



Natural Reserve System
UNIVERSITY OF CALIFORNIA



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UNIVERSITY OF CALIFORNIA

Division of Academic Affairs
Office of Research and Graduate Studies
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cover photograph: Lobsang Wangdu

2014 MATHIAS SYMPOSIUM

Bodega Marine Laboratory/Reserve
February 28–March 2

Welcome

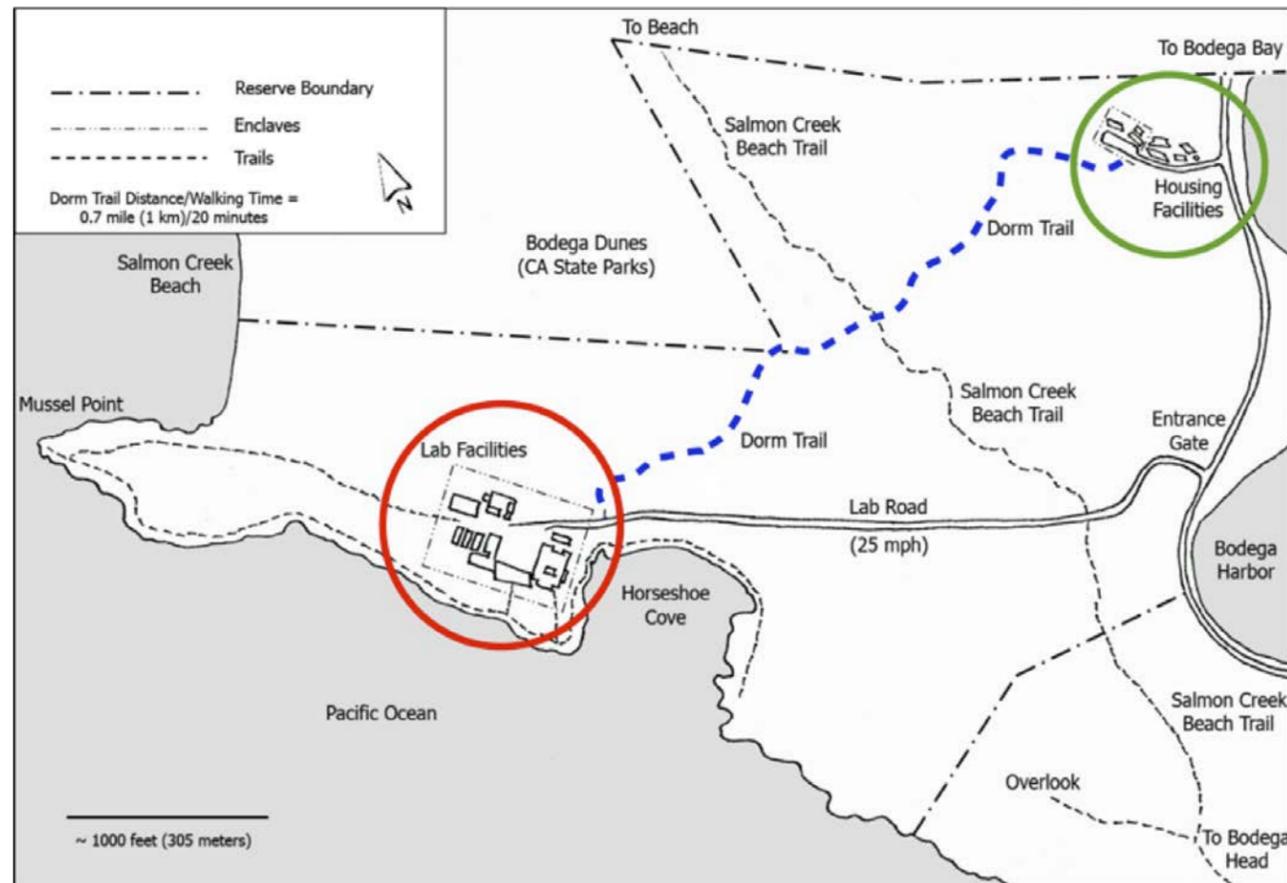
Bodega Marine Reserve Staff

Suzanne Olyarnik
Reserve Manager

Jackie Sones
Research Coordinator

Lewis Reed
Reserve Steward

Breakfasts will be served in the Dining Hall in the **housing area**.
All other symposium activities will be at the **Laboratory**.



FACULTY

Paul Barber

Associate Professor
Ecology and Evolutionary Biology, University of California, Los Angeles
PhD University of California, Berkeley

The Coral Triangle is the most biologically diverse marine ecosystem on Earth. My lab uses a combination of genetics, physical oceanography and ecological modeling to understand the drivers of speciation in this region. As one of the most critically threatened marine ecosystems on Earth, we also use our data to inform conservation planning in the Coral Triangle and use our research activities as a platform to build biodiversity research capacity in Indonesia, to raise awareness of the importance of marine biodiversity for the lives and livelihoods of the millions of inhabitants of this region.

Raymond M. Sauvajot

Deputy Associate Director, Natural Resource Stewardship and Science, National Park Service
Associate Adjunct Professor, University of California, Berkeley
PhD University of California, Davis

I provide leadership and oversight for natural resource programs, guide national parks on complex natural resource issues, and represent the National Park Service in broad-scale conservation science initiatives. As an adjunct professor, I connect faculty, post-docs, and students to national park management challenges through collaborative research and education. My own research has focused on the effects of development encroachment and habitat fragmentation on wildlife, including work on edge effects, roadway impacts on wildlife, and habitat linkages and corridors. My collaborative research interests are broader, and include conservation biology of parks and reserves, the interface between science, policy, and politics, and working to connect science to on-the-ground management decisions.

SCHEDULE

Friday *afternoon and evening*

- 12:00–1:15 p.m. **Lunch** (Food service 12:00–12:45 p.m.)
- 1:30–2:15 p.m. **Opening remarks**
Erin Marnocha, Program Coordinator, UC Natural Reserve System
Introduction to Bodega Marine Laboratory and Reserve
Suzanne Olyarnik, Manager, Bodega Marine Reserve
- 2:15–2:40 p.m. **Individualistic responses to environmental change: Comparing behavior and physiology in two chipmunk species**
Talisin T. Hammond, Department of Integrative Biology
University of California, Berkeley
- 2:40–3:05 p.m. **Spatial variation of enemy free space drives ontogenetic niche shift in an arctiid caterpillar**
Patrick Grof-Tisza, Department of Entomology and Nematology
University of California, Davis
- 3:05–3:30 p.m. **Hostplant alterations by an omnivorous bug and their effects on herbivore resistance**
Billy Krimmel, Department of Entomology
University of California, Davis
- 3:30–3:50 p.m. **Break**
- 3:50–4:15 p.m. **Northern elephant seals: integrators of persistent organic pollutants in the deep ocean**
Sarah Peterson, Department of Ecology and Evolutionary Biology
University of California, Santa Cruz
- 4:15–4:40 p.m. **Effects of habitat fragmentation on native bee assemblages and pollination services in a Southern California scrub ecosystem**
Keng-Lou James Hung, Department of Ecology, Behavior and Evolution
University of California, San Diego
- 4:40–6:00 p.m. **Tour of the laboratory**
Suzanne Olyarnik and Lewis Reed
- 6:00–7:15 p.m. **Dinner** (Food service 6:00–6:45 p.m.)
- 7:20–8:20 p.m. **LECTURE: Evolution and conservation of the Coral Triangle**
Paul Barber, Associate Professor, University of California, Los Angeles

SCHEDULE

Saturday *morning*

- 7:30–8:30 a.m. **Breakfast** (Food service 7:30–8:15 a.m.)
- 9:00–9:25 a.m. **Digging out the decomposer community from soil metagenomic data**
Emily E. Curd, Department of Ecology and Evolutionary Biology
University of California, Los Angeles
- 9:25–9:50 a.m. **Climate change effects on soil respiration: altered precipitation and invasion in a chaparral system**
Ellen Esch, Department of Ecology, Behavior, and Evolution
University of California, San Diego
- 9:50–10:15 a.m. **Impacts of environmental change on soil microbial composition and function across a habitat productivity gradient**
Kelly Gravuer, Department of Plant Sciences
University of California, Davis
- 10:15–10:35 a.m. **Break**
- 10:35–11:00 a.m. **Mound landscapes may emerge from small interactions: simulation and observation**
Chloe P. H. Lewis, Department of Environmental Science, Policy and Management
University of California, Berkeley
- 11:00–11:25 a.m. **Soil-landscape modeling of coastal California hillslopes using terrestrial lidar**
Samuel Prentice III, Department of Geography
University of California, Santa Barbara
- 11:25–11:50 a.m. **Geomorphic constraints on the temporal evolution of the Hilton Creek fault, Long Valley caldera, CA**
Jonathan Perkins, Department of Earth and Planetary Sciences
University of California, Santa Cruz

SCHEDULE

Saturday afternoon and evening

- 12:00–1:15 p.m. **Lunch** (Food service 12:00–12:45 p.m.)
- 1:20–1:45 p.m. **Reconstructing prehistoric plant use on Santa Cruz Island**
Kristin Hoppa, Department of Anthropology
University of California, Santa Barbara
- 1:45–2:10 p.m. **Cascading effects of the invasive pathogen *Phytophthora ramorum* on ectomycorrhizal fungal communities**
Sydney I. Glassman, Department of Environmental Science, Policy, Management
University of California, Berkeley
- 2:10–2:35 p.m. **Quantifying patterns of coastal fog deposition during the late summer drought**
Nathan Emery, Department of Ecology, Evolution and Marine Biology
University of California, Santa Barbara
- 2:35–2:45 p.m. **Break**
- 2:45–4:45 p.m. **Tour of the reserve**
Suzanne Olyarnik, Jackie Sones
- 4:50–5:15 p.m. **Spatial and temporal patterns in conifer encroachment into subalpine meadows in the central Sierra Nevada**
Kaitlin Lubetkin, Environmental Systems Graduate Group
University of California, Merced
- 5:15–5:40 p.m. **Panel discussion**
- 6:00–7:15 p.m. **Dinner** (Food service 6:00–6:45 p.m.)
- 7:20–8:20 p.m. **LECTURE: 21st-century conservation science challenges and opportunities for U.S. National Parks**
Raymond M. Sauvajot, Deputy Associate Director
Natural Resource Stewardship and Science, National Park Service

SCHEDULE

Sunday morning

- 7:30–8:30 a.m. **Breakfast** (Food service 7:30–8:15 a.m.)
- 9:00–9:25 a.m. **Evidence of diet specialization and prey switching in northern elephant seals (*Mirounga angustirostris*): Implications for responses to climate variability**
Chandra Goetsch, Department of Ecology and Evolutionary Biology
University of California, Santa Cruz
- 9:25–9:50 a.m. **Interactive effects of temperature and predation on mountain lake food webs and ecosystem fluxes**
Celia Symons, Department of Ecology, Behavior and Evolution
University of California, San Diego
- 9:50–10:15 a.m. **Does rafting help maintain gene flow in a brooding invertebrate?**
Lauren Schiebelhut, School of Engineering
University of California, Merced
- 10:15–10:35 a.m. **Break**
- 10:35–11:00 a.m. **Changes in marine resource use by California coastal coyotes (*Canis latrans*) over the last several thousand years**
Rachel E. B. Reid, Department of Earth and Planetary Sciences
University of California, Santa Cruz
- 11:00–11:25 a.m. **Colonization processes alter food web interactions and cause spatial variation in ecological systems**
Catherine Wade, Department of Ecology, Behavior and Evolution
University of California, San Diego
- 11:25–12:00 a.m. **Career opportunities**
- 12:00–1:15 p.m. **Lunch** (Food service 12:00–12:45 p.m.)

Individualistic responses to environmental change: Comparing behavior and physiology in two chipmunk species

Talysin T. Hammond, Department of Integrative Biology
University of California, Berkeley

Closely related, co-occurring species can respond to the same environmental change in divergent ways, often due to differences in behavior and physiology. While faunal climate change literature tends to focus on climate-matched range shifts in which species show concerted movement upward in elevation or latitude to track their climatic niches, there are also many species that experience climate change while maintaining static range boundaries. The lodgepole (*Tamias speciosus*) and alpine chipmunks (*T. alpinus*) in the Sierra Mountains of California are two closely related species that have dealt with the past century of human-induced climate change in divergent manners: *T. alpinus*'s range has contracted upwards while *T. speciosus*'s overlapping range has not significantly shifted. My dissertation research explores the question of why one species range would shift while its co-occurring congener's range did not, specifically examining stress physiology and behavior in different parts of these species' elevational ranges, including the trailing range edge and sites of co-occurrence. My research at the Sierra Nevada Aquatic Research Laboratory (SNARL) has developed new methods for studying the behavior and physiology of these two chipmunk species to examine whether these traits may explain their differing biogeographic responses. I conducted experiments in SNARL's controlled environment to validate the use of an enzyme immunoassay for measuring fecal glucocorticoid metabolites and an activity-logging sensor for remotely measuring behavioral activity budgets. I am now deploying these methods in the field to examine relationships between glucocorticoids, activity levels, and various environmental parameters (including climate, vegetation, species co-occurrence, and human impacts).

Spatial variation of enemy free space drives ontogenetic niche shift in an arctiid caterpillar

Patrick Grof-Tisza, Department of Entomology and Nematology
University of California, Davis

Despite the many organisms that shift niches during development, the reasons for ontogenetic niche shifts and the underlying selective pressures driving the evolution of complex life cycles are poorly understood. We studied the consequences and potential mechanisms of an ontogenetic niche shift (ONS) in an arctiid caterpillar, which moves from marsh to prairie habitat to pupate. We examined three non-mutually exclusive hypotheses for this apparent ONS: predator densities are higher in marsh habitat, caterpillars prefer to pupate on thistles – which occur in greater densities in prairie habitat – and rates of predation are higher on non-thistle host plants. Vertebrate exclusion experiments indicated that rodents and ants are the primary pupal predators in this system, but predator abundance did not explain the ontogenetic niche shift. We found that caterpillars within a mesocosm of transplanted host plants preferred to pupate on thistle and experimentally placed pupae suffered the least mortality on thistle compared to those on other host plants. A removal and addition manipulation experiment of prickles, thistle's primary defense, showed that pupae in association with prickles were more likely to avoid predation. These results suggest that penultimate instar caterpillars shift habitat and host plants, which provide an enemy free space from rodent predators. We propose that ontogenetic niche shifts can be driven by top-down processes: in this case, spatial variation of a non-trophic, stage-dependent resource which provides refuge from predation during a vulnerable life stage. This study demonstrates that host plants and life stage-dependent predation risk can interact to shape species' distributions.

Hostplant alterations by an omnivorous bug and their effects on herbivore resistance

Billy Krimmel, Department of Entomology
University of California, Davis

Omnivorous insects often feed both on their hostplant and other herbivores of the hostplant, making their role in tri-trophic interactions difficult to predict. We investigated how plant feeding by the omnivorous plant bug *Dicyphus hesperus* affected various phenotypic traits, including herbivore resistance, of its native host *Stachys bullata*. Feeding by *D. hesperus* caused *S. bullata* to grow extra stems and leaves (a process called "suckering"), and caused new leaves to grow in short and asymmetrical ("crinkling"), compared with undamaged plants. In the field, crinkled leaves are damaged more by the most abundant herbivore in the system, a leafhopper, which appears to be a key prey item of *D. hesperus*. We are currently conducting a multi-season experiment aimed at directly linking plant feeding by *D. hesperus* to leafhopper recruitment and *D. hesperus* performance, to determine whether *D. hesperus* increases its access to the leafhopper by inducing susceptibility in the shared hostplant.

Northern elephant seals: integrators of persistent organic pollutants in the deep ocean

Sarah Peterson, Department of Ecology and Evolutionary Biology
University of California, Santa Cruz

Northern elephant seals (*Mirounga angustirostris*) travel thousands of kilometers to forage in mesopelagic (200–1000 m) regions of the North Pacific. Lengthy foraging trips interspersed with time on land make elephant seals ideal integrators of difficult-to-study oceanic ecosystems. On land, elephant seals fast, resulting in extreme fluctuations in mass. Our study (1) measured the concentrations of persistent organic pollutants (DDTs, PCBs, and PBDEs) in adult seals during body condition extremes, (2) quantified correlations between contaminants to determine similarity of bioaccumulation patterns, and (3) used satellite-tagged females to describe contaminants in relation to foraging ecology. Full-thickness blubber cores and serum samples were collected from seals before and after their long (6–8 month) foraging trip (2011 and 2012). Female samples were paired (N=24), whereas unique males were sampled before (N=16) or after (N=17) the foraging trip. All females were instrumented with satellite- and time-depth recorder tags. DDTs, PCBs and PBDEs were detected in all samples, in decreasing mean concentration. Mean concentrations of \sum DDTs, \sum PCBs, and \sum PBDEs in blubber upon arrival to land from a foraging trip were twice as high for males compared with females. Upon arrival to land, \sum DDTs and \sum PBDEs in male and female blubber samples were highly correlated ($p < 0.001$; $r = 0.92$ and $r = 0.95$, respectively). Differences in male and female bioaccumulation may be due to behavioral differences in both foraging and reproduction. Our results support elephant seals as an integrator of deep-ocean contaminant exposure. Elephant seals are easily studied and their bioaccumulation patterns may reflect threats to more cryptic marine predators.

Effects of habitat fragmentation on native bee assemblages and pollination services in a Southern California scrub ecosystem

Keng-Lou James Hung, Department of Ecology, Behavior and Evolution
University of California, San Diego

Scientists estimate that over 85% of terrestrial flowering plants are pollinated by animals. Although studies show that pollinator communities respond idiosyncratically to anthropogenic disturbances such as habitat fragmentation, little is known regarding how disturbance affects pollinator assemblages in biodiversity hotspots or how ongoing pollinator diversity loss affects pollination services rendered to native plants in natural systems. To address these questions, we surveyed bee faunas in large natural reserves and small coastal sage scrub habitat fragments. We also monitored floral visitation by pollinators and measured pollen limitation for three focal native plant species: *Salvia mellifera*, *Bahiopsis laciniata*, and *Deinandra fasciculata*. Compared to bee assemblages in natural reserves, those in scrub fragments were less diverse both taxonomically and temporally and were represented by a larger proportion of species with broadly generalized diets. In reserve sites, *S. mellifera* was visited by a higher diversity of native bee species and *D. fasciculata* was visited by a higher diversity of native insects in general, compared to patterns of floral visitation in fragments. However, reserves and fragments did not differ from one another with respect to bee abundance, the frequency of pollinator visits to focal plant species, nor the degree of pollen limitation experienced by focal plants. Honey bees accounted for a large proportion of visits (30% to 90%) across all plant species and sites. These results show that pollinators in diversity hotspots may be especially threatened by anthropogenic disturbances, but suggest that generalist pollinators may potentially buffer pollination services against the loss of pollinator diversity.

Digging out the decomposer community from soil metagenomic data

Emily E. Curd, Department of Ecology and Evolutionary Biology
University of California, Los Angeles

Soils are an enormous reservoir of organic material and the largest accumulation of terrestrial carbon. The soil decomposer community is primarily responsible for the turnover of this organic matter. Extracellular enzymes produced by heterotrophic microorganisms degrade complex organic materials into less complex forms and ultimately mineralize the carbon, nitrogen, and phosphate. These organisms and the extracellular enzymes that they produce are incredibly important in global elemental cycles. Here we explore the relationship between microbial community composition, and function in soils under three vegetation types and at different soil depths. Due to differences in resources for these samples, we hypothesize that microbial community composition and function will differ by vegetation and depth. We assume that extracellular enzyme activity is proportional to the abundance of the organisms that produce those enzymes; therefore we expect that each vegetation type will have unique abundances patterns of decomposer species that are highly correlated with enzyme activity. We found depth and vegetation are significant predictors of enzyme activity and microbial diversity. Sage and oak enzyme activities and diversity are not usually significantly different, but they are significantly different from grass. Grass is the only vegetation type where enzyme activity correlates significantly with diversity. In general there is a weak relationship between microbial community and decomposer activity. Possible decomposers were identified. We are investigating the hypothesis that the class-level OTUs that correlate with extracellular enzyme activity do contain those genes.

Climate change effects on soil respiration: altered precipitation and invasion in a chaparral system

Ellen Esch, Department of Ecology, Behavior, and Evolution
University of California, San Diego

In arid and semiarid systems episodic rain events play fundamental roles in determining microbial activity and resulting effects on ecosystem level biogeochemical cycling. However, it is unclear how altered precipitation regimes coupled with changing community composition will affect soil microbial dynamics. To test this, we performed a wet-up and litter-addition experiment on soils collected following a 2-year rainfall manipulation where plots were subjected to low, ambient, or high rainfall. High and low water pulse treatments were applied to soils over eight weeks in combination with litter additions from two native and two exotic species. Microbial respiration and microbial biomass were measured following the pulses. Microbial activity was higher for soils receiving a large moisture pulse than for soils receiving a low moisture pulse, highlighting that decomposition is often moisture limited in arid and semiarid systems. In the high pulse soils, microbial activity was higher when exotic versus native litter was added. In the low pulse treatment, there was little effect of litter origin on respiration, suggesting strong moisture limitation overall in this treatment. In the low pulse treatment, average soil activity gradually increased over the experiment, showing that microbial communities can adapt to drought conditions. However, soils originating from different field rainfall treatments had no difference in respiration responses to lab manipulations. Microbial communities may be more responsive to current conditions rather than retaining legacy effects. These results show that altered rainfall regimes in combination with invasion by exotic species are capable of altering belowground processes.

Impacts of environmental change on soil microbial composition and function across a habitat productivity gradient

Kelly Gravuer, Department of Plant Sciences
University of California, Davis

Central to predicting how environmental changes will affect ecosystem function is understanding the context-dependence of their impacts – does an environmental change consistently increase or decrease a function across major ecological gradients, or do its impacts vary with site properties? We addressed this question at the McLaughlin Reserve, where three very different soil types (serpentine sand, serpentine clay and non-serpentine loam), supporting habitats of varying productivity, occur in close proximity. Since spring 2010, replicate plots on each soil have received late spring precipitation addition and NPK nutrient addition in a 2 x 2 factorial design. In spring 2013, potential activities of five soil enzymes were measured: β -glucosidase (BG), β -N-acetylglucosaminidase (NAG), acid phosphatase (AP), polyphenol oxidase (PPO) and peroxidase (PER). Nearly all enzyme activities differed among soil types. Effects of precipitation addition depended on soil type, in a manner fairly consistent across enzymes. In contrast, effects of nutrient addition did not - in all three soils, added nutrients increased activity of the hydrolytic enzymes involved in C and C+N acquisition (BG, NAG), while activities of the oxidative enzymes (PPO and PER) were unaffected. At the same time, we measured soil bacterial+archaeal composition by sequencing community 16S rRNA genes; in-progress compositional analysis will be discussed and compared to the functional (enzyme activity) measurements. Ultimately, we plan to integrate soil microbial and plant community data to understand how the impact of these environmental changes on the plant-soil system may depend on ecological context.

Mound landscapes may emerge from small interactions: simulation and observation

Chloe P. H. Lewis, Department of Environmental Science, Policy and Management
University of California, Berkeley

Mima mound landscapes, of meter-scale undulations over hectares of territory, are found throughout the world, usually over restricted drainage. Burrowing rodents in several mound landscapes have been observed moving soil toward the mound centers at rates sufficient to maintain the mounds against erosion, but the cause of this organized activity is debated. My cellular automata model coupling small-scale (10 cm, 1 day) interactions between topography, hydrology, plant growth, and underground rodent foraging generates and maintains mound-pool topography from rough or smooth original landscapes, and reproduces differences in mound arrangement observed on several landforms, if the rodents are attracted to the edge of the saturated regions. I mapped gopher tailings, soil moisture, and vegetation density and phenology over two years on six mounds in Jepson Prairie Nature Reserve to test the relations between burrowing activity and the other variables. Preliminary results show a weak association of activity with saturation, but a recent ground-based LiDAR scan of the mapping sites may increase accuracy. California mima-type landscapes are often vernal pool systems supporting endemic or endangered species, and understanding the short-term processes maintaining the niche habitats may be useful to landscape managers. Simulated systems can also model landscapes under rainfall regimes we have not observed historically.

Soil-landscape modeling of coastal California hillslopes using terrestrial lidar

Samuel Prentice III, Department of Geography
University of California, Santa Barbara

Digital elevation models (DEMs) are the dominant input to spatially explicit digital soil mapping (DSM) efforts due to their increasing availability and the tight coupling between topography and soil variability. This coupling is often modeled using techniques that assume the scale at which DEM terrain attributes are aggregated is appropriate for characterizing soil-landscape relationships. However, soil variability is driven by geomorphic process-response dynamics blending at multiple spatial scales and a physically meaningful specification of topographic scale in DSM efforts remains elusive. To address this dilemma we implement a DSM study that embeds conceptual models of soil distribution in a quantitative framework using fine scale (1 m) terrestrial lidar. Specifically we emulate a terrain segmentation model previously developed to extract and correlate hillslope positions with soil properties in a rolling post-glacial landscape. When implemented as published, the model does not translate well due to greater short-range topographic variability in our domain and high frequency spatial variability carried over from fine scale lidar data. To improve model portability, we propose an adaptive model based on quantitative diagnostic tools that identify topographic thresholds contained in the target landscape. Our adaptive hillslope segmentation approach leverages the richness of fine scale terrain data using conceptual models of soil-geomorphic linkages, and reduces the arbitrariness associated with specifying the scale of terrain attributes in soil-landscape modelling. Initial correlations between our categorical hillslope subdomains and soil properties reveal a breakdown in predictive power in areas transitioning from diffusion-dominated to advective in transport-limited landscapes.

Geomorphic constraints on the temporal evolution of the Hilton Creek fault, Long Valley caldera, CA

Jonathan Perkins, Department of Earth and Planetary Sciences
University of California, Santa Cruz

The Hilton Creek fault, adjacent to the Sierra Nevada Aquatic Research Laboratory in eastern California, is a prominent range-front normal fault bounding Long Valley caldera to the mountains of the southern Sierra Block. This fault is within the Eastern California Shear Zone (a diffuse zone of deformation between the Pacific and North American plates), and is hypothesized to be the epicenter of the 760 ka Long Valley caldera eruption, which ejected ~600 km³ of rhyolitic magma and blanketed a large portion of the southwest United States in volcanic ash. Recent seismicity in the caldera coincident with the growth of Long Valley's resurgent dome since 1980 has prompted renewed interest in studying the tectonics and magmatism of the area to better mitigate geologic hazards. Though we know the Hilton Creek fault has been active since the Last Glacial Maximum (~25 ka), little is known about its long-term evolution and possible relationship to the magmatic evolution of Long Valley caldera. Here we show through an analysis of deformed ancient lake shorelines that present activity along the Hilton Creek fault did not begin until after 175 ka. As the Hilton Creek fault has experienced significant pre-caldera offset, this temporal constraint reveals at minimum a ~500 kyr gap wherein regional tectonic stresses did not result in extensional faulting within Long Valley Caldera. Thus a dynamic relationship exists between regional tectonics, magma chamber evolution, and crustal rheology in Long Valley caldera that is at present poorly understood.

Reconstructing prehistoric plant use on Santa Cruz Island

Kristin Hoppa, Department of Anthropology
University of California, Santa Barbara

The Chumash and their predecessors have occupied the Santa Barbara Channel region, including both the mainland and the islands, for approximately 13,000 years. Studies of the island Chumash have traditionally focused on the importance of marine resources (i.e., fish, shellfish and sea mammals), to the near exclusion of terrestrial resources (i.e., plants). My research explores the use of plants as food, medicine and raw material during the Middle Holocene (approximately 4650-1350 BC). In particular, I focus on sites located within the Central Valley of Santa Cruz Island, testing the hypothesis that islanders moved inland during the Middle Holocene in order to take advantage of plant resources. As the first regional study to combine the analysis of charred seeds recovered from the soil matrix of archaeological sites with the analysis of microscopic starch grains recovered from the surface of ground stone artifacts, this project demonstrates the value of an integrated approach. Initial soil analysis revealed seeds from several medicinal plants, but a surprising lack of traditional plant foods. However, further analysis of groundstone residues resulted in the recovery of starch grains from both acorn and pine nut. Additionally, plant remains recovered in this study provide information on the variety of foraging locations (e.g., grassland versus riparian) and the seasonality of site occupation, allowing for a fuller understanding of prehistoric subsistence and settlement decisions.

Cascading effects of the invasive pathogen *Phytophthora ramorum* on ectomycorrhizal fungal communities

Sydney I. Glassman, Department of Environmental Science, Policy, Management
University of California, Berkeley

Phytophthora ramorum is a recently emerged, oomycete exotic plant pathogen that is responsible for the massive tree mortality caused by the disease sudden oak death (SOD). The pathogen has caused rapid decline of the locally dominant ectomycorrhizal tree (EM) tanoak (*Notholithocarpus densiflorus*), host to a high diversity of EM fungi, which are crucial tree root symbionts that contribute to N cycling in forest soils and form mushrooms that play important roles in local economic and cultural practices. As tanoak is the only EM host in many redwood forests and the largest biomass contributor to many coastal mixed evergreen forests, the loss of this tree may cause reductions in EM fungal richness and biomass that will likely have unexpected cascading effects on many ecosystem functions. Lack of quantitative pre-disturbance data has hindered our understanding of the effects of disturbances on forest ecosystems. By analyzing the effects of an emerging pathogen and taking advantage of two long-term SOD monitoring plot networks, I have an unprecedented opportunity to quantitatively analyze both above and belowground pre- and post- disturbance data. Thus far, 12 spatially explicit soil samples from 18 plots along a continuum of SOD infection have been collected for a total of 216 soil samples that await Illumina sequencing. Each plot has been characterized for a variety of soil parameters and mushrooms found in plots have been catalogued and sequenced. Discriminant analyses and generalized linear mixed effects models will be used to determine the effects of SOD infection on microbial communities.

Quantifying patterns of coastal fog deposition during the late summer drought

Nathan Emery, Department of Ecology, Evolution and Marine Biology
University of California, Santa Barbara

Water is a limiting resource for California's coastal shrubs during the prolonged summer drought. By August/September it may have been several months since the last rainfall. During the late summer, however, there can be significant fog in the Santa Barbara region and over much of the central coast. My study attempted to quantify fog presence and deposition for two coastal shrub species at Coal Oil Point Reserve. My overarching goal is to determine the relationship between fog deposition and plant water content. This study found a significant "fog shadow" effect of shrubs whereby the shrubs on the edge of a stand experienced more fog than those inside the stand. Also, deposition was highly variable throughout the summer and the relative influences on the quantity of fog deposited are still unknown. Further analysis of my data will relate fog deposited to rainfall equivalents as well as the importance of shrub position to prevailing winds.

Spatial and temporal patterns in conifer encroachment into subalpine meadows in the central Sierra Nevada

Kaitlin Lubetkin, Environmental Systems Graduate Group
University of California, Merced

Many grassland ecosystems worldwide are experiencing woody plant encroachment, including high-elevation meadows in the Sierra Nevada. Conversion of Sierran meadows to forest may result in loss of important ecosystem services, such as water storage and release, which they provide. During 2009-2012 we conducted detailed field surveys of 30 subalpine meadows in Yosemite National Park to examine overall density of encroaching conifers, and to look at age distributions of trees. There was a wide range of encroachment intensities in meadows, with encroachment essentially ubiquitous up to the krummholz zone (treeline). We therefore correlated encroachment density with environmental factors derived from PRISM data and the USGS National Elevation Dataset. Presence of surrounding lodgepole pine was the strongest predictor of encroachment density. In meadows with sufficient surrounding lodgepole pine, encroachment was most intense in lower elevation meadows, meadows with high mean monthly maximum temperatures, low precipitation, high solar radiation during the melt period (May-July), and south facing aspects. Meadow encroachment onset varied among meadows, though encroachment within meadows fit into three general patterns, with encroachment beginning either around 1904 (5 meadows), 1948 (9 meadows), or 1978 (4 meadows). The composite regional encroachment time series showed a strong peak in the early 1950s, followed by a dip after which encroachment increased fairly steadily since approximately 1964. We were able to model the regional time series based on 6 climatic drivers, divided into those during the 3-year "lag" period before germination (affecting seed supply) and the 6-year "lead" period following germination (affecting seedling survival).

Evidence of diet specialization and prey switching in northern elephant seals (*Mirounga angustirostris*): Implications for responses to climate variability

Chandra Goetsch, Department of Ecology and Evolutionary Biology
University of California, Santa Cruz

In response to climate variability, predators may change where they forage, how they forage, and which prey they target. Moreover, variability in diet due to individual specialization and prey switches may help buffer a population against environmental change, since both can serve to increase population niche width, facilitating a higher capacity to respond to change. Tracking data show that northern elephant seals have high individual foraging route fidelity, exhibiting little evidence of changing foraging locations in response to El Niño conditions. During the 2009–2010 El Niño, female seals dove deeper than in previous years, providing evidence that they alter foraging behavior. However, knowledge of diet is scant due to long foraging migrations, and it is unknown whether individual seals specialize in diet or if they respond to climate variability by switching diet. To determine the diet of elephant seals, I compared the fatty acid composition of blubber from adult female seals (2009–2012, n=119) with mesopelagic prey, using quantitative fatty acid signature analysis (QFASA). I found evidence for both high variability in diet as well as diet specialization between seals, with certain individuals focusing on fish and others on squid. Furthermore, fatty acid signatures for seals foraging in the 2009–2010 El Niño were significantly different than seals foraging in 2011 and 2012 (Permanova, $p=0.001$), suggesting a prey switch in response to oceanographic variability. The presence of individual diet specialization and prey switching suggests that elephant seals may be resilient to environmental changes.

Interactive effects of temperature and predation on mountain lake food webs and ecosystem fluxes

Celia Symons, Department of Ecology, Behavior and Evolution
University of California, San Diego

Understanding and predicting how global change will affect ecosystems is an increasingly urgent task in a world of ongoing climate change. Food webs are sensitive to the effects of both “top-down” and “bottom-up” forces as well as the influence of climate. Theory and experiments have shown that as temperature increases food webs become more influenced by top-down control. To determine if these patterns are present in natural systems, we sampled 29 lakes in Yosemite National Park. Lakes were chosen to vary in elevation, which provided a gradient in temperature, and 15 contained fish while 14 were fishless. In the summer of 2013 we sampled components of the food web including macroinvertebrates, zooplankton, phytoplankton and bacteria and measured ecosystem rates including pelagic production, benthic production and litter decomposition. We found that food web structure (i.e., the ratio of consumer to producer biomass) was interactively effected by temperature and fish (ANOVA, $F_{3,25}=12.82$, $p<0.001$). Fish exerted stronger top-down control at high temperatures, consistent with previous studies. Pelagic production increased with temperature (LME, temp $F_{1,24}=4.4$, $p=0.046$), while benthic production increased with both temperature and fish presence (ANOVA, $F_{3,17}=5.91$, $p=0.006$). Interestingly, decomposition rate decreased with temperature in the absence of fish, but was not affected by temperature in the presence of fish (ANOVA, $F_{3,19}=9.3$ $p<0.001$). This was likely the result of changes in the decomposer community composition and size structure. Together our results suggest that introduced fish predators will magnify the effect of climate change on food web structure and will interactively affect ecosystem fluxes.

Does rafting help maintain gene flow in a brooding invertebrate?

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Marine invertebrate brooders are perceived to have limited dispersal potential due to a lack of a free-swimming larval stage, although this can be quite the contrary if long-distance dispersal via rafting is found to be an important dispersal mechanism. To address this topic I have targeted the giant kelp (*Macrocystis pyrifera*) as a focal rafting substrate, which, when detached (e.g. by storms, wave action, herbivory), forms rafts that are subsequently transported via ocean currents. To assess how rafting might influence population genetic structure, I have selected a canopy-dwelling isopod (*Pentidotea resecata*), which broods its offspring to a crawl-away phase (lacks a pelagic phase) and is thought to have low intrinsic dispersal ability. Isolation by distance (IBD) best explains the genetic structure of *M. pyrifera* in populations studied in California, where close populations are genetically more similar than distant ones. My null expectation is that *P. resecata* will passively disperse with *M. pyrifera* and share a correlated pattern of IBD on a similar spatial scale. Preliminary analyses of cytochrome oxidase subunit I (COI) suggest *P. resecata* lacks the level of population genetic structuring that would be expected for a brooder and that phoretic dispersal via rafting likely contributes to gene flow in this species. As a next step, I plan to search for signals of natural selection in *P. resecata* using genetic assignment tests to identify likely source populations of detached kelp and test whether *P. resecata* genotypes are represented at sites to which they have the potential to disperse.

Changes in marine resource use by California coastal coyotes (*Canis latrans*) over the last several thousand years

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Marine and terrestrial environments are linked through the cross-habitat transfer of energy and nutrients, the flux of which can subsidize a diverse array of consumers with significant consequences for local communities and food webs. Although marine subsidies may enter recipient habitats at any trophic level, coastal or riparian predators are often agents of energy transfer from sea to land. Brown bears who feed on anadromous salmon in inland environments, for example, aid in transferring significant marine-derived nutrients from aquatic to terrestrial habitats. Coyotes, which have an expanding North and Central American range, have also been shown to facilitate and benefit from marine subsidies. Identifying the past and present role coyotes play in linking land and sea, and whether those links are lost or gained through time, has important implications for their future management. I sought to determine the magnitude of marine subsidies to coyotes in coastal California over the past several thousand years. To do so, I measured carbon and nitrogen isotope values in modern coyote scat and sub-fossil Holocene coyote bones. My data point to both the existence of a marine subsidy to modern coyotes, and to a positive impact on coyote abundance. Sub-fossil isotope data suggest that Holocene coyotes did not consume marine-derived foods, despite the nearby presence of a mainland seal rookery. These data suggest that the use of marine resources by contemporary coyotes is a new behavior relative to their recent ancestors, perhaps enabled by reduced competition with humans or other, now-absent consumers (e.g., grizzly bears).

Impacts of snow and rain change on native vs. invasive species and fire fuel properties in a sagebrush steppe ecosystem

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Sagebrush steppe is one of the most widespread ecosystem types in the western U.S., yet also one of the most vulnerable to large-scale ecosystem conversion due to a positive feedback between the non-native species *Bromus tectorum* (cheatgrass) and fire. One of the most ubiquitous invasive species in the western U.S., *B. tectorum* rapidly colonizes bare ground amid native steppe vegetation, completes an unusually early phenological cycle, and subsequently becomes a serious fire hazard. The continued rapid spread of *B. tectorum* throughout the West and into upper elevations is alarming and may be exacerbated by changing climatic conditions. This study examines effects of the type and timing of precipitation on *B. tectorum* and native species, using snow fences to simulate changes in snowpack (increased, decreased, and ambient depth) and irrigation to simulate increased frequency and magnitude of spring and summer precipitation. In spring 2013, the trend in *B. tectorum* phenology was advanced in the “minus” snow zone relative to the “plus” snow zone, while phenology of native species monitored did not respond to snowpack manipulations or had different patterns. Species richness, percent cover, and leaf area index did not differ by snow zone. *Bromus tectorum* physiological responses (CO₂ assimilation, stomatal conductance, quantum yield of Photosystem II, electron transport rate) to spring rainfall additions were more pronounced than those of native species. Native species physiology did not respond to summer rainfall additions (after *B. tectorum* senescence). Overall, results indicate that *B. tectorum* may be more sensitive than native vegetation to precipitation change.

