal communities. This can enhance future conservation efforts such as the reintroduction of native prairie species and ecosystem resilience as a whole.

217: Landscape genetics of raccoons (*Procyon lotor*) in a naturally fragmented coastal landscape

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We used mitochondrial (mtDNA) and nuclear DNA markers to identify past and present dispersal corridors of raccoons (*Procyon lotor*) on the Virginia barrier islands and adjacent Delmarva Peninsula mainland. We analyzed a 515-basepair fragment of mtDNA (containing the 3'-end of the cytochrome-b gene, the 5'-end of the d-loop, and the intervening tRNA gene) in 164 animals from 22 localities. We detected 8 unique mtDNA sequences and found north-south differentiation on the islands and on the mainland. To draw inferences about raccoon population dynamics and genetic connectivity, we genotyped 13 nuclear microsatellite loci in 314 individuals from 24 localities. We found complex patterns of spatial population structure and migration rates in this system. These patterns suggested nonequilibrium population-genetic dynamics, potentially caused by recent founding events on the islands and spatial variation in genetic connectivity within this system. Taken together, results of this study suggest that the metapopulation structure of raccoons on the Virginia barrier islands is highly dynamic, with most movement of raccoons occurring among groups of islands that are inter-connected by marsh and relatively shallow, narrow, open-water channels. These results are consistent with our direct observations of overwater movement by raccoons within this system. These genetic data also support predictions from our models based on cost-distance analysis of landscape resistance to movement by raccoons among islands and the mainland.

218^F: Insight into hantavirus evolution using phylogenomics

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Wild mammals are reservoirs for a wide array of zoonoses, yet our understanding of their evolutionary history with these pathogens is remarkably unknown. In particular, viruses infecting wild mammal populations, such as hantaviruses, have a history of causing severe pathology in humans. Hantaviruses (family Bunyaviridae, genus *Hantavirus*) are a group of globally distributed, negative-sense, single stranded RNA viruses with specific rodent borne strains capable of causing disease in humans. Although originally isolated in rodents, recent work demonstrates high diversity in non-rodent, insectivorous mammals of the orders Chiroptera and Soricomorpha. Full-length genomes are currently lacking for many of these strains, impeding progress in understanding pathogenicity, distribution, age, history, and evolution of hantavirus diversification. In this study we will use next generation sequencing techniques to generate genomes for nine divergent hantavirus strains isolated from shrews and moles. We are exploring three main questions: 1) What is the genetic diversity of hantaviruses across their distribution? 2) Can we elucidate the evolutionary history of pathogenicity in rodent-borne hantaviruses? 3) How can current viral screening techniques be improved to streamline and increase the efficiency of novel virus discovery? Addressing these questions provides the necessary baseline for future comparative studies into hantavirus evolution, global diversification, and pathogenicity of this emergent pathogen.

219: Small mammals of the Simien Mountains of Ethiopia

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The Simien Mountains of Ethiopia are well known for the endemic biota that occur on this exceptional massif. While many of its charismatic mammalian species such as walia ibex (*Capra walie*), Ethiopian wolf (*Canis simensis*), and gelada (*Theropithecus gelada*) are widely known, many of the rodents,

shrews, and bats have not received the same attention. We conducted an elevational survey of the small mammals of the Simien Mountains, marking the first systematic survey in this region since 1927. We used a standardized sampling regime that has been utilized in several other montane sites of eastern Africa over the past two decades in order to achieve the following principal goals: 1) to initiate intensive surveys of the elevational distribution and abundance of small mammals along the transect sampled; 2) to test for differences between rodents and shrews in their relationship to elevation and response to different trapping methodologies; 3) to compare the generated results to similar studies on other mountains of eastern Africa, and 4) to create tools to facilitate future biological study and educational outreach pertaining to the small mammals of the Simien Mountains and other localities within Ethiopia. Four sites were selected and sampled along an elevational gradient with center points at 2800, 3200, 3600, and 4000 m. Twelve genera of mammals were observed, including 9 rodent, 1 shrew, and 2 bat species.

220: Risk-driven behaviour in the African leopard

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In much of Africa, agricultural expansion is restricting carnivore species to smaller tracts of land, potentially forcing increased overlap between competitors by constraining spatial partitioning. Understanding competitor encounters is important because competition can influence species densities, distributions, and reproductive success. Despite this, little is known of the mechanisms which mediate coexistence between the African leopard (*Panthera pardus*) and its competitors. We used GPS radiocollar data and playback experiments to understand risk-driven changes in the leopard's behaviour and movement during actual and perceived encounters with lions (*Panthera leo*). Targeted playbacks of lion roars were used to elucidate behavioural responses of leopards when lions were perceived to be within the immediate area. To investigate the post-encounter spatial dynamics of leopard movements, we used datasets from high-resolution GPS radiocollars deployed on leopards and lions with overlapping territories in the Okavango Delta, Botswana. Leopards were found to adapt behaviours and movements when lions were perceived to be nearby. Specifically, roar playbacks elicited longer periods of vigilance than controls, and movement directions were influenced by speaker locations. Further, leopard movements were quicker and more directional after encountering lions. However, adjustments in behaviour and movement were short-lived. The results provide insights into mechanisms used by the leopard to coexist with its competitors and are a useful case study of methods which could be used to investigate encounter dynamics within other systems.

221: Natural history collection biorepositories and integrated databases as critical infrastructure for pathogen discovery and pathobiology

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Recent disease outbreaks caused by Ebola and Zika viruses have underscored the need for improvements in basic biodiversity infrastructure. One Health approaches, such as integrated collaborations between microbiologists, mammalogists, ecologists, public health agencies, and biorepositories, have reshaped our understanding of hantavirus systematics, evolution and ecology, and now serve as a new model for pathogen discovery and pathobiology. A full understanding of pathogens requires intimate knowledge of reservoir species, however, many pathogen sequences in GenBank are from taxa inconclusively identified and not associated with vouchers. We compiled known hantavirus symbiotypes as a case study in pathogen discovery. Of the 139 distinct hantavirus strains/species described, the host specimen (symbiotype) and biorepository could be determined for only 43. Thus,

critical host data for greater than two thirds of the currently recognized hantaviruses are compromised, severely limiting the ability to confirm host identity or extend previous work. Direct linkage between hosts, pathogens, genetic sequences, associated publications, and other data or materials related to these specimens not only ensures that the original sample will persist, but that the identity of the pathogen reservoir taxon will not be lost during the dynamic process of taxonomic revision. In light of this example, we advocate formal incorporation of museum infrastructure (i.e., unique catalog numbers, permanent archives, and web-accessible searchable databases) into pathogen research and present guidelines for pathogen discovery and symbiotype designation.

222: Diversity of medium-sized and large mammals through camera-trap surveys at northern Antioquia, Colombia

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Information about medium-sized and large mammals in the Andes is critical for conservation studies regarding their response to long-term and large-scale changes. Here, we present results of a comprehensive survey in northern Antioquia, Colombia, covering the western and central cordilleras between 450 and 3050 masl. From March to December 2015, we surveyed 1500 km² with 128 camera-traps and standard transects. Each camera station was characterized by its microhabitat variables and surrounding landscape, both at the field and using GIS layers. Accumulated effort reached to 6077 camera-nights, with a success of 1573 records for 29 wild mammal species. The most common species were the crab-eating fox (*Cerdocyon thous*) and the Central American agouti (*Dasyprocta punctata*). Other commons species included squirrels, opossums, raccoons, and tayra. Five felid species were recorded at the region, including puma and jaguar. Transect surveys yielded only ten species, but two additional ones: the river otter (*Lontra felina*) and the white-footed tamarin (*Saguinus leucopus*). Our results suggest that despite a long story of human activity in the region, it still supports a good portion of the original mammal assemblage. However, some species are restricted to small patches of suitable habitat that could not maintain healthy populations on the long term. Preliminary occupancy analyses provide some insights into the dynamics of these populations, suggesting feasible ways to increase connectivity within this complex matrix.

223^E: Fire effects on acorn use and demography of small mammals

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Fire can modulate small mammal population vital rates via changes in food resources and habitat characteristics. We examined the effects of prescribed fire on small mammals and the acorns upon which they rely for overwinter survival in central hardwood forests. We live-trapped and uniquely marked small mammals in pre-burn and post-burn areas alongside unburned controls. To assess the effect of fire on acorns, three species of oak (*Quercus*) acorns were placed in experimental burn plots that received fuel treatments representative of fuel loads in southern Indiana. Preferences of these burned acorns were tested with cafeteria-style presentation of acorns that varied in levels of charring. Photos from trail cameras were examined to determine species and char category for each seed removed by rodents. Preliminary results indicate that white-footed mouse (*Peromyscus leucopus*) abundance increased by 40% in the summer and fall following a spring burn relative to controls, while eastern chipmunk (*Tamias striatus*) abundance decreased by 21%. As expected, damage to acorns increased with greater fire intensity. White oak and chestnut oak acorns were selected by white-footed mice more often than black oak acorns, irrespective of char class. We discuss our results in terms of the implications of prescribed fire for short- and long-term responses of small mammals.

224^E: Potential reservoirs of *Borrelia burgdorferi* in a northern Illinois prairie species ecosystem

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Rodent species, particularly members of the genus *Peromyscus*, serve as reservoirs for tick borne diseases such as Lyme disease. Over the last twenty years, confirmed cases of Lyme disease in humans have markedly increased. In particular northern Illinois and southern Wisconsin are a particular hotbed of Lyme diagnoses. This area has also seen a large increase in efforts to restore tallgrass prairies during the same time. This study sought to identify rodent reservoirs of Lyme disease in prairie habitats. During the summer of 2015, tissues samples were collected from 223 rodents on a prairie restoration in Boone County, Illinois. Five species of rodents were captured: *Spermophilus tridecemlineatus*, *Microtus pennsylvanicus*, *Microtus ochrogaster*, *Peromyscus maniculatus*, and *Zapus hudsonius*. *Zapus hudsonius* was the most abundant (85 individuals) and *Microtus ochrogaster* was the least abundant (8 individuals). *Borrelia burgdorferi*, the causative agent of Lyme, was found in all five species via PCR amplification of Flagellin B using primers specific to *Borrelia*. Approximately 35% of rodents sampled were positive with infection rates ranging from ~20% in *P. maniculatus* to greater than 50% in *M. pennsylvanicus*. Engorged and questing ticks were also collected in the field, with a large percentage of those testing positive for Lyme as well. Data indicate that prairie restorations may harbor substantial amounts of Lyme disease and that several non-Peromyscine species may represent reservoirs of the disease.

225: The effect of a major drainage divide on the gene flow of the Eurasian otter

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Major drainage divides may significantly affect the dispersal, distribution, and genetic structure of semiaquatic animals. Assessing this effect is important for the proper management of endangered or invasive riparian species. I determined the fine-scale impact of a major drainage divide on the genetic structure and dispersal of the Eurasian otter (*Lutra lutra*) in the Bieszczady Mountains (Poland and Slovakia). I investigated the genetic structure of the otter population and assessed alternative dispersal models using landscape genetics methods. The analyses were based on 48 individual genotypes obtained from 622 spraint samples. Results indicate that the major drainage divide is not a barrier to gene flow for this population. This was established by analyses of population genetic structure and confirmed by analysis of the spatial distribution of samples originating from closely related individuals. In line with these findings, the best-supported dispersal model assumed that otters migrate through mountain passes, away from streams, thus revealing that they are able to cross a drainage divide. The genetic structure of the population studied exhibits an isolation-by-distance pattern; however, the locations of repeatedly recorded or closely related individuals revealed the occurrence of long-distance movements. Confirmed high mobility of otters and their ability to cross a major drainage divide ridge suggest that landscape obstacles and discontinuity of river network are unlikely to stop otter dispersal, gene flow, and recolonization of new areas.

226^F: Human influence on antibiotic resistance in the fecal matter of Itasca rodents

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Development of antibiotic resistance in human pathogens is of great concern to public health, but little is known about environmental reservoirs of antibiotic resistance genes (ARGs). The environmental origin of ARGs allows them to persist outside of clinical settings to some extent in most habitat types. We wanted to know if humans have some influence on the prevalence of ARGs in environmental populations of bacteria. In this study, we compared the prevalence of ARGs in fecal samples of rodent species (*Peromyscus* sp. and *Microtus pennsylvanicus*) between populations near established campsites and far from established campsites in Itasca State Park, Minnesota. Fecal samples were taken from five different sites (n=41) and tested for relative concentrations of two ARGs, tetM and a class 1 integron, using real-time quantitative PCR. Two sites had no evidence of the tetM ARG, and the three sites with tetM were not significantly different. The two sites with the closest proximity to humans had the highest relative concentration of the class 1 integron. These data suggest that rodent populations in Itasca State Park that are closer to established human activity have higher concentrations of ARGs in their fecal matter. It is

important to understand the extent to which humans influence the proliferation of ARG reservoirs in the environment so that we can work to prevent the formation of reservoirs for harmful ARGs.

227^F: Occupancy modeling to examine meso-mammal diversity and abundance at an urban-rural interface of Cheyenne, Wyoming

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Camera traps are a passive surveying method used to inventory and gather natural history and ecological information on vertebrates. In this study, camera traps were used to obtain occupancy estimates for meso-mammals in the Cheyenne Business Park Natural Area (CBPNA), an industrial complex on the edge of Cheyenne, Wyoming. Eight camera traps were deployed sampling forty three 100×100 m survey grids, with each grid surveyed by one camera for 7 days, totaling 301 trap days. Grids were assigned to 1 of 3 habitats (prairie, riparian, or woodland). Occupancy data were analyzed using a single-season, single-species model within habitats and across the CBPNA. In preliminary results riparian habitats hosted a more diverse meso-mammalian community in comparison to prairie habitats. At present, 4 mammal species (*Neovison vison*, *Ondatra zibethicus*, *Procyon lotor*, *Sylvilagus floridanus*) have been detected on the CBPNA and occupancy has been estimated. Neither *N. vison* nor *P. lotor* are well documented historically within Laramie County. While all of these species are known to be present in Laramie County, none have been documented on the CBPNA and this is the first study to estimate their abundance in southeastern Wyoming. Species expected, but not detected may have been due to anthropogenic or seasonal effects requiring further research. Results presented consist of winter data, but are part of ongoing research to elucidate meso-mammal population dynamics in southeastern Wyoming.

228: Mammal use of caves in Shoushan National Nature Park, Taiwan

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Caves provide important habitat for a wide variety of vertebrates and invertebrates. Caves could benefit mammals by providing sites for resting, mating, nursing young, protection, foraging, and hibernation. Shoushan, located east of Kaohsiung City, Taiwan, is an uplifted coral reef with altitude up to 350 m and many limestone caves. From November 2015 to March 2016, we assessed the occurrence of mammals as well as other wildlife in 44 caves to understand the cave fauna in Shoushan National Nature Park, a 9.3 km² isolated forest surrounded by urban Kaohsiung. We used echolocation call detection and spotlight survey along the passage inside each cave as well as camera traps at the entrances of eight caves. The caves varied in structure, length, and surrounding environment of the entrance. We recorded 12 mammal species in the caves, including three cave roosting bat species, two rodent and one tree squirrel species, Formosan gem-faced civet (*Paguma larvata taivana*), Formosan ferret-badger (*Melogale moschata subaurantiaca*), feral dog (*Canis familiaris*), Formosan Reeves' muntjac (*Muntiacus reevesi micrurus*), Formosan rock macaque (*Macaca cyclopis*), and human, and 11 non-mammal vertebrate and 85 invertebrate species. Bats (mostly *Rhinolophus monoceros*) were most abundant (>1500 individuals) and widespread (found in 16 caves) among mammals. Except bats, > 95% of the mammals were recorded by camera traps around the cave entrance, highlighting the importance of cave entrance to terrestrial mammals.

229: Comparing tree building approaches for a phylogenomic dataset with over 200 species

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DNA sequence datasets with hundreds of species and thousands of individual loci are challenging to work with. Some methods take shortcuts that might result in an inaccurate phylogeny. Other methods are

more robust but require a great deal of computational power. In this study, we compare several phylogenomic methods using a dataset of thousands of ultraconserved elements (UCEs) sampled from hundreds of crocidurine shrew species. We analyzed this massive data set using a supercomputer at Siena College and implemented two different phylogenomic methods: ASTRAL, a gene-tree-based method, and concatenated MrBayes analysis. In our poster, we compare these results, noting areas of agreement and areas of strong conflict. Overall, despite some cases of strong conflict, our results are largely in agreement, and provide a solid framework for ongoing taxonomic revisions.

230: Mammalian keratin as a useful source of high-quality DNA from museum specimens

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DNA derived from museum specimens is proving to be increasingly useful for projects related to phylogeography, systematics, taxonomy, disease, and conservation, among others. In particular, projects utilizing high throughput sequencing have facilitated obtaining large amounts of data from ancient/degraded DNA, thus resulting in a dramatic increase in destructive sampling requests to museums. Due to the destructive nature of sampling museum specimens for DNA extractions, a cost-benefit of loss of valuable specimen material relative to knowledge gained is required for any project utilizing destructive sampling. Variation exists in DNA preservation quality from historical specimens due to age, museum preparation types (e.g. dried, tanned, treated, formalin preserved), and other factors. Thus, it is important to assess DNA yield from different sources of museum specimens when considering the needs of a particular molecular project (e.g. mitochondrial versus nuclear datasets). We tested several common sources of DNA from museum specimens including osteocrusts, bone, skin+hair, and keratin. Analyses were performed on a variety of mammals including the orders Carnivora, Marsupialia, Lagomorpha, and Rodentia. DNA extractions included tests of two techniques (phenol chloroform versus silica-based). We quantified DNA quality by assessing average fragment size (Agilent Bioanalyzer electropherogram images), quantity (Qubit fluorometric quantitation), copy number (qPCR), and whole mitochondrial genome sequence coverage. Overall, keratin samples produced higher yields and larger fragment sizes of DNA than the other sources of museum specimens tested.

231: The efficacy of mammal urine as a lure in camera-trapping studies

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As part of a vertebrate biodiversity survey initiated at Georgia Southern University to obtain data for future sustainable development and management of the campus, we used camera trapping in combination with mammal urine to detect medium and large mammals. Mammal urine is advertised to gardeners as an herbivore deterrent and to hunters as an attractant. Camera trapping is widely accepted as an accurate, minimally invasive method for surveying mammals, and traps are frequently paired with bait or scent lures to increase detections, often of a target species, but the efficacy of specific lures is uncertain. We assigned four cameras to Georgia Southern's campus and four cameras to a rural area off-campus. We placed mammal urine of three different species, and water as a control (random, sequentially) at each camera trapping station and analyzed the relationship between presence of urine and mammal detections. The presence or absence of urine did not affect the number or species of mammals detected with camera traps, nor did prey species avoid camera traps with predator urine (i.e., the average number of "captures" for *Odocoileus virginianus* at predator, prey and water was $3.18(\pm 0.78)$, $1.37(\pm 1.1)$, and $1.87(\pm 1.1)$, respectively). Some animals (e.g., *Urocyon cinereoargenteus*) were curious about the urine as they were photographed sniffing the container. Based on the results of this study, mammal urine is ineffective as a lure for camera-trapping studies.

232^E: Human dimension of elephant conservation in South-East Bangladesh

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The 'human dimension' in wildlife management includes the participation of people in the stewardship of wildlife and related resources. It must be forefront in crafting effective management plans for countries like Bangladesh, where Asian elephants have been declared "critically endangered. Crop raiding, damage to houses, and other human values are proximate causes of human-elephant conflict, resulting in the death of at least 55 elephants and 200 humans since 2003. I have conducted face-to-face interviews on people's knowledge, interactions with elephants, and attitudes towards conservation, using structured questionnaires with 171 respondents across 109 villages in and near elephant habitat. Although analyses are in progress, preliminary results suggest approx. 73% of people favor elephant conservation, at least in principle. My second objective is to improve our understanding of how remaining elephant habitat has been altered as a consequence of human activities. I have collected Landsat images from the years 1989-2014 and conducted inventory in the remaining elephant habitat to identify land use changes and those patches that appear to be key to the perseverance of these animals. Preliminary results indicate the canopy coverage of remaining habitat is at present ≈31% of original habitat. In the past 25 years, ≈61% of elephant habitat has been lost. This information on habitat and human awareness and attitudes will be incorporated into desperately-needed plans for elephant conservation in Bangladesh.

233^E: Dangerous misperceptions: eastern cottontail survival in an agroecosystem

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Negative impacts of intensive agricultural practices on wildlife populations have resulted in the establishment of programs such as State Acres for Wildlife Enhancement (SAFE) to restore grassland habitat. One species that could benefit from such programs is the eastern cottontail (*Sylvilagus floridanus*). In Illinois, populations are estimated to have declined substantially over time, especially in agriculturally intense regions. To understand how mortality risk and perceived predation risk for eastern cottontails varies within an agroecosystem, we examined survival rates and perceived risk in restored grassland habitats and surrounding agricultural fields. To determine survival rates, we radio-collared eastern cottontails with VHF transmitters and tracked them year-round. To determine if habitats differed in perceived risk, we conducted giving up density (GUD) experiments in grasslands and adjacent agricultural fields. During the summer when crops (corn and soybean) were present on the landscape, mortalities occurred disproportionately in agricultural fields relative to grassland areas. However, GUD experiments suggested that cottontails perceived these same agricultural areas to be lower risk than grassland areas. This mismatch suggests that cottontail rabbits may be incorrectly assessing the risks of these habitats, and that agricultural fields may be acting as ecological traps. Our results can be used to inform selection of future SAFE sites, by considering landscape context, to more effectively manage eastern cottontail populations.

234^{E}: A temporal investigation of physiological stress for American pika (*Ochotona princeps*) in the Sierra Nevada**

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Non-invasive approaches to understanding physiological stress can be particularly informative for studying the response of a thermally sensitive species like the American pika (*Ochotona princeps*) to variation in its natural habitat especially in the face of anthropogenic climate change. Recent research validated the use of a corticosterone enzyme immunoassay for measuring glucocorticoid metabolites (GCMs) in pika feces as a proxy for chronic stress. The sampling of physiological stress in pikas holds great promise as a population monitoring tool. However, single measurements of GCMs may not accurately characterize natural fluctuations in chronic stress experienced by individuals over time. During the summers of 2013-2015, fresh fecal samples were repeatedly collected at occupied territories within

three pika populations located in the Sierra Nevada eco-region of eastern California to compare the variation in relative GCM concentrations: (i) among low and high elevation pika populations; (ii) among individuals and between sexes within populations; and (iii) within populations over time. Preliminary findings indicate that average GCM concentrations in Sierra pikas differ among individuals and populations with significantly greater chronic stress experienced at the lower elevations especially during the late summer months (July and August). Interestingly, average GCM concentrations did not differ significantly within or across seasons at higher elevations. Future analyses will investigate the combined effects of chronic stress, territory quality, and genetic variation on seasonal occupancy and individual pika survival. This research was supported by a Grants-in-Aid of Research awarded to Kelly Klingler in 2014.

235: Utility of whole mitochondrial genomes for species-level phylogenetics of *Maxomys spiny rats*

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Mitochondrial genes like cytochrome *b* have commonly been used to build species-level phylogenetic trees for mammals. With falling sequencing costs, it is now relatively cost-effective to obtain sequences from the entire mitochondrial genome for tree-building. Does this type of data produce more robust phylogenies than single mitochondrial genes? Or are individual mitochondrial genes sufficient and effective? To study this question, we worked with mixed pools of millions of nuclear and mitochondrial DNA reads sequenced from nearly 50 *Maxomys* specimens representing most of the recognized species. We compared both referenced-based and *de novo* whole mitochondrial assembly methods. We tested for the best partitioning strategy in PartitionFinder and then built phylogenies using MrBayes and RaxML for individual mitochondrial genes and for the whole mitochondrial genome. Overall, the trees produced from whole mitochondrial genomes had higher nodal support than trees produced from single mitochondrial gene analyses. We discuss potential benefits and tradeoffs of analyzing whole mitochondrial genomes.

236^E: Phylogeography of two northcentral Asian shrews (*Sorex tundrensis* and *Sorex caecutiens*)

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Shrews are one of the most abundant, widely dispersed and temporally persistent mammals. Shrews from the genus *Sorex* have a Holarctic distribution, a region characterized by dynamic climate change where fluctuating glacial and interglacial warming cycles were major historical factors that structured the demography and distribution of shrews. We examined DNA sequence variation (1140 bp of the mitochondrial cytochrome *b* gene) in recently collected (2015) Mongolian specimens to further test the role of LGM glacial refugia in phylogeographic structure of *Sorex tundrensis* ($n = 70$) and *Sorex caecutiens* ($n = 13$). We estimated intraspecific evolutionary histories and demographic parameters to help clarify the history of response to past climatic conditions. *Sorex caecutiens* was divided into two distinct clades, Eurasian clade and the Hokkaido Island clade. The Mongolian samples cluster with members of the Eurasian clade, with no phylogeographic structuring. *Sorex tundrensis* was divided into seven distinct clades: MNA, Central Siberia, East Siberia, Far West Siberia, Amga Basin, West Siberia, and Nearctic. Samples of *S. tundrensis* from Mongolia are clustered within the West Siberia clade. We calculated segregating sites, haplotype diversity, nucleotide diversity, Tajima's *D*, Fu's *F*, and R^2 for both species. Because climate change is greatest at high latitudes this background on historical demography provides an extraordinary opportunity to understand how northern mammals and their biotic communities are responding to rapidly warming conditions.

237: Population dynamics of an extinct cotton rat (*Sigmodon curtisi*) from the early Pleistocene of Florida

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Plotting the occlusal area (length x width) against the enamel height of m1s reveals distinct age cohorts, supported by morphological characters, within the population of *Sigmodon curtisi* from the late Blancan (early Pleistocene) Inglis 1C fauna from the west coast of Florida. These cohorts allow demographic studies of the *Sigmodon* sample, an approach that is seldom possible in small-rodent paleopopulations. Individuals at birth had a life expectancy of only 1.25 months due to high juvenile mortality seen in rodents. In this population the mortality rate in the first month was 75%, and 80% before the animal reached sexual maturity. Individuals that persisted into the second month of life had a total life expectancy of 3.5 months. Population dynamics studies require, among other items, a cyclic birthing regime. Unlike that seen in large mammals, the cyclicity in the Inglis 1C *Sigmodon* population may be the result of extremely rapid and continuous breeding after a reproductive hiatus. If correct, this is the first example of a seasonal curtailment of reproduction in a fossil population.

238^F: Shifting to a new place: influence of developmental timing on life-history schedules in order Carnivora

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During development energy demands for survival, growth, and reproduction must be balanced. Trade-offs occur between competing traits. These trade-offs are expected to have profound consequences for life-history schedules. We ask whether interspecific differences in the timing of morphological maturity are reflected in life history schedules. We characterize the patterns of evolutionary change in the timing of morphological maturity of the cranium and mandible for 7 species representing the suborders Feliformia and Caniformia and test the hypothesis that Feliforms reach morphological landmarks later in their life cycle (because of foraging differences) than Caniforms. Skulls representing individuals ranging from 1 day to several years of age were photographed and digitized in three views (ventral cranium, lateral cranium, and lateral mandible). Ontogenetic change in skull size (centroid size) and shape (Procrustes distance from the average for the youngest specimens) were plotted for each species and the ages at maturity compared. Age at maturity for skull size and shape, was defined as the 95% of the asymptotic (adult) value from nonlinear growth models selected using Akaike Information Criterion. We fit an Ornstein-Uhlenbeck model of character evolution to our age of maturity estimates. This model uses a reverse jump MCMC approach to consider clade-specific optimum trait values (thetas). Preliminary data suggest marked differences in timing of development between Feliformia and Caniformia.

239^F: Simulating patterns of home range selection by the American marten in northern Wisconsin
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Habitat selection occurs at multiple spatial scales. Factors selected for at the scale of the home range may differ from factors selected for within the home range. In addition, how an individual perceives the landscape may be more relevant than the actual suitability of the landscape and its associated habitat. We investigated mechanisms of home range selection by American martens (*Martes americana*) in northern Wisconsin using the spatially-explicit, individual-based modeling tool SEARCH (Spatially-Explicit Animal Response to Composition of Habitat). Using SEARCH and a pattern-oriented modeling approach, we simulated the dispersal of reintroduced American martens to test alternate models of habitat suitability for their capacity to reproduce empirical movement patterns observed from actual martens. Habitat suitability models varied based on whether martens perceived habitat types as suitable or unsuitable, and also varied based on the scale at which martens selected habitat. Minor changes in suitability models resulted in disproportionate shifts in response metrics. Our results demonstrate the sensitivity of the process of home range establishment to models of habitat suitability and emphasize the need for accuracy and rigor in the development of species-specific suitability models. Furthermore, our results demonstrate the utility of individual-based simulation tools for management applications, particularly when working with species that occur at low densities or are of conservation concern.

240:** Determinants of multiple paternity in a fluctuating population of ground squirrels

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Multiple paternity is common in vertebrates that produce several offspring in the same reproductive bout, but the rate often varies among and within populations. Three primary explanations for this variation have been advanced: null models based on encounter rate of mates, socioecological models dependent on the ability of males to monopolize females, and age- or condition-dependent models of female choice. We used 18 years of genetic and demographic data to examine the mating system and patterns of multiple paternity in a free-living population of golden-mantled ground squirrels (*Callospermophilus lateralis*). The mating system was polygynandrous, but opportunity for sexual selection was lower for females than for males. Annual reproductive success of males was low for yearlings and new immigrants, and increased with breeding tenure in the population. Multiple paternity was evident in 62% of litters. In accordance with the socioecological model of male monopolization, rates of multiple paternity decreased with female spatial clustering, unless male-male competition, as indicated by male density, was also high. From Bateman gradients, we found no fitness benefit of multiple paternity for females, and in support of the female choice model, multiple paternity decreased with maternal age and peri-oestrous mass. Together, our results suggest that variation in the rate of multiple paternity in golden-mantled ground squirrels was determined primarily by the active strategies of males and females. This research was supported by Grants-In-Aid of Research awarded to Caitlin Wells.

241^E: Why did the wolf poop in the road? Road density doesn't impact wolf road usage

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Large carnivores demonstrate road aversion by avoiding roads during movements and choosing territories with reduced road density. Wolves exhibit similar aversions to major roads, but often use minor roads as travel corridors. However, it remains unclear if wolves preferentially choose the minor roads they use. We utilized scat collections to evaluate the hypothesis that road use by wolves is independent of distance to other roads. We analyzed Global Positioning System coordinates of 22 scats collected in Wisconsin and Michigan. For surveys conducted, 42.9 wolves were detected and 9.9 scats were collected per 100km. We added a 1km buffer around each scat and surrounding randomly placed points along study area roads using ArcGIS. We created a Euclidean distance to roads raster file and calculated zonal statistics of each buffer set. If the random buffers are in areas of greater road density, the average pixel value should be lower. The average road value per pixel within the scat buffers (274.68 ± 116.78) was not significantly different ($t=2.03$; $p=0.78$) from the average road value per pixel of the random buffers (263.55 ± 119.82). Our results indicate wolves do not exhibit preference for roads used as travel corridors relative to overall road density.

242^{F}:** Examining the relationship between cortisol levels and ectoparasite loads in degus (*Octodon degus*)

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The endocrine stress response allows vertebrates to appropriately react to stressful stimuli such as predator presence, low food availability, and social instability. By releasing glucocorticoids (GCs) into the bloodstream, the endocrine stress response essentially redirects energy from unnecessary physiological processes (e.g. reproduction, digestion) to those immediately necessary for survival (e.g. energy mobilization, heightened fight-or-flight response). Ectoparasitism may be one such stressor that elevates GC levels, yet the relationship between ectoparasite loads and the endocrine stress response has not been well defined. We measured ectoparasite loads and GC (cortisol) concentrations in two ecologically and geographically distinct populations of free-living degus (*Octodon degus*) in central Chile. Exotic fleas have been identified as the predominant ectoparasites in one population. Between populations, there may be variation in the ectoparasite species and their bacterial communities, potentially influencing cortisol levels. Thus, our aim is to explore the relationship between cortisol levels and ectoparasite loads in two populations of degus. This research was supported by a Grants-In-Aid of Research awarded to Madeline Strom.

243: Ancient DNA and NGS bring new insights on *Mustela* systematics

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With at least 18 full species the genus *Mustela* shows a wide distribution through Eurasia, Africa, and the Americas. Recent molecular phylogenies have shown different arrangements in genera systematics. The study with the largest taxonomic coverage up to now included 16 species on a time-scale, but based in a single gene. Other works with greater gene sampling included the mitochondrial genome for some species, but with less taxa. The necessity to better understand the systematic arrangement of *Mustela* led us to sample three species not considered in previous studies dealing with mitochondrial genomes: *Mustela africana*, *M. felipei* and *M. itatsi*. Samples of all three species were collected from museum skin or skeleton vouchers. Ancient DNA was extracted using different protocols to proceed with library-prep for Illumina Mi-Seq NGS. The mitochondrial genome of *M. africana* and *M. felipei* are being assembled, and *M. itatsi* will soon be sequenced. We aim to assemble the mitochondrial genome, as well as capture other nuclear markers through bioinformatics tools. Based on a more comprehensive data matrix (new sequences + GenBank) we hope to present a clearer view of *Mustela* systematics with stronger support. Moreover, with a Bayesian relaxed clock and ancestral state reconstruction approaches we will be able to better trace hypotheses concerning the followed pathways by its lineages through time.

244^E: Canid collision: range expansion by coyotes (*Canis latrans*) and crab-eating foxes (*Cerdocyon thous*) in Panama

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Coyotes (*Canis latrans*) and crab-eating foxes (*Cerdocyon thous*) are two generalist canids that are aggressively expanding their ranges in human-disturbed habitats in Central America. However, the current distribution and future expansion potential of the two species remains poorly characterized. To determine occupancy patterns for both species along the frontiers of their ranges, we deployed 112 camera traps across a human-modified landscape in eastern Panama during March – June 2015. We also compiled recent occurrence records from 120 camera traps in protected forests in Panama, roadkill records along the Pan-American Highway, and observation in Colombia from the Global Biodiversity Information Facility (GBIF), producing four auxiliary datasets. We jointly analyzed all datasets in a novel

data fusion framework, allowing us to study broad-scale spatial patterns while accounting for sampling differences among the datasets. We used this model to characterize major habitat associations and predict possible expansion routes for coyotes and foxes in Panama. Our findings contrast the predictions of previous models and reassess the role of deforestation in the recent range expansions by these species.

245^E: Challenging perceptions of Afroinsectiphilia mammal radiations through comparative macroevolutionary analyses

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Afroinsectiphilia mammals provide an excellent opportunity for comparative study of seemingly 'exceptional' and 'unexceptional' radiations along the diversification spectrum. This intriguing subclade of Afrotheria includes aardvarks (Orycteropodidae), elephant shrews (Macroscelididae), golden moles (Chrysochloridae), and tenrecs (Tenrecidae). Each of these families is unique with contrasting degrees of phenotypic specialization. Preliminary findings from Bayesian Approximation by Macroevolutionary Mixtures (BAMM), based on a phylogeny built from available nuclear and mtDNA sequences, show unexpectedly high speciation rates among golden moles – a relatively homogeneous fossorial family – and low rates among tenrecs – a family that adaptively radiated on Madagascar. However, body mass diversification rates are not correlated with these trends. Rates are only high in the aardvark and a single species of elephant shrew and, depending on sampling coverage, low among tenrecs. These preliminary results indicate that common perceptions of these radiations might be incomplete – for example, golden moles might be more 'exceptional' than previously hypothesized. Consistently low rates of diversification among elephant shrews, with the exception of a single species, is also striking and sets the backdrop for further study.

246^E: The impact of prairie restoration on rodent population and community dynamics in northern Illinois

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Anthropogenic destruction for agricultural, residential, and commercial purposes has caused tallgrass prairies to become one of the most endangered habitat types in the world. Restoration efforts have been at least partially successful in reestablishing native plant populations through methods such as seeding and controlled burns. However, it is necessary to assess the effects of these efforts on animal communities as well. This study focused on the community dynamics of small mammals in a small prairie restoration over the course of three years. Animals were trapped in two prairie patches in different stages of ecological succession during the summers of 2013, 2014, and 2015. *Spermophilus tridecemlineatus*, *Microtus ochrogaster*, *Microtus pennsylvanicus*, *Peromyscus maniculatus*, and *Zapus hudsonius* were captured over the course of 3 years and the abundances of each were compared. Species richness, Simpson's diversity index (D), Shannon's diversity index (H), species evenness, and Peterson's homogeneity index were calculated for each patch for each year and comparisons were made between the patches. Vole populations experienced a decrease from 2014 to 2015. Other species have shown large population increases, particularly *Zapus hudsonius*. Diversity also increased over the course of the study, with a slight decrease in 2014 due to the high prevalence of voles compared to other species. Additional monitoring is necessary to understand long-term population trends in small prairie patches such as this.

247: The importance of cliffs in the roosting and foraging ecology of eastern bats

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Sport climbing is a rapidly growing sport in the US and elsewhere. Although several species of bats commonly roost in cliffs, the potential for impacts of climbers on bats has not been examined. We initiated a pilot study on the potential impacts of climbing on bats in Obed Wild and Scenic River, Tennessee to: 1) determine if small-footed bats (*Myotis leibii*) avoid climbed cliffs for roosting, and 2) determine if overall bat foraging and commuting activity varies between climbed and unclimbed areas. We used radio-telemetry to track small-footed bats to day roosts, and Anabat SD2 detectors to compare bat activity between climbed and unclimbed areas of regularly climbed cliff faces, and between climbed and unclimbed cliffs. Four adult male small-footed bats were tracked to nine day roosts, all of which were in various types of crevices including five cliff face roosts (three on climbed and two on unclimbed faces). Overall bat activity was significantly higher along climbed cliffs than unclimbed cliffs although species richness did not differ between climbed and unclimbed cliffs. Lower activity along unclimbed cliffs may have been related to lower cliff heights and more clutter along these cliff faces. High bat activity along cliff faces suggests that these are important roosting and commuting sites and that additional study of bat use of cliffs is warranted.

248:** Behavioral and hormonal differences between juvenile and adult brush mice (*Peromyscus boylii*)

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Behavioral traits such as exploration, activity, and boldness have been suggested to influence dispersal movements of young animals, as have hormones such as corticosterone. We compared multiple behaviors between juvenile and adult brush mice (*Peromyscus boylii*), using open-field and social odor tests to quantify behavior. Behavioral trials were recorded and later scored to quantify boldness (emergence into an open field), activity (cm traveled in the open field), exploration/novelty seeking (time spent investigating novel odors), and social preference (preference for the scent of an unfamiliar conspecific vs. a non-social odor). We also collected a fecal sample from each animal to measure fecal glucocorticoid metabolites (CORT). We predicted that in comparison to adults, juveniles would be bolder, more active, and more exploratory, but did not necessarily expect to find a difference in social preference between age classes. Preliminary analysis indicates that juvenile brush mice have higher levels of exploratory and novelty-seeking behavior than adults, but we did not detect any differences in activity or social preference. Bold individuals had lower levels of fecal corticosterone across all ages. Juveniles also had higher levels of fecal CORT than did adults. Our results suggest that in brush mice, both behavioral traits and hormones previously implicated as influencing dispersal behavior in other species may be elevated during the juvenile life stage. This research was supported by a Grant-in-Aid of Research awarded to Rebecca Kelley in 2014.

249: Prevalence of raccoon roundworm (*Baylisascaris procyonis*) in a semi-urban environment in northwest Missouri

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Raccoons are the only member of their family to naturally occur in Missouri, and are very adaptable to life around humans. Their proximity to humans can cause some health concerns. They can carry diseases and parasites that could be transmitted to humans. One such parasite is raccoon roundworm (*Baylisascaris procyonis*). Raccoon roundworm larvae can infect the central nervous system of humans, causing disease and in rare cases death. Since raccoons live in urban and suburban environments, there is increasing awareness of the possibility of human infection from raccoon roundworm. Roundworm eggs are shed in raccoon feces, and can remain viable in the environment for long periods of time. We began a survey of raccoon latrines on the MWSU campus (> 650 acres) to determine the distribution and prevalence of raccoon roundworm. We established 100 x 100 m grids on the campus of MWSU and have begun to systematically search each grid. We recorded the location of each fecal sample and latrine using mapping grade global positioning systems (Trimble Navigation, Ltd., Sunnyvale, CA). We analyzed each sample for raccoon roundworm using standard fecal floatation technique. We evaluated 345 samples and found raccoon roundworm eggs in 32; an approximately 9.3% infection rate. The extent to

which our preliminary results accurately reflect infection rate and prevalence, will depend upon analyzing additional samples, expanding out into the surrounding landscape.

250: Starting an LCCMR prairie restoration grant: monitoring of small mammals

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Minnesota State University Moorhead (MSUM) was recently awarded a Legislative-Citizen Commission on Minnesota Resources (LCCMR) grant to restore old farmland (called the “Houston Property” HP) owned by the MSUM Regional Science Center (RSC) (near Glyndon, MN) and an adjoining former Golf Course (GC) back to native prairie habitat. One main grant objective is to live-trap small mammals to determine species composition, abundances, habitat use, and behaviors before, during, and after restoration. During summer 2015, small mammals were live-trapped on HP and GC to monitor “pre-restoration” populations. For comparison, 2 reference sites were also live-trapped on the nearby Bluestem Prairie. Trapping was conducted from 2nd July - 30th August 2015. HP was re-trapped in September as part of the LCCMR grant to integrate restoration efforts into related college courses. HP had the highest species diversity, including masked shrews (*Sorex cinereus*), a meadow jumping mouse (*Zapus hudsonius*), meadow voles (*Microtus pennsylvanicus*), deer mice/white-footed mice (*Peromyscus* spp.), and thirteen-lined ground squirrels (*Ictidomys tridecemlineatus*). Not surprisingly, the GC yielded only 1 *Peromyscus* spp. and 1 meadow vole. Surprisingly, 1 of the reference sites yielded only 1 *Peromyscus* spp and thirteen-lined ground squirrels. The other reference site had higher diversity including 2 Richardson’s ground squirrels (*Uroditellus richardsonii*) and 1 short-tailed weasel (*Mustela erminea*).

251^F: The long-term effects of post-fire succession on small mammal communities in the Greater Yellowstone Area

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Fires are an important and increasingly common driver of habitat structure in the intermountain west. Through an ongoing study of burned and adjacent unburned areas along the John D. Rockefeller, Jr. Memorial Parkway, we examine the long-term effects of the 1988 fire season on community assembly, succession, and ecological processes. We compare mark/recapture and removal data for insectivorous mammals and rodents, as well as habitat measurements and invertebrate samples from 2 burned and 2 unburned grids at 8 regular intervals across 27 years of post-fire succession. Since the beginning of this long-term study, the total number of mammal species has increased across all sites, and relative abundance in burned areas has shifted from early successional species (*Peromyscus maniculatus*) to those more associated with the adjacent old growth forests (e.g., *Myodes gapperi*). With the exception of 1991, the burned grids have consistently harbored more diverse small mammal communities than unburned control grids. Significant, long term differences in vegetation based upon burn history were observed, including changes in ground cover, less canopy cover, and more coarse woody debris in burned sites. These cover characteristics may explain differential movement distances observed in small mammals. This work provides a unique long-term picture of the interrelationships of small mammal communities and correlated habitat variables as these ecosystems undergo post-fire succession.

252^F: An overview of detection methods for plains spotted skunks (*Spilogale putorius interrupta*) in Texas

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The plains spotted skunk (*Spilogale putorius interrupta*) experienced a range wide decrease in population during the second half of the 20th century and currently is being reviewed for threatened or endangered

status under the U.S. Endangered Species Act. Sampling for the plains spotted skunk is difficult due to the rareness of the species and its cryptic nature. Two methods were used to record spotted skunk detections in Texas. The first was a combination of field techniques (live traps, track plates with hair snares, and camera traps) deployed in 5 counties throughout the state. The second method used was the solicitation of verifiable *S. putorius interrupta* observations from wildlife professionals and the general public. This outreach included the request that future detections are recorded and tissue samples be taken, if possible. We surveyed 416 professionals via email and collected citizen science data from multiple projects on iNaturalist.org. Fifteen (n=12 verified and 3 unverified) detections have been compiled using all methods to date. In 3931 survey nights, only 3 skunks were detected using the field techniques (detection rate=0.076%). The surveys of professionals resulted in 7 verified and 1 unverified account (success rate=1.7%) and the iNaturalist.org data resulted in 2 verified and 2 unverified accounts.

253: Discovering the Andean diversity: long-term mammal inventory in Parque Nacional Natural Las Orquídeas (Colombia)

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The Neotropics, one of the most species-rich regions in the world, harbors 5 of the world's biodiversity hotspots. Two of such hotspots are found in Colombia, the Andes and the Choco; both of which account for 50% of the 1700 species of neotropical mammals. *Las Orquídeas* National Park is located in the northern terminus of the western slope of Cordillera Occidental and notably it protects areas of both Chocoan rainforest as well as a wide elevational gradient (300 to 3450 meters) of Andean forests. Despite its status as a protected area, the park must orient its conservation strategies towards the species present on this area, nonetheless, no rigorous inventories have been developed in the park and a species list is currently lacking. Previous mammal research has only recorded 37 species of mammals of a minimum estimated diversity of 183 for this area. This work presents the results of the first two years of a five-year inventory of mammals at Orquídeas National Park. So far, this has been the inventory with the largest trapping effort for Colombia and the 80% of the total captured species represent first records in the park, including highly relevant biogeographical records (e.g., *Marmosa waterhousei*, *Thomasomys bombicinus*) and endemic or threatened species (e.g., *Handleyomys fuscatus*, *Microsciurus otinus*), which are important candidates for the park's Valuable Conservation Objectives.

254: Behavior (not) under pressure: personality and behavioral syndromes in laboratory Siberian dwarf hamsters

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In many species, individuals show consistent behavior patterns relative to other individuals (personalities). Specific behavioral combinations (behavioral syndromes) particularly correlating activity, aggression, and boldness are common. In several non-mammals this syndrome is present only in populations under predation, suggesting that the phenotypic combination is maintained through selection. We investigated whether Siberian dwarf hamsters (*Phodopus sungorus*) in a laboratory colony displayed personalities, and if so whether an active-aggressive-bold syndrome was present under this relaxed selection pressure. Each animal was tested multiple times in a tunnel maze assay for activity, and then same-sex aggression trials in a neutral arena against different opponents. Anti-predator boldness was assessed as decreased foraging in the presence of mink scent; we have only one score per animal from this pilot test. Dwarf hamsters showed consistent individual personalities in all three behaviors. Preliminary analysis suggests positive correlation between activity and aggression in males but not in females. Such a partial behavior syndrome in captivity would be consistent with behaviors at least partially linked through common physiological pathways in this rodent. In the wild, *P. sungorus* are highly territorial; a behavioral syndrome suggests that high fitness consequences of aggression strategies may then also shape other ecological characteristics such as home range, foraging, and dispersal activities.

255^F: A molecular diet analysis of the western bonneted bat (*Eumops perotis*) from southwest Texas

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The western bonneted bat (*Eumops perotis*), the largest North American bat species, is a known insectivore, yet information regarding the specific insect families, genera, and species consumed by this bat species remains unclear. Using next generation sequencing technology, COI mtDNA sequences from prey-items present within a fecal sample obtained from an adult female western bonneted bat inhabiting Big Bend National Park, Texas were extracted and compared to known sequences in GenBank. A neighbor-joining tree was used to cluster the resulting 221 nucleotide sequences along with 15 published sequences obtained from top GenBank matches. At least 2 orders (Lepidoptera and Hemiptera) and 6 families of insects have been documented as targeted prey-items of the western bonneted bat from this fecal sample. Identification to genus and species level has proven more difficult due to a lack of reference sequences. Results from this study have served to expand previous knowledge regarding the diet of this species, and additional analyses from fecal samples of western bonneted bats will help to further elucidate prey items consumed by this species.

256: Population genetics of isolated Abert's squirrel populations

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In much of the southwestern United States, forests are restricted to high elevations. This has led to the separation of these forested "sky islands" from similar environments. Many forest obligates are unable to travel across the deserts that separate forests, and thus form isolated populations. One such species is the Abert's squirrel, which inhabits high elevation conifer forests of the southwest. In addition to natural, long term isolation, Abert's squirrels were successfully transplanted by state game agencies to several mountain ranges in Arizona and New Mexico from 1940-1977. The numbers of individuals, sex ratios, and dates of these transplants are documented, allowing us to compare genetic diversity of transplanted populations to each other based on the number of individuals transplanted. In addition we will compare genetic diversity of transplanted to natural populations in both isolated and more continuous habitats. To determine the effects of this isolation we will use tissue samples acquired from live trapping squirrels, hunter kills, and road kills. We will then extract and amplify DNA for 10 microsatellite loci by using primers designed for the eastern gray squirrel and the eastern fox squirrel. We will then calculate heterozygosity, inbreeding levels, and genetic distance for the Abert's squirrel populations. This work will expand our understanding of genetics of isolated populations and inform the future management and conservation of isolated tree squirrel populations.

257: Rodents from the Upper Pleistocene of Quebrada Chalán and their paleoecological context

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Currently, Ecuador harbors more than 102 species of rodents of which 65 belong to the Family Cricetidae. Despite the presence of abundant paleontological sites along the Andes, the Quaternary rodent fauna of Ecuador has been little studied. Here we analyze the rodent fauna retrieved from the Cangagua Formation - a distinctive and typical volcanoclastic succession in the Andean valleys - in Quebrada Chalán, located in the Chimborazo province. The samples were collected in 1950 by Claudio Reyes and Robert Hoffstetter, and 2009-2010 by the authors. We identified the following species: *Microryzomys altissimus*, *Microryzomys* sp., *Akodon mollis*, *Akodon* sp., *Phyllotis andium*, *Phyllotis* sp., *Thomasomys aureus*, *Thomasomys baeops*, *Sigmodon inopinatus* (Cricetidae), and *Cavia* sp. (Caviidae). This faunal association suggests a Paramo environment (high elevation grasslands) with wetlands and meadows that served as shelters for fauna in the upper Pleistocene. Currently, this site shows typical mid-elevation vegetation. This environmental shift could be attributed to glaciations along the Andes during the Pleistocene.

258^F: Taxonomy, fossils and phylogeny of Ecuadorian shrews

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Little is known about the phylogenetics and fossil record of South American shrews despite their scant diversity in the region. To alleviate this lack of knowledge, we conducted an integrative systematic review of Ecuadorian shrews using extant and fossil specimens. Our efforts resulted in: 1) The description of a new species, *Cryptotis niausa*, which is the largest of the Ecuadorian species. Also, this new species has the lightest coloration and a characteristic yellow patch on the chest, while the other Ecuadorian species - *C. equatoris*, *C. montivagus*, and *C. osgoodi* - are uniformly black or dark grey. 2) The first molecular phylogenetic assessment of Ecuadorian shrews (*thomasi* group), reveals that this group is likely paraphyletic, implying at least two colonization events of South America. 3) We identified fossil remains of shrews, by multivariate morphometric analyses, as *C. niausa*. Radiocarbon dating of associated fossils retrieved from the same outcrop in Quebrada Chalán, Chimborazo province, revealed this outcrop as being 41,000 years old, meaning that these fossils of shrews constitute the oldest records in South America. Our results contribute to the understanding of the diversity of South American shrews, but it is evident that to have a deeper understanding of their phylogenetic relationships and biogeographic history we should study Colombian and Venezuelan species as well.

259: Sex influence in the habitat use of the frugivorous bat *Sturnira hondurensis* in agricultural landscapes

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Habitat loss influence growth and extinction rates in animal populations. The response of an animal to habitat change depends on its mobility, territorial behaviour and reproductive state. Phyllostomid bats respond in multiple ways to habitat fragmentation in terms of richness and abundance. However, population aspects as sex or reproductive state have been taken into account for a few studies. Using as a model of habitat loss the replacement of cloud forest by coffee plantations in Veracruz, Mexico, we set as our objective to determine habitat use and foraging behaviour between males and females of the frugivorous bat *Sturnira hondurensis*. In general, females showed larger home ranges than males ($F = 4.31$, $p = 0.05$). The minimum area of foraging showed no significant differences between sexes, however, the interaction between habitat and sex itself was significant ($F = 5.192$, $df = 1$, $P = 0.03$). In cloud forests, males and females differed in the frequency they consumed fruits, mainly of the Solanaceae family ($X^2 = 6.21$ ($df = 2$, $n = 120$, $P = 0.05$)). Whereas apparently females are more sensitive to modified habitats, more knowledge should be generated about habitat needs for females in different reproductive stages (i.e pregnant females) that are particularly susceptible because of their higher energy demands. Forest fragments represent an important source of resources and their conservation should be a priority.

260: Long-term data reveals influence of removal trapping on wild small mammal populations

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Research archives are experiencing a marked increase in use of specimens for collection-based science, while simultaneously facing an overall decrease in new accessions and declines in support necessary for curation and long-term maintenance. Considering immediate and projected conservation needs, there exists an ethical responsibility to preserve biological materials that will vouch for the existence of a given species both temporally and spatially, enable often unrealized future research potential, and qualify substantial investments in field efforts. Yet, techniques such as removal trapping are too often avoided by researchers due to “ethical” concerns, increasingly not permitted by agencies, and generally are perceived as resulting in negative impacts on wild populations. I investigated the impact of repeated

removal trapping by comparing changes in richness and diversity of small mammals between removal versus non-removal sites. The Sevilleta National Wildlife Refuge in central New Mexico supports a high diversity of small mammals. Between 1992-1998, standard trapping webs were systematically sampled across six habitats, reflect non-removal methods for three webs, and removal trapping for two webs. Preliminary comparisons indicate no significant effect on richness or overall densities from removal methods, although short-term changes in relative abundance within communities may occur. Specimen collection as part of field survey efforts can provide rich archives for numerous studies, and should continue for research aimed at assessing environmental change across temporal and geographic scales.

261^E: Endoparasite richness, genetic diversity, and co-evolutionary dynamics of the endemic Pribilof Islands shrew (*Sorex pribilofensis*)

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St. Paul Island in the Bering Strait between Alaska and Far East Siberia supports one native mammal species, the Pribilof Islands shrew, isolated there following fragmentation of the Bering Land Bridge (~16,000 ya). This shrew is the only species in the subgenus *Otisorex* (having a Nearctic common ancestor) that is listed as endangered (IUCN red list), although this status largely reflects a deficiency of data. To better understand challenges facing management of this small isolated population under rapidly changing environmental conditions, we will investigate both parasite and genetic diversity associated with this mammal species. We aim to test three hypotheses: 1) that this population exhibits very low genetic diversity due to both prolonged isolation and phylogeographic history; 2) that parasite diversity is low due to faunal relaxation; and 3) that associated endoparasites reflect a Nearctic origin of this shrew (ie. coevolution) rather than acquisition of new parasite taxa as shrews shifted their historic distribution. We will assess mtDNA diversity within a population of ~30 specimens donated by the Native Aleut Tribe of St. Paul, and use molecular and morphological methods to identify endoparasite taxa. Both host and parasite genetic sequences will be compared with mainland taxa from Russia and Alaska using tree-based methods. Preliminary analyses have identified multiple new endoparasite species records from this locality including cestodes, nematodes and trematodes.

262: Multi-locus phylogenetic inference of the howler monkey radiation (*Alouatta*)

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Howler monkeys (*Alouatta*) are the most widely distributed New World primates. They occur in tropical rain forests, flooded and gallery forests, and deciduous and semi-deciduous seasonal environments. Despite their importance as seed dispersers and ecological indicators, many species are threatened by habitat loss and alteration. Available phylogenetic hypotheses for this genus have used chromosomal characters or a limited number of molecular markers and sampled specimens. Yet, branching patterns conflict between studies or remain unresolved. We provide a new, highly resolved and supported phylogenetic hypothesis for *Alouatta*, including South American (*A. guariba*, *A. caraya*, *A. belzebul*, *A. guariba*, *A. seniculus*, *A. sara*) and Mesoamerican taxa (*A. pigra*, *A. palliata*) based on 13 non-coding nuclear loci under a concatenated Bayesian approach (MrBayes) and a coalescent-based species tree method (*Beast). Contrasting with previous studies, we found that *A. guariba* and *A. belzebul* are not sister taxa; *A. belzebul* composes a clade with *A. caraya*, *A. seniculus* and *A. sara*, and *A. guariba* was recovered as sister to the remaining South American species. Moreover, we found for the first time a highly supported sister relationship between *A. sara* and *A. caraya*. We discuss the biogeography of the group in the light of the new results.

263: Investing in biodiversity collections for the future: a new century at the UMMZ

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The University of Michigan Museum of Zoology (UMMZ) is a recognized leader in biodiversity research and education. It houses approximately 13 million specimens organized in six divisions (Birds, Insects, Fishes, Mammals, Mollusks, and Reptiles and Amphibians). All collections rank in the top 10 in size for their discipline and most rank in the top five nationally. As collections associated with a university, some of the collections rank first in the world. In 2009, UM addressed storage limitations and safety issues for the UMMZ's enormous ethanol-preserved collection by relocating the collections to a newly renovated facility, referred to as Varsity Drive. In August 2015, an additional renovation at Varsity Drive, which also included space for the UM anthropological, botanical, and paleontological collections, increased total renovated space to approximately 97,000 gross square feet with new 1) environmentally-controlled collection space, 2) preparatory laboratories, 3) research offices and laboratories, 4) compact storage for paper collections and libraries, 5) administrative support offices, and 6) a demonstration room for teaching and public programs. The installation of new archival specimen cabinets will be completed by June 2016, and the relocation of specimens will begin May 2016 with an expected completion date within 12-18 months. Solutions for public transportation and a new building name are under consideration. Total university investment is ~\$44,450,000.

264^E: Does translocation alter resource selection during parturition in desert bighorn sheep (*Ovis canadensis nelsoni*)?

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Translocations are a key management strategy for recolonizing populations, introducing species into new habitats, and increasing population size and genetic diversity in many species of wildlife. This strategy is especially popular in the management of ungulate species such as desert bighorn sheep (*Ovis canadensis nelsoni*), whose populations have dwindled across their range over the last several decades. In an effort to reestablish populations and reduce population level die-offs, managers across the western United States have increased translocation efforts of bighorn sheep. However, the effects of these translocations on parturition site selection and resource selection associated with raising neonates is not well documented. In an effort to increase the understanding of translocation effects on these life history traits, the University of Nevada, Reno and Nevada Department of Wildlife captured and collared 30 adult, female sheep on Lone Mountain, of which 15 were translocated to the Garfield Hills range. In addition to receiving collars, all individuals were given vaginal implant transmitters (VITs) to provide valuable parturition timing information. Following captures, we monitored parturition events, adult resource selection, and neonate survival in both study areas. We used mixed effects logistic regression to identify parturition site selection and resource selection following parturition events in each area and compared results to determine changes in selection. These results will help biologists implement translocation techniques that increase recruitment potential in translocated populations.

265^E: Cryptic pika (Ochotonidae) species revealed by genetic, morphological and ecological evidence

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The genus *Ochotona* Link, 1795 (Family Ochotonidae), commonly known as pikas, represents one of the most common cold-adapted herbivores occurring in the higher altitudes of the Himalaya. The genus is largely Asian, with 26 of 28 known species having been reported from Asia (Lissovsky, 2014). Most Asian pika species have similar morphology and overlapping geographic ranges, which leads to uncertainty in

their in-field identification and can lead to confusions in taxonomy. We field-sampled, measured and genotyped pikas from the Sikkim region of the eastern Himalayas to assess their diversity. Our analyses revealed the occurrence of a cryptic lineage - *Ochotona sikimaria*, previously reported as a subspecies of *O. thibetana*, based on morphological similarity. Estimated species tree, mitochondrial gene tree and morphometric analyses clarifies the *O. sikimaria* is not a taxon of subspecific rank. Our results support the elevation of this lineage to the species level, as it is genetically divergent from *O. thibetana*, as well as its sister species, *O. cansus* (endemic to central China) and *O. curzoniae* (Tibetan plateau inhabitant). Further, the distribution range of *O. cansus*, *O. thibetana*, *O. curzoniae* and *O. sikimaria* demonstrate isolated range of *O. sikimaria* from its sister species. We estimate the Sikkim lineage diverged from its sister species about 1.7–0.8 myr, coincident with uplift events in the Himalayas.

266^F: A non-invasive and comparative approach to assess reintroduction efforts of American martens in Wisconsin

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Despite the targeting of carnivores for reintroductions in an attempt to restore ecosystem function, the majority of reintroductions fail or require periods of prolonged recovery. American martens (*Martes americana*), one of the most widely reintroduced carnivores in North America, have faced similar challenges in repatriating parts of their range, and currently are endangered in Wisconsin following serial reintroductions. Using non-invasive genetic mark-recapture techniques our partnership of University of Wisconsin- Madison, Wisconsin Department of Natural Resources, United States Forest Service, and Great Lakes Indian Fish and Wildlife Commission are quantifying the status and viability of martens at two sites in Wisconsin: the Nicolet and Chequamegon National Forest. We have concluded our demographic study on the Chequamegon National Forest, identifying limitations to recovery including isolation and potential competitive interactions with fishers, and are currently sampling martens in the Nicolet National Forest to similarly quantify viability. Ultimately, we will combine assessments into a comparative framework to assess marten reintroductions statewide and understand the mechanisms limiting recovery.

267: Modeling microhabitat parameters as predictors of trapping likelihood for four species of small mammals

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A small mammal capture-recapture study was conducted in 2013-2015 utilizing two 0.65 hectare deer exclosures constructed in the oak-maple-eastern hemlock forest of northeastern Pennsylvania heavily browsed by white-tailed deer (*Odocoileus virginianus*). Forty Sherman trap locations were utilized in each exclosure and in two sites adjacent to each exclosure. Nine microhabitat characteristics were quantified for each Sherman trap site. We modeled abundance for white-footed mice (*Peromyscus leucopus*) and eastern chipmunk (*Tamias striatus*) and presence for northern short-tailed shrews (*Blarina brevicauda*) and southern red-backed voles (*Myodes gapperi*). The white-footed mice top habitat model included plant cover (positive effect) and distance to the nearest tree (negative effect). The top model for the eastern chipmunk had plant cover and leaf litter as negative effects and another model with ferns as a positive effect. The top models for the northern short-tailed shrew included ferns and plant cover as positive effects. The top model for the southern red-backed vole (*Myodes gapperi*) also included ferns as a positive effect. Our results demonstrate the importance of plant cover and fern species on small mammal communities in a disturbed forest habitat.

268: Midwest range expansion of the Virginia opossum impacted by agriculture and snow cover

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Range expansions are key demographic events driven by factors including climate change and human intervention that shape the genetic composition of peripheral populations. The expansion of the Virginia

opossum (*Didelphis virginiana*) into Michigan has been documented over the past 200 years, indicating relatively new colonizations of Northern Michigan and the Upper Peninsula. The opossum offers an opportunity to examine the compounding influence that climate change and anthropogenic processes have on a species' distribution. To investigate the genetic consequences of two range expansions, opossums from Michigan, Ohio, and Wisconsin were genotyped for 11 microsatellite markers. Two genetic clusters were identified using the Bayesian clustering program STRUCTURE: one on either side of Lake Michigan. Numerous geographic outliers between these clusters suggest there have been instances of long-distance dispersal in addition to substantial gene flow. Across twelve counties, measurements of genetic diversity are most strongly negatively correlated with days of snow on the ground. A positive correlation between allelic richness and farmland also suggests increased carrying capacity in agricultural landscape. Accounting for days of snow using a stepwise linear regression indicated winter temperature has no significant impact on genetic diversity. Taken together, these data suggest opossum expansion is facilitated by resources provided by farms and limited by their ability to forage in snow.

269^{E,TA}: Impacts of human disturbance on carnivores in protected areas of the Southwest

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Mammalian carnivores are a vital component of many ecosystems, often affecting community diversity and stability, as well as important surrogate species for biodiversity conservation. Additionally, carnivores can be particularly sensitive to human disturbance and development, even within protected areas, and may serve as important indicator species within these areas. The objective of this study was to understand how human disturbance affects the carnivore communities in southern Arizona through studying occupancy in three protected areas with different levels of human disturbance. We utilized non-invasive methods including: wildlife cameras, open and closed track plates, and sign surveys. We also conducted vegetation surveys to determine habitat associations related to carnivore presence. Our results indicate that carnivore occupancy varies based on human disturbance variables (i.e., visitors, roads, trails, etc.). Common carnivore species had high occupancy in highly disturbed sites, while rare carnivores had a higher probability of occupancy in low disturbance areas. Additionally, carnivore diversity was higher in areas with low human disturbance. As the population of Arizona continues to grow, annual visitation rates to its protected areas have increased as well. Increased disturbance generally accompanies increases in visitation to protected areas, which likely results in impacts on the areas' wildlife. To adequately manage and conserve carnivore species within protected areas, obtaining information on how they are influenced by human disturbance is essential.

270^F: When the cat's away: how anthropogenic disturbance alters puma subsidies to scavengers

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The fear induced by predators on their prey is known to cause behavioral adjustments by prey that can ripple through food webs. Little is known, however, about the analogous impacts of humans as perceived top predators on the foraging behavior of carnivores. Our previous work suggests that pumas (*Puma concolor*) spend less time at their kills when they are disturbed by development. Therefore, greater carcass availability may alter community dynamics by augmenting food resources for scavengers. Here, we investigate the influence of human-induced fear on puma foraging behavior using motion-sensor video camera data from 12 GPS-tagged individual pumas living along a gradient of human development. We also quantify carcass use by vertebrate scavengers and catalog scavenger behavior at puma kills. For this study, we deployed 44 cameras on fresh puma kills located with satellite or GSM data from collars, allowing us to collect full carcass life cycles of consumption. Our results indicate that puma kills near residential development are visited by a greater diversity of carnivore scavengers, and that some scavenger behaviors, including feeding and vigilance rates, appear to be related to housing proximity. In light of the extensive and growing impact of habitat modification, our study emphasizes that knowledge of the indirect effects of human presence on animal behavior is a necessary component in understanding anthropogenic impacts on community dynamics and food web function.

271^{E,TA}: The spatial ecology of domestic dogs along Kenya's human, wildlife and livestock interface

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Domestic dogs represent an ecologically important host and reservoir for many wildlife diseases known to impact endangered carnivores. Developing a deeper understanding of the spatial and behavioral ecology of domestic dogs (*Canis lupus familiaris*) is therefore essential for mitigating disease transmission between domestic animals and wildlife, especially for large carnivores of conservation concern (e.g., lions and wild dogs). Using a population of dogs in Kenya's Laikipia County, we set out to examine how differential space use patterns associated with different functional roles impact pathogen dynamics. Applying new GPS tracking technologies (iGotU data loggers), we collared 40 domestic dogs and to date, an equal number of herding versus home dogs (20 and 20) have been monitored since March 2015, recording GPS locations every 15 minutes. Spatial patterns qualitatively indicate that both herding and home dogs appear to maintain close associations with their home bomas, although individuals utilized multiple bomas throughout the study period. Results from the wet season (April and May) indicate that domestic dogs infrequently move into surrounding conservancies, with dogs found along conservancy borders showing more frequent incursions. This study provides one of the most in-depth assessments of domestic dog ecology and pathogen burdens along Kenya's human-wildlife-livestock interface, providing vital information for effective management of carnivore communities.

272: Muskrat populations in Canada and the U.S. do not necessarily behave the same: an examination of population cycles and Moran effects based on harvest data.

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Analyses of harvest data (1925 – 1949) from the Hudson Bay Company in Canada have suggested that some populations of muskrats (*Ondatra zibethicus*) show cycles that may be related to predator-prey relationships with American mink (*Neovison vison*). We examined harvest data (1970 – 2011) from the U. S. for comparison. After controlling for economic influences on harvest (e.g., pelt price), we found no evidence that muskrats showed population cycles in our 41-year data set. Muskrat and mink dynamics were highly correlated without time lags, providing no support for a classic predator-prey cycle. Muskrat harvest was related to seasonal weather conditions in a few states, but factors related to harvest varied by state. Autoregressive models, usually interpreted to infer density dependence, showed the greatest power for predicting population dynamics, but the mechanisms underlying the relationships remain unclear. We caution against making generalizations about "North American muskrats" based on data from a limited part of their geographic range, and especially without controlling for factors affecting trapper effort and participation.

273: Does recreation or hunting affect wildlife communities in protected areas?

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Managed public wild areas have dual mandates to protect biodiversity and provide recreational opportunities for people. These goals could be at odds if recreation disrupts wildlife enough to alter their

space use or community structure. We evaluated the effect of managed hunting and recreation on 12 wildlife species in 32 protected areas in the Eastern USA. Coyotes were the only species where recreation covariates were stronger predictors in distribution models than habitat covariates. The three most hunted species (eastern gray squirrels, white-tailed deer and raccoons) were commonly detected throughout the region, but relatively less at hunted sites, while coyote use of hunted areas increased compared to unhunted controls. Most species did not consistently avoid human-made trails, and some predators positively selected them. The models for bobcats and black bears showed different relationships with human trail use depending if the local area was hunted or not, suggesting that hunters may be having indirect predator effects on those species, but not others. Although we found that hikers and managed hunting has significant effects on the distribution of some species, these were relatively minor compared with the importance of habitat covariates associated with land use and habitat fragmentation. This result suggests that the present practices for regulating recreation in the region are in balance with wildlife protection, and may be facilitated by decades of animal habituation to humans.

274^{E}: Anthropogenic effects on bat roosting behavior in Atlantic Forest of South America**

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When organisms occupy heterogeneous environments, their behaviors should manifest variation across a continuum. We explored this habitat use concept by examining a likely density-dependent resource: bat day roosts. If landscape types differ in roost abundance, we expected to see changes in the behavioral patterns of roost use. Furthermore, roost use should be balanced by considering both roost characteristics and roost use by conspecifics. The great fruit-eating bat (*Artibeus lituratus*) occurs as a common bat species across both contiguous and matrix landscapes in interior Atlantic Forest of eastern Paraguay. We examined differences in roosting behavior of these bats between contiguous forest and surrounding fragments. The average number of roosts used per bat did not vary by landscape type, yet the manner they utilize those roosts did. Despite using similar numbers of roosts, group sizes of individuals were larger in the matrix habitat. The social network of bats in the matrix is more cohesive relative to bats in contiguous habitat, suggesting greater roost sharing. Bats would startle and flee with unequal frequency between landscapes, perhaps due to a heightened level of fear in the matrix. Our findings implicate the matrix as roost-limited, with anthropogenic activities that seem to act as environmental stressors. Understanding plasticity regarding habitat use is critical for mitigating ecological degradation as contiguous habitat becomes increasingly fragmented. This research was supported by a Grant-in-Aid awarded to Garret D. Langlois in 2014.

275^{}: Anthropogenic development influences on puma behavior, movement, and energetics in a fragmented landscape**

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Human development has strongly influenced large carnivore survival and persistence globally. Changes in behavior are often the first measureable responses to human disturbances, and can have dramatic ramifications on animal populations. Understanding how apex predators respond to anthropogenic changes can greatly inform management and conservation of these predators. We used 3 years of GPS location data for pumas in the Santa Cruz Mountains to study how their movements and behaviors were affected by human development. We used log-linear analyses to examine how habitat, time of day, and proximity to housing influenced the activity patterns of male and female pumas. We also used 15-minute GPS sampling points to evaluate how development density affected the average distances pumas traveled and calculated their daily energetic expenditures. We found that pumas responded to development differently depending on the time of day. Pumas generally were more active and moved further when they were in developed areas at night. In contrast, during the day, pumas either did not change their activity or moved less in developed areas. Higher nighttime activity in developed areas increased daily caloric expenditure in both and females. Our integration of energetic and movement

models indicates that pumas have higher energetics costs and requirements in human-dominated habitats. We recommend that future conservation work consider the ramifications of behavioral shifts on animal energetic costs and fitness. This research was supported by Grants-In-Aid of Research awarded to Yiwei Wang.

276: An apex urban predator: the coyote establishes predator functions in the Chicago area

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In recent years, coyotes (*Canis latrans*) have colonized major metropolitan areas across North America. For the past 15 years, we have captured and marked nearly 1,000 individuals in the Chicago area to determine how coyotes function in urban systems. Stable isotope analysis revealed substantial inter- and intra-individual variation in diet, although most coyotes continued to consume natural prey, even in the most developed parts of the city. In addition to our previous work on coyote impacts on geese, foxes, and feral cats, we are currently measuring white-tailed deer (*Odocoileus virginianus*) fawn survival within urban parks. During 2013-15, 29 of 45 fawns died in their first year ($S=0.34$, $SE=0.06$). Predation by coyotes was responsible for >80% of mortalities, all of which occurred in the first 30 days following birth. Predation rate varied across years, possibly influenced by availability of alternative prey. It appears coyotes influence these species through direct predation (e.g., at the nest or neonatal stage for geese and deer) and intraguild competition (foxes, cats). Predation by mammalian carnivores had been lacking from urban landscapes. The colonization of Chicago by coyotes illustrates their importance at influencing community structure through their role as an apex predator.

277: Developmental and social constraints on early reproduction in an asocial mammal

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For short-lived species, selection for early reproduction should be strong, yet females often delay reproduction beyond what appears to be optimal. Delay in age of first reproduction due to developmental constraints, such as food availability, or social constraints, such as the inhibitory presence of breeding adults, has been documented for social ground-dwelling squirrels, but their effects on the reproductive maturation of asocial ground squirrels are unknown. We used 21 years of demographic data from a free-living population of golden-mantled ground squirrels to evaluate the developmental and social factors that may constrain early reproduction in this short-lived, asocial species. We found that females who would reproduce as yearlings were weaned earlier in the summer, and that early weaning was associated with higher growth rate during the natal summer. Females were more likely to reproduce as yearlings when there were more adult males present, possibly because exposure to males accelerates reproductive maturity or because more mates increases the likelihood of conception. Maternal presence had no facilitating or inhibitory effect on yearling reproduction, but yearlings with a littermate sister present were only 22% as likely to reproduce as females without a sister present. Competition among siblings before or after weaning may reduce growth rates in female rodents, and if sisters remain in close proximity in their natal range, developmental delays may extend to delays in reproductive maturation.

278: Temporal scaling in analysis of American marten locomotor activity

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Spatial scale influences resource selection and multi-spatial-scale studies are now commonplace. Temporal scale also influences resource selection and likely influences patterns of locomotor activity, but studies of activity have not explicitly examined potential influences of temporal scale. We used a multi-temporal-scale analysis framework to study winter activity of American martens (*Martes americana*) that were fitted with radiocollars containing activity switches. We found that support for the mortality risk, prey

activity, thermal conservation, and competition hypotheses for activity varied by temporal scale. The mortality risk hypothesis was supported at only the broader scales examined, but not at the finest scale, making this the first study to support the hierarchy of limiting factors hypothesis using a multiple-temporal-scale framework. Marten activity was polyphasic and activity bouts occurred across the 24-h period, which may be due to digestive and metabolic constraints. Our results indicate that a multi-temporal-scale analysis framework can expose influences of temporal scale on patterns of locomotor activity that would otherwise remain obscured.

279: To forage or to guard: movement analysis of a solitary larder-hoarding rodent (*Callospermophilus lateralis*)

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Foraging competition within granivore guilds regulates the populations of participating species and also aids in the persistence of seed species being harvested. Golden-mantled ground squirrels (*Callospermophilus lateralis*) of the North American Sierra Nevada range have a unique role to play in this interaction. Unlike many of its competitors, *C. lateralis* larder-hoards seeds year-round and does not actively pilfer seeds from caches made by other individuals. Additionally, *C. lateralis* is solitary, meaning its one larder of food is left vulnerable while foraging. Competitors such as chipmunks can easily detect these larders with their acute olfactory sense and have the ability to steal seeds while the burrow is unprotected. How *C. lateralis* manages the conflict of needing to forage away from the burrow and also be sentinel at the burrow to protect the larder is unknown. The central focus of this study is to determine if *C. lateralis* uses a defensive strategy to coexist in the highly competitive granivore guild. To address this question, locations from novel mini-GPS technology were collected on a narrow time interval. Cost distance modeling, resource selection function, and time local convex hull methods were used to analyze spatial and temporal patterns. Preliminary results indicate that patterns in *C. lateralis* activity are correlated with forage availability, time of day, and canopy cover type.

280^E: Foraging behavior and social interactions of white-tailed deer (*Odocoileus virginianus*) at a concentrated food resource

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Prey animals maximize fitness by balancing resource acquisition and anti-predator behaviors. Additionally, social interactions, breeding chronology, habitat characteristics, and abiotic factors influence foraging decisions made by each sex-age class within a population. To investigate factors affecting foraging behavior and presence at feeding sites, we analyzed 6,992 camera trap photos of white-tailed deer (*Odocoileus virginianus*) collected at 22 feeding sites from September 2013-January 2014. We characterized the behavioral state of each individual as either feeding or not and documented presence. We fitted generalized linear mixed models (GLMMs) to estimate the probability of feeding and presence at feeding sites, and treated feeding site as a random variable. We compared competing sex- and age-dependent hypotheses based on breeding chronology, time-of-day (diurnal vs. nocturnal), habitat (distance-to-escape-cover), and social factors (group size, presence of opposing sex-age class) using an information theoretic approach. Breeding chronology and social interactions were important predictors for feeding and presence for all sex-age classes. Increasing distance-to-escape-cover reduced diurnal adult feeding and presence. Presence of a mature male had a negative effect on immature male feeding. Finally, each sex-age class' presence was negatively affected by the presence of a competing sex-age class, especially mature males and females. Our results suggest habitat characteristics associated with the feeding site, breeding chronology, and intra-specific competition drive temporal resource partitioning and foraging behaviors at concentrated resources.

281^E: Temperature-induced changes to plant chemistry and forage selection by moose

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Since 2005, the moose population in Minnesota has declined by nearly 50%. While climate change has been implicated as the primary driver behind this decline, the ecological and physiological mechanisms connecting climate change to this decline are not well understood. Plant secondary metabolites (PSMs) play an important role in defense against herbivory and can impact herbivore survival and reproduction. Several studies suggest that plants increase production of PSMs due to heat stress, but this has not been tested in a controlled setting. Here we investigated the effects of increasing temperatures on the production of PSMs in balsam fir (*Abies balsamea*) and paper birch (*Betula papyrifera*) and assessed if temperature-induced changes to phytochemistry are correlated with diet composition. We analyzed PSM composition in plants reared under three different temperature regimes - ambient, ambient + 1.7°C, and ambient + 3.4°C. To examine how moose diets changed across a similar temperature range, we used stable isotopes of carbon and nitrogen from forage and hair to reconstruct the diets of moose from areas that span a 6°C summer temperature gradient. Results indicate that temperature influences PSM production in forage, and that moose diets vary as a function of ambient temperature. We discuss how this pattern could be driven by a combination of forage availability and forage selection, and how changes in forage chemistry may influence population-wide demographic rates.

282^F: Variation in personality, foraging behavior, and demography of a ground-dwelling sciurid across structurally distinct habitats

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Variation in personality exists both within and among populations. Boldness, the tendency to take risks, is often associated with individual difference in foraging behavior and space use, eventually modulating the survival and fecundity of individuals. Thus, variation in boldness among and within populations can influence their demography and trophic interactions. We used mark-recapture trapping from 2013-2016 and in-field personality assays to compare the personality, foraging behavior, and population demographics of Piute ground squirrels (*Urocitellus mollis*) in two structurally distinct habitats in southwestern Idaho, USA. Structural variation of a habitat influences both the direct and indirect predation risk and can mediate the consequence of risky behavior. Individuals were more bold and boldness was more variable within a sagebrush-dominant habitat than within a native grass-dominant habitat. Time budgets of individuals at feeding stations differed significantly both within and among habitats and were significantly by individual boldness. Demographic characteristics of ground squirrels were similar across the 4 years of the study in both habitats. Thus populations in structurally distinct habitats can have similar demographic characteristics but can differ in risk-related personality traits of individuals both within and among populations. The interaction between habitat structure and the distribution and variation of personality traits in heterogeneous habitats could influence susceptibility of individuals to predation and the acquisition of food and therefore play a role in spatial and temporal population patterns.

283: Running on empty: nest burrow relocations by Franklin's ground squirrels (*Poliocitellus franklinii*)

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Mammalian den or nest-site movements have been attributed to unfavorable abiotic conditions, variation in habitat quality, social factors, or pressure imposed by presumptive predators and parasites. A three-year study of telemetry-collared Franklin's ground squirrels (*Poliocitellus franklinii*) near Delta Marsh Manitoba revealed that 31 of 32 females relocated their nest burrows one to four times over the course of lactation. In the context of each relocation, pups were transported individually by their dam between nest burrows over distances up to 1 km, resulting in daily above-ground travel up to 20 km. Such movements are presumably costly, both energetically and in terms of enhanced predation risk, and thus must impart some offsetting benefit. PIT-tag based monitoring of conspecific nest visitation revealed that visits to nests of lactating females significantly increased the likelihood of nest relocation, while experimental reduction of ectoparasite abundance via the application of the topical insecticide fipronil reduced the frequency of nest relocation relative to sham-treated females. Presumably then, nest relocation among lactating Franklin's ground squirrels reduces contact with conspecifics, which may serve to reduce infanticide, but most certainly reduces ectoparasite-related costs for dams and their young.

284^F: Individual variability in reproductive strategies among females shape the mating system of tree sloths

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Mating systems are broad generalizations of reproductive strategies made at the population level, and individuals can exhibit significant variation in their reproductive behavior. Taking advantage of a long-term genetic, demographic and movement dataset of brown-throated three-toed sloths (*Bradypus variegatus*) and Hoffmann's two-toed sloth (*Choloepus hoffmanni*) in northeastern Costa Rica, we aimed to quantify the mating system for these two species of mammals that are both uniparous and exhibit nominal parental care or mate guarding. Our findings support that sloths are broadly polygynous but that females of both species frequently mate with multiple males over their lifetime: 70% of female *B. variegatus* and 50% of female *C. hoffmanni* switched mates between years. Consequently, reproductive skew in males was intermediate when compared to mammals exhibiting strong polygyny or strict monogamy. Further, females that mated with males with low reproductive output tended to have an increase likelihood of switching mates. Although many factors can contribute to multi-male mating and modulate reproductive skew, we suggest that the mating system of sloths is ultimately one driven by female choice.

285: Ecological structure of modern mammalian faunas in relation to climate and landscape

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The ecological structure of mammalian faunas refers to the number of species in ecological functional groups, such as size and trophic categories. We analyzed the ecological structure of modern faunas in relation to climate, topography, and vegetation for terrestrial regions worldwide. One goal of our analysis was to identify which environmental variables are the best predictors of ecological structure—for developing mechanistic models of environmental sorting. A second goal was to identify which components of ecological structure are robust predictors of environmental variables—for application to fossil faunas. We assembled a database of 344 modern faunas distributed across five continents and representing all biomes. For >2100 species, the database includes measures of body size, feeding habit, and habitat use. For each locality, 10 climatic, two physiographic, and three vegetation variables were recorded. We used regression trees to identify geographic subsets of the global database characterized by a common ecological structure, and regression analysis to develop predictive equations. Temperature seasonality, mean annual precipitation, and biome are strong predictors of species richness in individual faunal categories. The number of frugivores, semi-fossorial species, and species in size class 1 (1-10 grams) predict climatic and biomes variables well. Continental datasets show stronger relationships than the global dataset, and these relationships differ among continents, reflecting the different bioclimatic attributes of each continent and the different evolutionary histories of their faunas.

286: A latitudinal gradient in dimensionality of biodiversity

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Biodiversity is multifaceted and represented by numerous dimensions expressing variation in richness and abundances of species, their ecological functions, phylogenetic relationships, morphology, traits and interactions. Such dimensions are correlated to varying degrees and recent research has attempted to better understand magnitude and behavior of such correlations. Dimensionality of biodiversity refers to degree of correlation in spatial or temporal variation among dimensions of biodiversity. Here we evaluate whether dimensionality of biodiversity exhibits spatial gradients in particular related to latitude. One fundamental question regarding dimensionality of biodiversity is whether it too is spatially dynamic and whether complementarity among dimensions of biodiversity exhibits similar increases towards the poles thereby contributing to increased equatorial complexity. We find that dimensionality does indeed exhibit a latitudinal gradient. Moreover, empirical increases in dimensionality of biodiversity towards the equator are faster than expected given two null models. Correlations among different dimensions of biodiversity depend to some extent on geographic position and interpretations of such correlations should be geographically explicit. Moreover, dimensionality provides a deeper context within which to evaluate efficacy of competing mechanisms proposed to explain latitudinal gradients; mechanisms need not only account for gradients of biodiversity, but gradients in dimensionality as well. Lastly, a gradient in dimensionality suggests that conservation strategies that rely on maximization of a single metric, for example species richness, may be of varying utility in different geographic contexts.

287: Rule reversals: patterns of body size variation in the common treeshrew (Scandentia: Tupaiidae)

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The island rule predicts that populations of larger mammals on islands evolve smaller size than their mainland counterparts, whereas smaller mammals evolve larger size. These patterns are modulated by the size and remoteness of the islands: in small species, body size tends to increase less with island area and as distance to the mainland decreases. Bergmann's rule describes the pattern in which populations of a species in colder climates have larger mean body sizes than conspecific populations in warmer climates. These two rules are rarely tested together and have never been rigorously tested in treeshrews. The common treeshrew, *Tupaia glis*, distributed on the Malay Peninsula and several offshore islands east, west, and south of the mainland, is a good candidate for study. Using craniodental dimensions, we investigated how island size and distance from the mainland relate to body size of insular *T. glis* populations while controlling for latitude. Of 13 island populations examined, none were sufficiently distinct from the mainland population to warrant taxonomic recognition. There was a strong negative effect of latitude on size, indicating the inverse of Bergmann's rule. At a given latitude, individuals were smaller on islands than on the mainland. Furthermore, among island populations of treeshrews, size increased with island area. Hence, although there are latitudinal and island effects, neither Bergmann's nor the island rules apply to the common treeshrew.

288^F: Biogeography and phylogeny of the two most diverse murid rodent genera on Sulawesi, Indonesia

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The oceanic island of Sulawesi is a global hotspot of endemism with many endemic species evolving after crossing Wallace's line. Within island speciation following colonization is the main source of diversity. Patterns of regional endemism within Sulawesi suggest that within island speciation is driven by the island's peninsular structure. Murid rodents comprise about 40 percent of mammal species on Sulawesi with nearly one-third of murid species in two genera, *Bunomys* and *Taeromys*. Here we present the results of our recent collections of these species across the northern peninsula of Sulawesi, where a major biogeographic divide is centered on Gorontalo in the middle of the peninsula. Using both morphological and phylogenetic analyses we provide the first test of this divide in murid rodents. We found that at least two species thought to be endemic to east of Gorontalo are distributed to the western end of the peninsula. Our phylogenetic analyses show that the genera *Bunomys* and *Taeromys* are part of an endemic Sulawesi clade including the genera *Eropeplus*, *Lenomys*, and *Paruromys* that evolved from a single colonization of the island. Phylogenetic differences across the Gorontalo divide provide evidence for the significance of this boundary in the evolution of Sulawesi's endemic rodents.

289: Preliminary phylogeographic analysis of *Sciurus variegatoides*

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Despite its impressive biodiversity and geographic variation, Central America is grossly understudied in a biogeographic context. This is especially true for mammals even though intriguing morphological variation is apparent for many species across this region. The variegated squirrel (*Sciurus variegatoides*) is an exemplar species exhibiting this variation, showing multiple, distinct pelage patterns across its range from southern Mexico to central Panama. Hypotheses for the variable pelage of *S. variegatoides* include possible adaptations to primary habitat and/or consequences of the variable climatic ranges seen in the region. Despite this, no studies have investigated this variation or these hypotheses using morphological or molecular means. In fact, the last revision of this species in 1937 identified 15 subspecies based solely on pelage differences. Given this, we undertook a phylogeographic assessment of this species using both molecular and morphological methods. Capture hybridization was used to collect mitochondrial genomes from museum specimens, while two-dimensional geometric morphometrics was used to assess cranial shape differences between subspecies and localities. Analysis of cranial landmark data suggests that many current subspecific designations do not reflect morphological differences between individuals. Understanding the evolutionary patterns in this species will add to the current, sparse literature of Central American mammal evolution and increase our understanding of the biogeographic patterns affecting species in this region.

290^E: Museum and citizen science records change distributional estimates for the recently described olinguito (*Bassaricyon neblina*)

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In the context of global change, a necessary first step for conservation of species is gaining a good understanding of their distributional limits. This is especially important for biodiversity hotspots with high endemism such as the Northern Andes. The olinguito (Procyonidae: *Bassaricyon neblina*) is a newly described, medium-sized carnivoran found in Northern Andean cloud forests, with distributional estimates recently published (2013). In this study we build ecological niche models in Maxent, calibrated using occurrence data (georeferenced museum records and citizen science photo-vouchers) and bioclimatic variables. Optimal models were selected via two different approaches, AIC and performance on withheld

data. The AIC optimal model was chosen because visual inspection indicates that it aligns more closely with our current knowledge of the species in terms of elevation. This model highlights areas for future sampling, such as the central portion of the Western Cordillera of Colombia, mid- and northern portions of the Central Cordillera of Colombia, Southwestern Colombia, and the eastern slopes of Eastern Andes in Ecuador. The occurrence data used here indicate climatic space different from data used in the original description of the species, with our final model showing more extensive suitable area in Northern Colombia. Based on these results, we will perform a formal conservation assessment, taking into account climate change and deforestation.

291: Biodiversity assessment of small rodents in northern Peruvian Amazonia near Iquitos

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The Amazonian lowland forests is characterized by a large diversity of rodents; however it faces a rapid lost of biodiversity by an accelerated deforestation, mining, and oil megaprojects. Even places near large cities like Iquitos have not been adequately studied and are the first to disappear converted by anthropogenic activities. We surveyed rodents from the surrounding of the Reserva Nacional Allpahuayo-Mishana (RNAM), near Iquitos, combining several trapping methods such a combination of Sherman/Thomahawk/snap traps on the ground and on the trees, and 160 m pitfall, repeated in three types of forests with distinct degree of deforestation in a typical dry season. Based on an effort of 12484 trap-nights and more than 80 bucket-nights, in 30 days of continuous survey, we register thirteen species of rodents, in two families and eight genera. As expected, the more deforested sample site obtained only 6 species, but the more pristine sample sites registered from 6 to 9 species. In addition, we provide evidence for new species of the genera *Neusticomys*, *Neacomys*, *Oecomys*, and *Proechimys*, based on a detailed analysis of morphological traits, karyotype, and sequence of cytochrome *b*. We support the hypothesis that the Amazonian river has a deep role in the diversification of these rodents. Additional work on the wet season might reveal the existence of seasonal changes, and probably a higher diversity. Funds came from project N°096-2014-FONDECYT-DE.

292: Roosting ecology of Amazonian bats: resource partitioning and guild structure in hyperdiverse mammalian communities

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Amazonian bat communities are known to include almost 80 sympatric species at some localities, and >100 species might be sympatric throughout much of the region. What ecological mechanisms sustain such high diversity? Most research on Amazonian bat ecology assumes that food is a limiting resource, so community structure is usually quantified in terms of trophic-guild membership. Diurnal roosts, however, are another crucial resource for bats, so roost availability might also affect community structure if some species are roost specialists. We obtained information about roost occupancy from a multiyear field project in northeastern Peru and a subsequent review of previously published studies. Statistical analyses of these data (>500 observations of Amazonian bat roosts) provide evidence for a novel classification of roosting guilds. Roost availability is proposed to have a filtering effect on Amazonian bat communities, which (among other peculiarities) are notably deficient in cave-inhabiting taxa. Likewise, seasonally inundated forests may routinely lack species that roost under fallen trees or in understory foliage, and young secondary growth may often lack species that roost in large hollow trees. Before a roosting-guild classification can be genuinely useful for studies of Amazonian bat community structure, however, much additional fieldwork is required to determine the roosting behavior of many data-deficient species.

293: Stable isotope ecology of sympatric rodent species in a mixed forest ecosystem in northern Minnesota

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To assess forage availability for furbearers, volunteers for the 1854 Treaty Organization have been trapping small mammals by re-occupying the same trap grids every year in early fall across northern Minnesota. Here we report on an isotopic study of diet in sympatric rodent species trapped in three grids (four traps each) from 2001-2013. The grids span about 5 km and are in different plant associations: northern mesic mixed forest (grid 1), black ash-conifer swamp (grid 2), and early successional forest (grid 3). The total sample is 164 specimens of six species, but we focus on two species with samples large enough for robust statistical analysis. Mean $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of hair for *Myodes gapperi* (n=55) do not differ significantly among the grids, indicating an isotopically consistent diet over time independent of plant association. *Microtus pennsylvanicus* (n=52) occurred only in two grids, and mean $\delta^{13}\text{C}$ is significantly lower and mean $\delta^{15}\text{N}$ significantly higher in grid 2 relative to grid 3, indicating spatial variability in diet. However, in these grids, *Myodes gapperi* has significantly higher mean $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values, indicating consistent differences in carbon sources and differences in higher trophic level. Sympatry of these species could be maintained by competitive displacement of dietary niches in local populations or by characteristic diets generally for each species with little overlap, which could be tested at other sites.

294: Habitat segregation in two competing species of rodent

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The prairie vole (*Microtus ochrogaster*) and cotton rat (*Sigmodon hispidus*) co-occur in oldfield habitats in Kansas. The two species have similar diets and habitat requirements and likely compete. This competition could result in the spatial segregation of the habitat. We used Spatially Explicit Capture Recapture (SECR) analyses to assess the spatial distribution of these two species at a site in northeastern Kansas. Rodents were live-trapped approximately monthly on a 10 x 10 grid from 1974-2003. We used these data to estimate the spatially explicit density of the two species both annually and monthly. The distribution of the two species varied among years, suggesting that habitat quality also varied spatially among years. At an annual scale, the density of the two species was positively correlated indicating a lack of spatial segregation of habitats. However, spatial distribution of each species differed seasonally suggesting that though the two species use similar habitats, they may not use them at the same time. Seasonal differences in habitat use could indicate habitat segregation or competitive exclusion of the prairie vole by cotton rats.

295: Integration of stable isotope and stomach content analysis to infer diets of arid grassland rodents

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Stable isotope analysis (SIA) and stomach content analysis (SCA) are commonly used to provide insight into mammalian feeding ecology, but they differ in limitations and biases. Integrating SCA and SIA can provide greater detail for small mammals, many of which consume diverse mixtures of leaves, seeds, and invertebrates. We compare variation in $\delta^{13}\text{C}$ (consumption of C_3 and C_4 plants) and $\delta^{15}\text{N}$ (trophic level) values for 11 rodent species in relation to dietary category, macrohabitat, and complete SCA in a central New Mexico arid grassland (Sevilleta NWR). Results from 248 individuals indicate that diets in riparian forest are significantly different from those in all other macrohabitats and reflect greatest consumption of C_3 derived resources. Diets in all other macrohabitats are not significantly different and consist of varying mixtures of C_3 and C_4 derived resources. A positive correlation between $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values indicates

consumption of C₄ derived resources increases with trophic level evidenced by increasing $\delta^{15}\text{N}$ values with $\delta^{13}\text{C}$ values. For all species, $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values do not vary with the amount of seeds, arthropods, or seeds consumed. However, species-specific diet responses to macrohabitat and season better explain the isotopic variance, which indicates food resource partitioning among species in macrohabitats. Our integration of SCA and SIA provides enhanced dietary interpretations that reveal species-specific foraging ecologies in relation to community composition, habitat structure, and food resources.

296^E: Examination of gut microbial compositions of genera in Rodentia

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Differences in gut microbiomes can be a result of various ecological, behavioral, and physiological factors such as diet, age, physical activity, and habitat. Some of these gut microorganisms play a pivotal role in digestion as well as other metabolic and neurological aspects. Research has shown that gut microbiomes of rodents can aid in the digestion of various toxic plants, seeds, and arthropods that rodents may consume, and help with the degradation and metabolism of dietary substances such as fiber and carbohydrates that may otherwise be indigestible. Here we examined gut microbiome differences among multiple genera within the Order Rodentia. Rodent samples were collected from Oklahoma and Texas over a 2 week field period, and field effort was prioritized to collect rodents of different dietary niches. 16S amplicon sequencing was performed on gDNA of collected colon samples. Sequences were then processed using our microbial diversity analysis pipeline, which includes assignment of operational taxonomic units (OTUs) and corresponding relative abundances. Significant differences in both alpha and beta diversity were found among genera. Significant differences in abundance of bacterial taxonomic lineages were inferred among rodent genera microbiomes, and these differences may relate to differential functions of host microbiomes. By comparing differences in microbial diversity to life history and taxonomic relationships, we can better understand the role of specific microbes in the evolution of life histories and niche utilization.

297: Small-mammal communities as indicators of change in ecosystem restoration

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Ecological restoration projects have been initiated world-wide with the goal of recovering damaged or degraded ecological systems, increasing biodiversity, and providing ecosystem services. Project assessment is essential for improving their implementation and justifying their costs, but comprehensive monitoring and evaluation have rarely been incorporated into projects. We developed a cost-effective monitoring program for lands managed by 5 Native American tribes in Washington and Idaho. Key ecological objectives of restoration are that the restored area (1) has an assemblage of species characteristic of a reference ecosystem that provides appropriate community structure, and (2) consists largely of indigenous species. We established 24 reference points representing the best extant representatives of 8 habitat types, and 83 sampling points on 39 management units under restoration. Composition and structure of vegetation, and composition and relative abundance of small mammals, birds, and larval amphibians were monitored over 3 years for reference points and at 5-year intervals on restoration sites. Similarity indices that incorporate relative abundance (Chao-Jaccard) were calculated to compare managed lands to the reference for each habitat. Non-metric multidimensional scaling was used to visualize the relationships of restoration to reference sites for each habitat type. Small-mammals appear to be appropriate indicators of change particularly for habitats such as shrub-steppe where there are clear linkages with herbaceous vegetation, and for structurally simple habitats like wetland meadows.

298^{E}: Structure of bat assemblages from tropical lowlands on both sides of the Ecuadorian Andes**

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The Ecuadorian Andes constitute an important area in terms of biodiversity, endemism and conservation of several taxonomic groups. The Order Chiroptera is currently the most diverse, collected, and studied group of mammals in Ecuador. The aim of this study was to evaluate bat assemblages in terms of species richness, relative abundance, and trophic guild structure for 89 species of bats collected across eight sampling localities (below 1000 m) from both sides of the Ecuadorian Andes. The sampling localities analyzed corresponded to the Tropical Northwestern Forest, Tropical Southwestern Forest, and Tropical Eastern Forest. The Andersen's fruit-eating bat (*Artibeus aequatorialis*) and the dwarf little fruit bat (*Rhinophylla pumilio*) were the most abundant species on western and eastern localities. The feeding categories demonstrated that insectivores are more common and well represented in southwest and east Ecuador, whereas frugivores are more common in the humid localities of northwest Ecuador. However, distribution is not proportional for all feeding guilds and some are equally represented on both subdivisions. This research was supported by a Latin American Fellowship awarded to Juan Pablo Carrera-E in 2012.

299^F: Examining species richness and phylogenetic diversity of bat communities across Mexico

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Biodiversity is a multidimensional concept that once focused solely on species abundances, but now extends to other aspects including phylogenetic and functional diversity. Analyzing the interaction between these dimensions can help us better understand the mechanisms that drive community structure. In this study, we created a null distribution based on random phylogenetic inertia, using R, to serve as a basis to test for phylogenetic over- or underdispersion. Communities that fall above the 95% confidence envelope display phylogenetic overdispersion in which the species within a community are more distantly related than expected indicating higher evolutionary divergence. Mechanisms that could potentially contribute to overdispersion include niche partitioning, character displacement, and competition within clades. Communities falling below the 95% confidence envelope exhibit phylogenetic underdispersion where species within the community are more closely related than expected showing more evolutionary convergence. Mechanisms that could contribute to underdispersion are biotic and abiotic filtering, as well as competition among clades. To test the utility of this approach, we analyzed 32 bat communities distributed throughout Mexico to examine patterns of phylogenetic dispersion and potential structuring mechanisms. We chose bats because they are the second most diverse group of mammals following rodents and are important bioindicators of climate change and habitat loss. We chose these specific communities because they have been studied previously, allowing us to make connections with previous empirical results.

300: Improving diversity and training of future mammalogists

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There is a growing body of literature demonstrating the barriers (and solutions) to improve the successful selection, retention, and development of underrepresented (UR = low income, minority, and first generation) students in ecology and evolutionary biology. A summary of recommendations and examples of successful programs will be highlighted and the latest research on graduate selection and training. Additionally, a summary of undergraduate research training conferences (SACNAS, AISES, and ABRCMS) will be presented as an under-utilize pool for recruitment and training of UR-students. Time will be given for questions from the audience to discuss ways to broaden the pool of future mammalogists.

301: Citizen science and ecology in the Zooniverse: turning data into discovery

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As technology changes the way that we collect data, citizen science is changing the way we turn data into discovery. Engaging volunteers to interpret large datasets that computers can't easily process can expand the scope and scale of scientific research – allowing us to answer bigger, broader questions about the world around us. The Zooniverse citizen science platform engages 1.5 million volunteers around the world in this large-scale data interpretation – on projects that range from plankton to penguins, astronomy to archaeology, cancer research to Martian craters. By implementing generalized approaches for converting volunteer effort into expert quality scientific data, these projects have yielded >100 peer reviewed publications across disciplines as well as increased scientific literacy and engagement among volunteers. The Zooniverse has now launched a new “build your own” platform that allows researchers to easily and effectively harness the power of the crowd to interpret their own large-scale datasets. In this talk, Zooniverse lead ecologist Ali Swanson will review key aspects of this new approach to citizen science and explore the implications of this approach for transforming the shape of scientific research.

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**97TH ANNUAL MEETING OF THE AMERICAN
SOCIETY OF MAMMALOLOGISTS**

ASM
University of Idaho
2017



Please join us June 20-24, 2017, in Moscow, Idaho for the 97th Annual Meeting of the American Society of Mammalogists. The conference will be held on the campus of the University of Idaho, nestled in the hills of the Palouse region of the Great Northwest. Learn about the latest advances in the study of mammals and interact with researchers and educators specializing in the biology of these fascinating animals. Come and enjoy everything this picturesque region has to offer!

On-campus housing will be available in the Living and Learning Community, Idaho's newest residence halls. In addition, hotel blocks will be made available to meeting attendees. Detailed conference and registration information will be made available on the conference website (<https://conferences.k-state.edu/mammalogists/>).

The scientific program will include contributed oral and poster presentations as well as symposia, plenary speakers, and workshops. A full social agenda is being planned that includes multiple mixers (and a downtown "mammal crawl"), an awards social, a picnic, our annual Run-for-Research, and fieldtrips. Details for these events will be made available on the conference website.

For more information about the 2017 meeting, contact the chair of the Program Committee, Cody Thompson, University of Michigan Museum of Zoology (734-615-2810 or mammal.meetings@gmail.com), local co-hosts from the University of Idaho (Janet Rachlow 208-885-9328, jrachlow@uidaho.edu and Ryan Long 208-885-7225, ralong@uidaho.edu), or Tony Ballard, Kansas State University Conference Services (785-532-2402 or tballard@k-state.edu).

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