Ecological Dynamics Annual Meeting

University of California, Merced

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Wednesday, November 29

Ariadna Cairo
Dynamics of a system composed of phytoplankton and microbes
Phytoplankton are microscopic,one-celled, photoautotrophs organisms that drift in the sunlit surface areas of water bodies, and use light energy from the Sun, carbon dioxide and important ocean nutrients such as nitrogen, phosphorous, iron, and vitamin B. They convert the carbon dioxide and water into sugars and other carbon compounds. Then, phytoplankton return carbon dioxide and oxygen to the atmosphere when they respire. Over 50% of the world's oxygen needed by us to breath is produced by phytoplankton, only a small fraction of the carbon drawn into the ocean by plankton blooms makes it into the depths where it no longer can be exchanged with the atmosphere. The plankton communities, in which many microalgae (phytoplankton) and bacteria are included, establish interactions with heterotrophic bacteria by not not only decompose organic matter but also promote plant growth by certain complex communication mechanisms and nutrient exchange. There is three types of interactions: mutualism (two or more partners of different species benefit each other, commensalism (only one partner benefits) and parasitism (one species benefits at the expense of the other and exerts negative effects on it). In this project, I am going to analyze the dynamics of a system composed of phytoplankton and microbes. These microbes establish mutualistic, parasitic or commensalistic relationships with phytoplankton. The purpose of this analysis is to know the dynamical consequences of these microbes serving different purposes to phytoplankton, and also to know what can we say about the system depending on the proportions of each microbe type.

Ritwika VPS
A population dynamics approach to strategies in carnivore foraging
Predator behaviour during foraging can fall on a continuous spectrum between hunting and scavenging. In an ongoing study, I investigate the behaviour of a group of predators that can actively hunt for prey, or scavenge from the foils of a fixed pool of predators, either by eating leftovers (passive scavenging) or by stealing from a predator (active scavenging), based on the fitness value associated with each behaviour. While this approach gives tremendous discerning power at the individual level, it lacks analytical tractability. I propose a population dynamics approach to this problem, where the interactions between the predator and prey populations are summarised in a set of 6 differential equations, describing the three predatory modes (hunting, active scavenging, and passive scavenging) and their corresponding sources of food (live prey, prey being eaten by the hunter, and dead prey, respectively). In the proposed analytical model, the prey population can grow due to reproduction, and shrink as a result of predation through any of the three predatory modes. Each predator sub-group can grow either due to resource-dependent reproduction (we make the assumption that the offspring of one predator sub-group exhibits the same behaviour as the parent), and shrink due to mortality associated with the predatory mode. In addition, the size of each predator sub-group can also fluctuate as a result of exchange between the three sub-groups. This approach facilitates the incorporation of reproduction, as well as prey density-dependent effects in the system. We will solve this system numerically to investigate the evolution of prey and predator populations as a function of the governing parameters. We will also solve for fixed points and bifurcations in the system, and understand what they mean in a realistic predator-prey system.

Brandon Hendrickson
Virus-Host Dynamics: Modeling the range of virulence and spread rate traits in a changing host population using a Bounded Nicholson-Bailey Model.
Background: Traits associated with virulence and infection rate have been discovered to change given selection, however the actual environmental selective causes of this evolution remain elusive. The types of viruses are very diverse though they are all share a dependence on host survival. Viruses require a host to survive and reproduce,

and therefore viral fitness is dependent upon the virus's ability to spread and to kill the host while also maintaining a combination of these traits so the host population survives **Methods:** The Nicholson-Bailey Model is a host parasitoid model that measures host and viral density in a specific population where the amount of host that is not preyed upon is determined by a Poisson distribution, $e^{(-aV)}$, while the amount that is preyed upon is determined by another Poisson distribution, $1-e^{(-aV)}$. In the Virus-Host modified model, the proportion of hosts that are preyed upon have a likelihood of being recovered, denoted by c in $(1-e^{(-aV)})c$, which is not included in the NB model. This modification is like the SIR model, where a proportion of the infected individuals have a probability of overcoming the disease. Different a, b, and c values will be used in combination to find how each is affected by the other. **Results:** Initial host density did not change the steady state host and viral densities, though a low initial host density does result in complete die off the virus and host. Viruses have a natural range of a and c values that can be used for hosts, though the range of values increases for both a and c when the intrinsic growth rate of the host is increases. Conclusion: The first is that the host density can be reduced to a point to cause local population extinction of the virus. This means that the host characteristics can be modified easily over one generation as to cause viral extinction in a small period of time, which verifies the tactics used by the CDC in quarantine procedures. When virulence rises, the spread rate values that permit viral/host coexistence are smaller and vice versa. This limitation is seen in natural viral lineages where viruses that spread well are easily recovered (rhinovirus) while viruses that have high virulence happen to spread at a low rate (AIDS and Hepatitis). The model created supports these natural observations. Future research will include experimentation.

Jonathan Anzules

An essential part of the immune system to function properly in it's attack of intruders, and not self antigens, is the tolerance mechanism. During the development of T cells medullary thymic epithelial cells (MTEC) present potential antigens that can be found in our own body. These antigens can be anything from blood cells to muscle structures. If a developing cell recognizes any of these antigens, it is eliminated. The cause of autoimmune disease is the escape of any of these self-recognizing cells into our bodies. They then have the potential of recognizing our body as an intruder and initiate an attack on something as essential as one of our blood cells or bone marrows. In an attempt to understand the conditions that would allow the escape of these self-recognizing T cells I propose a probabilistic model of the tolerance mechanism. During the development process there are many MTECs present, it is theorized that 99% of antigens are presents, but how has not been well studied. I hypothesize that a series of MTECs do not need to present all antigens, only a few. The combined effect is a cumulative wall created to prevent passage of these self recognizing cells. My model sets out to explore what percentage of the bodies antigens is expressed in each cell to be efficient. In the figure below, each MTEC presents 30% of the bodies antigens, resulting in a 70% chance of not being found in each interaction. **Conclusion** In in an ideal situation, where MTEC's are not constrained by time, energy, and demand 9 MTEC's that present only 30% of the bodies self antigen is enough to capture 94.16% of all the self-recognizing cells. As for the ones that got away there are other mechanisms that eliminate these cells. **Future Work** In my model I wish to further explore what are the conditions that would cause autoimmune disease. There are a multitude of other factors to consider here. For instance, the chances of encountering the antigen, how efficient is the tolerance mechanism in the periphery of the body, and a self recognizing cell needs the support of another to instigate an autoimmune disease what are the chances of this?

Monday, December 4

Nathaniel Fox

Stochastic dynamic programming and stable isotope analysis reveal apex predator impacts on coyote prey selection
Terrestrial ecosystems are changing at unprecedented rates due to anthropogenic factors including overpopulation, overconsumption of resources, pollution, and climate change. These changes will likely have devastating effects on much of Earth's terrestrial biota, though it can be difficult to predict which species will be negatively impacted and how. Such predictions are challenging because trophic cascades caused by the removal of certain taxa can be difficult to anticipate. One type of cascade that has gained attention in recent years is a phenomenon known as mesopredator release. The mesopredator release hypothesis predicts that mid-trophic level predator populations will surge if apex predators, which often keep mesopredator populations in check, are removed from a system. In this scenario, mesopredators may overconsume small-bodied prey, thus resulting in an overabundance of large-bodied herbivores and mesopredators. Despite interest in the effects of mesopredator release on anthropogenically modified systems, little has been done to quantify these "before and after" effects because it is difficult to study systems where apex predator populations have not been reduced or eradicated by humans already. It is therefore largely unknown whether mesopredators (over)consume the same prey types after apex predator removal or whether they subsequently modify their prey selection. Though, it might be expected that mesopredators will consume the most

energetically efficient prey when other constrains such as competition and predation are lessened. Here, I use stochastic dynamic programming (SDP) to simulate whether one mesopredator, Canis latrans (coyote), consumes the same prey items before and after apex predators are removed from the system. Coyote prey selection is modeled based on three foraging scenarios: hunting large-bodied prey (mule deer), hunting small-bodied prey (cottontail rabbit), and scavenging an emaciated carcass. Parameters including foraging cost, prey capture probability, energetic gain, and mortality risk are modeled based on field observations from the literature. Results indicate that, in the absence of apex predators, coyotes will preferentially select large-bodied mammals over small mammals or scavenging. However, small mammal predation and, to a lesser extent, scavenging becomes more profitable when apex predators are included in the system (though large-bodied prey are still most profitable when coyotes are close to starvation). Further, changes in prey capture probability due to competition with apex predators appear to have the most significant impact on coyote prey choice, while changes in coyote mortality rates due to large carnivore predation has comparatively little impact on their prey selection. Stable isotope analysis of coyote, small herbivore, and large herbivore fossils from Rancho La Brea will reveal whether coyote prey selection in these models are reflected in a natural "high competition" system as well.

Vicky Espinoza
The American River is the spawning location for tens of thousands mixed run hatchery and naturally produced fall-run chinook salmon and Folsom Dam, a Central Valley Project facility built in 1955 and regulates flows in the reach that is accessible to salmon. In natural conditions (without the dam) the river supported both fall-run and spring-run chinook salmon populations, but the spring-run chinook are no longer supported since the river was dammed. Historical salmon migration data shows that salmon populations were devastated by California's hydraulic gold mining in 1866, but proved to be resilient about 44 years after the damming of the river. This project demonstrates differences in pre-and- post dam relationship effects between river conditions (water temperature and depth) and salmon populations trends. This project also shows changes in fecundity of chinook salmon population in both the presence and absence of the Folsom Dam.

Qingqing Xu
Ecosystem resilience is of great concern with global change. Fire is as a major disturbance of vegetation changes and vegetation properties in turn alter fire regimes. Mediterranean-type ecosystems (MTEs), which dominated by grassland (G), shrubland (S), and forest (F), are a prime example of ecosystems disturbed by climate and fire. I developed a theoretical model which incorporates: (1) the rate of vegetation succession from G to S and S to G; (2) the feedback of fire to set F back to S and G. The stability of this dynamic system is examined (results will come later).

Jeffrey Lauder
Fight or Flight: Carbon allocation in conifers under drought stress
The California drought of 2012-2016 was more severe than any observed in the previous 1200 years and left an estimated 110 million standing dead trees in the Sierra Nevada. This mass tree mortality may have myriad implications for water resources, fire prevalence, and land management. However, it also provides a unique opportunity to test hypotheses regarding drivers of tree mortality in a natural setting. The specific mechanisms of tree mortality or survival under drought are still mostly unknown. Under drought stress, trees close stomata leaf pores to reduce water loss, but at the expense of decreased photosynthesis. This means that under drought stress, trees are taking in less food needed to grow and produce tissues. As stress intensifies or is prolonged, trees may use different strategies of resource use. I propose that under extreme stress, a tree may face a choice between two options: to "fight" by allocating more energy to survival-enhancing features such as growth; or "flight" - allocating more resources to reproduction, increasing the probability that offspring will reach more favorable sites, or have a chance to germinate in a lower-competition environment after adults die. I also hypothesize that while the fitness maximizing behavior of perennial plants is survival under stress to enhance future reproductive success, drought stress may increase the prevalence of flight behavior instead, as drought may stress trees beyond "normal" thresholds of survival strategies. Here I present a model of fight-or-flight dynamics in conifers relative to stochastic drought frequency and intensity. The model incorporates carbon storage dynamics and impacts of seed production or growth on those dynamics as a function of drought tolerance. I will then present results from solutions computed using stochastic dynamic programming that simulate the expected fitness maximizing behavior – either fight or flight – under drought stress.

Wednesday, December 6

Dana Swarth
Quercus douglassii age structure modeling to predict long term population shifts

Many California oak woodland species rely on Quercus douglasii (Blue Oak) as a food source and for nesting cavities. Blue oaks, endemic to California, are known to be one of the more drought tolerant oak trees in the state, but since the recent 2012-2015 drought, blue oaks are experiencing a surprising amount of tree mortality. A prior stress that has affected blue oak populations is a lack of sapling recruitment to reproductive age, causing an age structure that is made up of more mature old-growth trees (150-300years old) and less young trees (20-150 years old). Based on these factors, there is an uncertainty of how the age structure of the population will progress in the coming years. I plan to model the age structure of an average blue oak population and simulate the model over time using different variables that affect tree mortality and sapling recruitment, such as elevation, precipitation, and herbivory in order to predict how blue oak populations will change over time related to potential future environmental conditions. I predict that blue oak species will experience a continued increase in mortality, that the populations as a whole will suffer in the next 100 years and that acorn production will decline, limiting food availability for oak woodland species. I also predict that there will be a higher survival rate at higher elevations than at lower elevations, and a higher survival rate in woodlands that are not grazed by cattle. The results of these models could inform land managers who are interested in finding restoration locations that have the greatest need and greatest chance of success. The age structure model that I will create could be used for predicting population changes in other plant species as well.

Laura Van Vranken

Determining population size for a long-lived, secretive, semi-aquatic reptile presents physical, logistical, and monetary challenges in understanding how that species is distributed across a landscape. This knowledge is also critical in resolving areas of biological importance for a species with multiple years at different life stages and with differing ecological requirements. The western pond turtle, Emys marmorata, is one such species. The status of western pond turtle populations in the central California to Sierra Nevada region is relatively unknown, and this knowledge is of ecological importance to advise turtle reintroduction efforts in this region. This study aims to model population sizes for adult and juvenile western pond turtles from central California to Yosemite National Park using factors that affect population size that are also ecologically significant to their life history, using a modified logistic equation for population size: $rN(1-N/K) - L$. Predicted population sizes were calculated using three variables important to this semi-aquatic turtle: [1] temperature, which influences the population growth rate (r); [2] primary productivity, which caps population sizes (K); and [3] predation, which represents a loss in population size based on predator abundance (L). Using estimates for each variable based on findings from the literature, databases, and expert opinion, population size was calculated for each grid (100 m2) across a 100 km transect, from the San Joaquin Valley to Yosemite Valley. Calculated values were mapped in ArcGIS to display population densities as a gradient across the transect. Based on the results, adults and juveniles display differing population sizes at different areas along the transect, corresponding with their distinct thermal requirements. Modeling predicted population sizes based on species life history traits can reveal optimal suitable localities for a species without the time-consuming and expensive task of estimating population size through long-term capture and survey studies, or molecular population genetic work. These results also offer predictions for areas of high conservation importance, and the opportunity to focus on localities important for different life stages which can directly inform conservation and management for this species. Future directions for the results from this model are to compare these population size estimates with population data for western pond turtles in this region, which is currently in the works through existing population genetic research to determine effective population sizes from genetic samples.

Daniel Toews

Ecological Niche Model Of An Annual California Vernal Pool Endemic Limnanthes douglasii ssp. rosea (Meadowfoam)

Over 95% California's vernal pool habitat has been lost to agriculture and urban development. The 5% of remaining vernal pool habitat hosts some of California's rarest endemic plants and animal species, many of which have specific habitat requirements that we are just recently beginning to explore. In this paper, will combine plant community and environmental data to build a theoretical ecological niche model for the vernal pool endemic Limnanthes douglasii ssp. Rosea (Meadowfoam), Benth. C.T. Mason. This work will highlight parameters important for structuring Meadowfoam populations that may be used as a first approximation for understanding the ecological and environmental habitat parameters responsible for structuring vernal pool plant populations.

Megha Suswaram

Reaction-Diffusion (RD) systems, have applications in ecology, developmental biology, physiology and many other fields. This study relates the appearance and propagation of patterns in population dynamics to the process of speciation (specifically, appearance of new biological species). The objective of this research is to model, characterize and predict the evolutionary speed of phenotypic spread in an expanding population. It is developed on a

framework that combines existing population dynamics systems and RD systems to study the process of a speciation. It examines the interaction between a quantitative trait and population density. I develop and analyze a diffusion model of the distribution of a phenotypic trait in a population. I explore the spatio-temporal dynamics for population density and of a quantitative phenotypic trait which is related to the adaptation of individuals to their environment. It considers a species distributed continuously across a one-dimensional spatial domain. This species is subjected to a pattern of selection on the quantitative trait that varies spatially. Using numerical simulations, I demonstrate that populations spread by advancing as two synchronic traveling waves, one for population density and one for trait adaptation. It could be possibly inferred that dispersal rate and evolutionary speed of phenotypic evolution are inversely related. This is expected because dispersal moves individuals further, it homogenizes populations. This simple model of phenotypic evolution within populations show how multiplicative changes can produce macroevolutionary patterns.