Global change at the nexus of climate, biodiversity, and disease

8 August 2022 | 9:00 – 5:00

Peter Wall Institute for Advanced Studies, Seminar Room

Watch from Zoom (password: 443015)

9:00 Welcome

9:15 Allan Carroll (UBC): Predicting biotic disturbances to forested landscapes under global change

9:50 Claire Kremen (UBC): Managing landscapes to reduce the triple Anthropocene threat

10:25 Lizzie Wolkovich (UBC): Is the global fingerprint of climate change driving species asynchrony?

11:00 Coffee Break

11:30 Alyssa Gehman (Hakai Institute): Untangling the interacting influence of disease, host biodiversity and climate change in sea star wasting

11:45 Johannah Farner (Stanford University): Local tree cover and land use predict mosquito biodiversity and disease vector presence

12:00 Jayme Lewthwaite (University of Southern California): Species, phylogenetic and community-level responses of Canadian butterflies to a century of global change

12:15 Sally Otto (UBC): TBA

12:30 Lunch Break

1:30 John Drake (University of Georgia, Athens): Patterns in emerging pathogens of livestock

2:10 Lauren Buckley (University of Washington): Characterizing how organisms experience climate change to forecast biodiversity and disease implications

2:50 Patrick Stephens (Oklahoma State University): Using biodiversity to predict Ebolavirus outbreaks

3:30 Snack Break

4:00 John Gittleman (University of Georgia, Athens): One Health: what is it, what should it be?

4:15 Alaina Pfenning-Butterworth (UBC): Making connections: climate change, biodiversity, and infectious disease

4:30 Closing discussion

Talk Descriptions

9:15 Allan Carroll (UBC): Predicting biotic disturbances to forested landscapes under global change

To facilitate sustainable harvests, forest management agencies throughout most of western North America have for many decades conducted regular assessments of forest disturbances (fire, insect/disease outbreaks) and forest structure/composition. These long-term spatial databases, along with weather/climate projections, can be combined with empirical models of eruptive forest insect dynamics to quantify factors affecting the temporal and spatial attributes of outbreaks, and predict the independent and interacting impacts of climate change and forest management activities. This presentation will comprise an overview of the efforts by the UBC Forest Insect Disturbance Ecology Lab to predict biotic forest disturbances under global change.

9:50 Claire Kremen (UBC): Managing landscapes to reduce the triple Anthropocene threat

Biodiversity loss, climate change, both fueled by continued unsustainable extraction from land and sea, make up the triple Anthropocene threat. How can we manage landscapes to reduce these threats? This talk will discuss the "working lands conservation" concept and develop several examples to show how regenerative agricultural techniques both support biodiversity and depend on it to produce ecosystem services, including pest and disease regulation, while promoting climate mitigation and adaptation.

10:25 Lizzie Wolkovich (UBC): Is the global fingerprint of climate change driving species asynchrony?

Twenty years ago researchers reported the first 'globally coherent fingerprint' of climate change on natural systems. Plants and animals are shifting earlier with warming. Within a decade concerns that such shifts could reshape the timing of species interactions and, in turn, communities and ecosystems were met with data suggesting upper trophic levels shift slower than lower ones. But recent meta-analyses have led to contrasting findings, some supporting major differences across trophic levels and others finding little support. Such discrepancies could be driven by ecology, with responses explained by the level of species interactions, or by differences in warming or sampling across space. New results provide robust tests of these hypotheses and address how globally coherent trophic asynchrony is across systems.

11:30 Alyssa Gehman (Hakai Institute): Untangling the interacting influence of disease, host biodiversity and climate change in sea star wasting

Sea star wasting, with an epidemic outbreak in 2013-14 and continued disease outbreaks through 2022, can infect up to 20 sea star species, and the many hosts interact directly as competitors and predators. In addition, sea star wasting has been associated with anomalous temperature, suggesting a role for the interaction between disease outbreak and climate change. I will outline ongoing work to 1) identify causative agents of disease, 2) the influence of competition and disease response on interacting hosts and 3) explore the relationship between temperature and disease.

11:45 Johannah Farner (Stanford University): Local tree cover and land use predict mosquito biodiversity and disease vector presence

Mounting evidence from Latin America shows that percent tree cover at small spatial scales of < 100 m is a reliable predictor of biodiversity for many taxa, suggesting local tree cover management as a promising conservation tool in this region. However, the generality of this pattern across taxa and its relationship to disease risk are unknown. Here, we use a field survey of mosquito community assembly along a tree cover and land use gradient in southern

Costa Rica to assess how landscape context relates to mosquito biodiversity and the presence of key disease vector species.

12:00 Jayme Lewthwaite (University of Southern California): Species, phylogenetic and community-level responses of Canadian butterflies to a century of global change

Species' responses to anthropogenic change have been varied and complex. Some species and areas have flourished, whilst others have been reduced to a fraction of their previous extent or diversity levels. Are these responses idiosyncratic or are there generalizable patterns that we can extract in order to prevent further losses of biodiversity by prioritizing those species that require it most? I examine spatial and temporal responses of approximately 300 species of Canadian butterflies over the past century over a wide spatial and environmental gradient. I test whether species' intrinsic biology as well as the magnitude and direction of both climate and land use change have dictated biological responses at 3 levels: species, community and phylogenetic. These results may help resolve the recent discrepancy between global and local diversity trends (no net change vs an extinction crisis).

12:30 Sally Otto (UBC): TBA

1:30 John Drake (University of Georgia, Athens): Patterns in emerging pathogens of livestock

Dr. Drake will discuss the results of a recent data-driven horizon scan aimed at identifying attributes of bacterial species associated with wildlife that confer a propensity to spill over into livestock populations. A machine learning approach was used to select characteristics that serve as risk factors and a screen was developed to identify those species most likely to associate with pigs, sheep or cattle. Wildlife reservoirs of known and novel bacteria were shared among all three species, suggesting that targeting surveillance and/or control efforts towards these reservoirs could contribute disproportionately to reducing spillover risk to livestock.

2:10 Lauren Buckley (University of Washington): Characterizing how organisms experience climate change to forecast biodiversity and disease implications

Common forecasting approaches often fail to predict what appear to be individualistic responses of organisms to environmental change. Accounting for physiology and other aspects of organismal biology may account for the variable responses, but how can we tractably incorporate organismal biology in general models? Challenges include generalizing how biological mechanisms mediate responses to spatial and temporal environmental variation and assembling the required biological data. I will discuss paths toward better accounting for biological mechanisms in forecasting biodiversity and disease responses to environmental change.

2:50 Patrick Stephens (Oklahoma State University): Using biodiversity to predict Ebolavirus outbreaks

The primary reservoirs of Ebolavirus in the wild remain elusive. We explored how host traits, phylogenetic identity and cell receptor sequences relate to infection status and mortality from ebolaviruses in the first comprehensive study to consider all African mammals. We gathered exhaustive databases of mortality from ebolavirus after exposure and infection status based on PCR and antibody tests. We performed ridge regressions predicting mortality and infection as a function of traits, phylogenetic eigenvectors and separately host receptor sequences. We found that mortality from ebolavirus had a strong association to life history characteristics and phylogeny. In contrast, infection status related not just to life history and phylogeny, but also to fruit consumption which suggests that geographic overlap of frugivorous mammals can lead to spread of virus in the wild. Niemann Pick C1 (NPC1) receptor sequences also predicted infection statuses of bats included in our study with very high accuracy, suggesting a promising avenue for future work. We combine the predictions from our mortality and infection status models to differentiate between species that are infected and also die from ebolavirus versus species that are infected but tolerate the virus (possible reservoirs of Ebolavirus). The results of this study are feeding into ongoing work to build more accurate maps of Ebolavirus spillover risk in sub-Saharan Africa.

4:00 John Gittleman (University of Georgia, Athens): One Health: what is it, what should it be?

One Health, the integration of animal, human and environmental approaches to identify and solve health related issues, is universal to understanding modern problems in society and life at large. Like so many universals - climate change, extinction, poverty - the fact that everyone has a general understanding of One Health does not necessarily translate into effective application and advancement of the field. To some extent this is a reflection of the terminology and familiarity of working across individual fields (silos) of animal, human and ecological disciplines, making common language difficult to carry out. A One Health approach is now more important than ever, with emerging infectious diseases causing 9.6 million deaths globally and costing about $120 billion in the U.S. alone. Such diseases have a complex history, yet it is clear that most originate and pass through animal and environmental contexts before moving onto humans. Therefore, we need to develop integrative, broad-scale approaches that identify determinants of pathogens and predict their responses to animal, human and environmental changes. In this talk, I will summarize the state of the field: describe useful definitions of One Health; identify important and key examples of how One Health is uniquely effective in solving difficult health problems (e.g., Ebola, West Nile, human emerging diseases); show new forecasting methods to determine where, when and pace of emergent pathogens; and, generally characterize why this approach though difficult is critical to predicting, solving and finding common ground for health issues. To advance the field we must expand interdisciplinary databases to rapidly access information on biodiversity, public health and ecosystems and, to be truly successful, widen One Health applications into agricultural, clinical and environmental issues.

4:15 Alaina Pfenning-Butterworth (UBC): Making connections: climate change, biodiversity, and infectious disease

We are experiencing an increase in global climate, emerging infectious diseases, and species extinction. While pairwise combinations of climate change, biodiversity, and infectious disease are often associated (and sometimes causally linked), we lack a framework that integrates all three, while recognizing the positive and negative feedbacks between them. I will show the current focus of research effort and discuss how the integration of mechanistic links between climate, disease, and biodiversity can inform future research.