FRALIN LIFE SCIENCES INSTITUTE
GLOBAL CHANGE CENTER
VIRGINIA TECH

IGC Graduate Research Symposium
April 21, 2023

The Moss Arts Center

- AGENDA -

8:00 – 8:55	• Welcome Table with name tags (Entrance to Main Lobby) • Coffee & refreshments - 1st Floor Fife Lobby • Poster setup - 2nd Floor Fife Lobby
8:55-9:00	**Welcome,** by Dr. Bill Hopkins - The Cube
9:00-10:00	**IGC Platform Presentations Session 1** - The Cube Moderator: Heather Wander **9:00-9:15** - Sugar-feeding by Invasive Mosquito Species on Ornamental Plants, **Forde Upshur** **9:15-9:30** - How do spatial scale and species traits influence genetic structure of freshwater invertebrates?, **Sam Silknetter** **9:30-9:45** - An interdisciplinary approach enhances understanding the efficacy of agricultural best management practices for protecting stream health, **Joshua Mouser** **9:45-10:00** - Anoxia begets anoxia: increased air temperatures drive a self-reinforcing cycle of anoxia in stratified lakes, **Abby Lewis**
10:05-11:00	• **Poster Viewing: Morning Session** - 2nd Floor Fife Lobby • Coffee & refreshments - 1st Floor Fife Lobby - Dynamically Coupled Hydrologic and Economic Models Using Systems Modeling Language (SysML) and Hetero-Functional Graph Theory (HFGT) to Create an Extensible Computational Framework, **Megan Harris** - Agroforestry with Refugees and Hosts in Northwestern Uganda, **Sarah Juster** - Characteristics of Success and Unsuccessful Strategies to Recruit Underrepresented Populations into Clinical Research, **Amanda Hensley** - Subsewershed Surveillance in Rural Central Appalachia Reveals Enteropathogen Signal is Influenced by Inflow and Infiltration, **Amanda Darling** - Will frugivores enable Appalachian plants to track climate change?, **Abir Jain** - How sensitive are stream macroinvertebrates to variations in land use?, **Sergio Sabat-Bonilla** - Why Do Birds Join Mixed Species Flocks?, **Noah McNeill** - Assessment of Bull-Run River Microbial Communities Using 16S Amplicon Sequencing, **Idowu Okeshola** - Tributary junction, what's your function? Stream confluences alter carbon and nutrient cycling in freshwater networks, **Stephen Plont**

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11:00-12:00	**IGC Platform Presentations Session 2** - The Cube Moderator: Macy Kailing **11:00-11:15** - Unraveling migration patterns of catfish in the Amazon, **Luciana Pereira** **11:15-11:30** - Purple Reign: Increasing proportion of probiotic bacteria in tadpoles through embryo inoculation, **Korin Jones** **11:30-11:45** - Metabolic patterns of non-perennial stream pools, **Kristen Bretz** **11:45-12:00** - Strategies for private lands research and exploration of its potential as a means of conservation outreach, **Rebecca O'Brien**
12:00-1:15	**Lunch Break** - 1st Floor Fife Lobby *What did I order for lunch?*
1:15-2:00	**IGC Platform Presentations Session 3** - The Cube Moderator: Stephen Plont **1:15-1:30** - How Our Urban Arthropod Communities Differ from their Rural Counterparts, **Isaac VanDiest** **1:30-1:45** - Long-term effects of habitat corridors on ant communities, **Melissa Burt** **1:45-2:00** - Putative prophages of chytrid inhibiting bacterial isolates, **Emma Bueren**
2:00-2:50	**Capstone Flash Talks** - The Cube Moderator: Dr. Bill Hopkins **2:00-2:10** - An interactive website on environmental justice within the New River Valley **2:10-2:20** - A Community-Science Driven Invasive Species Inventory and Management Guide for Brush Mountain **2:20-2:30** - Weather or Not? Documenting the hardships and barriers of energy costs in off campus housing to identify local weatherization needs and opportunities to implement energy-saving strategies. **2:30-2:40** - Learning to engage with values in science **2:40-2:50** - I Can SciComm: a grad student-led podcast on science communication

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2:50-3:45	• **Poster Viewing: Afternoon Session** - 2nd Floor Fife Lobby • Coffee & refreshments - 1st Floor Fife Lobby - Can acoustic monitoring give new insights to the spatial and temporal distribution of an invasive and a threatened amphibian?, **Grace O'Malley** - Flood pulse effects on fish catch in the Amazon River, **Gabriel Borba** - Urban male song sparrows show flexibility in aggression over sustained challenge, **Taylor Fossett** - Zooplankton community structure is more variable over time than space, with implications for water quality management, **Heather Wander** - Linking greenhouse gas concentrations and changing inundation regimes in wetlands, **Carla López Lloreda** - A Triassic stem caecilian and the evolutionary and origins of living amphibians, **Ben Kligman** - Causal inference to scope environmental impact assessment in multisector systems: the case of trans-border hydropower exports, **Amir Mortazavigazar** - Incidence of per-polyfluoroalkyl substances (PFAS) in private water supplies in Southwest Virginia, **Kathleen Hohweiler** - Growing Cover Crops for a Diverse Soil Microbiome, **Prashasti Agarwal**
3:45-4:45	**Keynote Speaker -** The Cube Keynote Title: *Centering Culture & Mentorship in Research* **Dr. Laura Schoenle,** the Associate Director of the Office of Undergraduate Biology at Cornell University
4:45-6:00	**Reception and Platform Award Announcements -** 3rd Floor Fife Lobby

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PLATFORM PRESENTATION:

Sugar-feeding by Invasive Mosquito Species on Ornamental Plants

Upshur, I.F. [1]*, *Fehlman, M.*[2], *Parikh, V.*[1], *Lahondere, C.*[1]

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Feeding on plant-derived sugars is an essential component of mosquito biology that affects key aspects of their lives such as survival, metabolism, and reproduction. Mosquitoes locate plants to feed on using olfactory and visual cues. Aedes aegypti and Aedes albopictus are two mosquito species invasive to the US, and are vectors of diseases such as dengue fever, chikungunya, and Zika. These species live in heavily-populated, urban areas, where they have a high accessibility to human hosts as well as to plants in backyards and town landscapes. Therefore, it is important to understand what plants may attract / repel mosquitoes to inform citizens and municipal authorities accordingly. Here, we observe Ae. aegypti and Ae. albopictus sugar-feeding behavior with eleven different commonly-planted ornamental plant species. We then assessed feeding activity using the anthrone method and identified volatile composition of plant headspace using gas-chromatography mass-spectroscopy. Finally, we determined the sugar-feeding activity of local mosquitoes using the plant DNA barcoding technique and compared these results with the eleven ornamental species tested in the lab. The potential for application to disease vector control is also discussed.

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PLATFORM PRESENTATION:

How do spatial scale and species traits influence genetic structure of freshwater invertebrates?

Silknetter, S.C[1]*, *Allen, D.C.[2], Atkinson, C.L.[3], Bogan, M.T.[4], Boersma, K.S.[5], Busch, M.H.[6], Datry, T.[7], Gill, B.A.[4], Corey A. Krabbenhoft, C.A.[8], Lytle, D.A.[9], Martinez, Y.[1], Messager, M.[7,10], Olden, J.D.[11], Rogosch, J.[12,13], Ruhi, A.[14], Shogren, A.J.[3], Tonkin, J.D.[15], Trumbo, D.R.[1], Walker, R.H.[16], Mims, M.C.[1]*

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[7] INRAE, UR RiverLy, Centre Lyon-Grenoble Auvergne-Rhône-Alpes, Villeurbanne, France
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[10] Department of Geography, McGill University, Montréal, QC, Canada
[11] School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA, USA
[12] Department of Natural Resources Management, Texas Tech University, Lubbock, TX, USA
[13] U.S. Geological Survey, Texas Cooperative Fish & Wildlife Research Unit, Lubbock, TX, USA
[14] Department of Environmental Science, Policy, & Management, University of California, Berkeley, CA, USA
[15] School of Biological Sciences, University of Canterbury, Christchurch, New Zealand
[16] Department of Biology and Chemistry, Upper Iowa University, Fayette, IA, USA

Investigations of genetic structure, or genetic variation within and among populations, offer insights into ecological and evolutionary processes in freshwater ecosystems and beyond. However, there exists no framework to organize our understanding of how the spatial scales at which genetic structure is detected may vary with biological and environmental factors, limiting the generality of findings from one area to another. In our study, we investigated the spatial scale at which population genetic structure is detected for freshwater invertebrates and how this was mediated by species traits, including dispersal (mode and strength), longevity (lifespan and voltinism), and reproduction (mode and fecundity). We hypothesized that dispersal, a key driver of gene flow, would most strongly influence the scale at which genetic structure is detected, but that longevity and reproduction may be important for poor dispersers or if dispersal potential is reduced by low habitat connectivity. First, we conducted a systematic literature review to obtain > 30 microsatellite datasets for freshwater invertebrates located across four continents. We calculated FST', a standardized measure of genetic differentiation, for all population pairs per dataset. We then tested for isolation-by-distance using Mantel correlograms to relate pairwise FST' to pairwise Euclidean and river network distances. Trait data have been compiled for all species, and analyses to quantify the effect of traits on observed genetic structure are ongoing. Identifying how species traits may mediate the effects of spatial scale helps inform how genetic diversity is structured, and can be used to guide future freshwater biodiversity conservation efforts.

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PLATFORM PRESENTATION:

An interdisciplinary approach enhances understanding the efficacy of agricultural best management practices for protecting stream health

Mouser, J.B.[1]*, *Ciparis, S.[1,2], Dayer, A.[1], Czuba, J.[3], Brown, B.[4], and Angermeier, P.[1,5]*

[1]Dept. of Fish and Wildlife Conservation, Virginia Tech
[2]U.S. Fish and Wildlife Service, Gloucester, VA
[3]Dept. of Biological Systems Engineering, Virginia Tech
[4]Dept. of Biological Sciences, Virginia Tech
[5]U.S. Geological Survey, Virginia Cooperative Fish and Wildlife Research Unit, Virginia Tech

Agricultural best management practices (BMPs) have been installed across the U.S. to protect stream health while maintaining agricultural sustainability. Unfortunately, stream health continues to decline because landscape conditions and social factors can cause BMPs to be less effective than expected. Understanding these shortfalls in BMP efficacy requires understanding and integrating approaches from many fields including, but not limited to, engineering, ecology, and social science. Therefore, our goal was to use an interdisciplinary approach to understand how water quality, habitat quality, and social factors influence stream health in southwest VA. We used the Soil and Water Assessment Tool to model long-term water quality in streams. We also mailed surveys to 889 landowners to understand their continued use of BMPs and those data were used to alter BMP density in our models. Finally, we collected water quality, habitat data, and macroinvertebrates from streams. We then built regression models to understand the relative influences of long-term water quality, BMP density, instream habitat, and instream water quality on stream health, as indicated by macroinvertebrate assemblage composition. We found that BMPs improved water quality, but those improvements only increased stream health up to a certain BMP density, after which stream health decreased. Further, we found that the stream health response to BMPs changed when BMP density was altered. Our results demonstrate that more time may be needed for water quality improvements from BMPs to affect the macroinvertebrate assemblage and that an interdisciplinary approach is necessary to fully understand stream health responses to BMP implementation.

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PLATFORM PRESENTATION:

Anoxia begets anoxia: increased air temperatures drive a self-reinforcing cycle of anoxia in stratified lakes

Lewis, A.S.L.[1]*, *Lau, M.[2], Jane, S.[3], Rose, K.[4], Be'eri-Shlevin, Y.[5], Burnet, S.H.[6], Clayer, F.[7], Feuchtmayr, H.[8], Grossart, H.[9,10], Howard, D.[1], Mariash, H.[11], Martin, J.D.[12], North, R.[13], Oleksy, I.[14], Pilla, R.M.[15], Sommaruga, R.[16], Verburg, P.[17], Wain, D.[18], Weyhenmeyer, G.[19], and Carey, C.C.[1]*

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[19] Department of Ecology and Genetics/Limnology, Uppsala University, Uppsala, Sweden

Declining oxygen concentrations in the bottom waters of lakes worldwide pose a pressing environmental and societal challenge. As bottom-water oxygen concentrations decrease, low concentrations could potentially trigger a positive feedback loop where anoxia (no oxygen) during a given year begets future years of increasingly severe anoxia. Specifically, anoxia could promote internal phosphorus release, increased phosphorus concentrations could stimulate phytoplankton growth, and increased phytoplankton biomass could fuel heterotrophic respiration, further accelerating oxygen declines. However, while some of the individual links in this cycle are well-established, to our knowledge there has not been a systematic analysis within or across lakes demonstrating all of the mechanisms needed to characterize a positive feedback to deoxygenation. Here, we compiled data from >700 widespread lakes to analyze the proposed mechanisms by which anoxia begets anoxia. Using linear mixed models, we found support for each of the hypothesized causal relationships between oxygen concentrations, nutrient concentrations, chlorophyll-a concentrations, and oxygen demand both within and among widespread lakes. Our results indicate that the anoxia begets anoxia feedback loop operates on top of additional and ongoing influences of climatic drivers: within lakes, spring air temperatures tended to be positively correlated with end-of-summer bottom water temperature and oxygen demand rates and negatively correlated with end-of-summer oxygen concentrations. Combined, these results suggest the existence of a positive feedback mechanism that could magnify the effects of climate change and land use on the development of anoxia in lakes around the world.

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PLATFORM PRESENTATION:

Unraveling migration patterns of catfish in the Amazon

Pereira, L.A[1]*, *Castello, L.[1], Hallerman, E.[1], Orth Donald[1], Duponchelle, Fabrice[2]*

[1] Department of Fish and Wildlife, Virginia Tech
[2] Research Institute for Development, France

Most fish movements in Neotropical river floodplains coincide with the flood pulse, which is the predictable annual flooding of large rivers. We studied the migration of a species of catfish in the Amazon basin, Pseudoplatystoma fasciatum, which is threatened by poorly regulated fishing activities and the construction of hydropower dams that block its migratory movements. Despite these threats, the migrations performed by this catfish have not yet been studied. We, therefore, are addressing the following questions: What is the migration ecology of P. fasciatum in the Amazon Basin? To answer this question, we will characterize the movement ecology of this catfish by analyzing the trace-chemical composition of Strontium isotopes on their otoliths, i.e., ear bones. Otoliths record the chemical signature of the water in which the fish live as they grow and move between waters of different trace chemical compositions. Our analysis of the trace chemical composition of the otoliths provided the profiles of Strontium isotopes, which revealed migration patterns along with the life of individuals. We found that 90% of individuals stayed in waters with the same Sr isotope signature and did not migrate among different types of water (white, black, and clear water). The average distance migrated was 410.55 Km, with all individuals that migrated being adults and moving bi-directionally. These results will inform stakeholders about the migration patterns and critical habitats used by the species to avoid overfishing and guide dam construction.

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PLATFORM PRESENTATION:

Purple Reign: Increasing proportion of probiotic bacteria in tadpoles through embryo inoculation.

Jones, K.R.[1]* *and Belden, L.K.[1]*

[1] Department of Biological Sciences, Virginia Tech

Globally, amphibian populations have seen heavy population declines in recent years. Many factors likely contribute to this loss of biodiversity, however the fungal pathogen Batrachochytrium dendrobatidis (Bd) has been implicated as a major contributor to amphibian declines and extinctions. Depending on composition, the communities of bacteria present on amphibian skin can mitigate Bd associated morbidity and mortality. Understanding how these communities assemble is, therefore, a goal of amphibian conservation research. Differences in colonization order during initial assembly can have lasting impacts on the structure of host-associated bacterial communities by conferring advantages to early arriving bacteria. Utilizing these priority effects, it may be possible to augment host amphibians with target bacteria that persist through development, forming bacterial communities capable of mitigating the impacts of Bd. To determine if priority effects can be used to augment hosts with probiotics, we selectively inoculated the embryos of spring peepers (Pseudacris crucifer) with bacteria isolated from the skin of wild, adult conspecifics. Through 16S rRNA gene amplicon sequencing, we observed compositional shifts in the bacterial communities associated with newly hatched tadpoles due to priority effects. Our results suggest that priority effect-based inoculation of embryos with probiotic bacteria may serve as an effective mechanism to increase the proportion of probiotic bacteria present within the host microbiome during early stages of development, but that the effectiveness will depend on the traits of the target bacteria.

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PLATFORM PRESENTATION:

Metabolic patterns of non-perennial stream pools

Bretz, K.A.*[1]**, *Gannon, J.P.*[2]*, and Hotchkiss, E.R.*[1]

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[2] Department of Forest Resources and Environmental Conservation, Virginia Tech

Non-perennial streams are increasingly common in the southeastern United States as climate change alters precipitation regimes to cause longer, more intense periods of drying. Despite growing interest in non-perennial streams, we have few estimates of how flow contraction alters ecosystem processes, including in-stream metabolism of terrestrially-derived organic matter. Surface-subsurface connections, catchment vegetation, and regional precipitation all influence stream-specific contraction, meaning that drivers at multiple scales can have unique controls on metabolism along a contracted stream. We tracked changes in stream chemistry and hydrology and estimated metabolism in two non-perennial headwater streams, with unique valley characteristics and situated on opposing sides of a mountain ridge, in the Valley and Ridge physiographic province of southwest Virginia. Our objective is to identify what hydrologic and biotic factors most influence non-perennial stream metabolism over time. We measured high-frequency dissolved oxygen in three persisting pools of each stream to estimate how metabolism changes as the stream contracts and expands. We also sampled dissolved CO2 along both streams. Dissolved oxygen was more variable among pools of the same stream than between the two streams. Stream water dissolved CO2 was similar between the two streams before fragmentation, but after drying, CO2 nearly doubled in isolated pools compared to connected reaches of both streams. Ecosystem respiration did not differ between streams or pool habitats, but GPP was influenced by rewetting events. Differences in flow permanence between the two catchments was less important than expected, providing insight into the links between stream flow regime and ecosystem function in a changing world.

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PLATFORM PRESENTATION:

Strategies for private lands research and exploration of its potential as a means of conservation outreach

O'Brien, R.[1]*, *Greene, R.[1], Johnson, A.[2], Hopkins, W.[1], Dayer, A.A.[1]*

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[2] Virginia Working Landscapes

Increased attention on the importance of private lands for achieving conservation goals has highlighted the need for conservation research on private property to inform these efforts. However, the unique challenges of research in this context means that many scientists avoid working on private land. This is a problem because results from research undertaken on public lands does not always apply to private lands and may lead to misinformed decision making. In this paper, we seek to break down barriers to private lands research by sharing suggestions on how to overcome some of the challenges this type of research presents. Specifically, we discuss how to gain access to private lands and tips for successful engagement with landowners. Using a case study of private lands research in rural Virginia, we also explore the potential value of harnessing private lands research as a means of conservation outreach.

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PLATFORM PRESENTATION:

How Our Urban Arthropod Communities Differ from their Rural Counterparts

VanDiest, I.J.*[1]**, *Jones, K.R.*[1]*, Lane, S.J.*[2]*, Fossett, T.E.*[1]*, Sewall, K.B.*[1]

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[2] Biological Sciences Department, North Dakota State University

Most work in urban ecology has focused on charismatic fauna despite lower trophic level taxa, such as arthropods, being vital to the function of ecosystems. Urbanization often lowers diversity and abundance of arthropod communities. However, few studies have investigated how urbanization changes community structure, and how it relates to prey abundance. In the current study, using vacuum sampling that collects arthropod taxa with diverse life histories, coupled with multivariate comparisons, we investigated how arthropod communities differ between replicate urban and rural sites in southwest Virginia. We found that rural sites had higher average arthropod biomass and abundance compared to urban sites, and that higher trophic level arthropods (e.g. Araneae and Coleoptera) were more common in rural areas. Additionally, we found urban habitat to have lower alpha diversity, and that beta diversity differed between urban and rural habitat. Our findings are consistent with other studies of the effects of urbanization on arthropods and suggests that higher trophic level species in urban areas may be impacted by prey availability and quality. These results were further used as the basis for questioning how predators of arthropods might be affected by having different prey communities to rely on. This is likely an issue for urban birds that exist in these same field sites, specifically song sparrows (Melospiza melodia), where they are found in lower abundance and density than in our rural sites.

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PLATFORM PRESENTATION:

Long-term effects of habitat corridors on ant communities

Burt, M.A.*[1]**, *Whitehead, S.R.*[1]*, and Resasco, J.*[2]

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[2] Dept. of Ecology and Evolutionary Biology, University of Colorado

Corridors are linear strips of habitat used to connect isolated habitat patches and are often used by land managers to mitigate the effects of habitat fragmentation. However, due to the potentially confounding effects of connectivity and patch shape, how corridors function to impact biodiversity is often not well understood. Here, we used a long-term, landscape-scale experiment that manipulates both habitat connectivity and patch shape to investigate the effects of corridors on ant communities in restored longleaf pine savannas. Each experimental landscape (N=7) contains a central square habitat patch surrounded by four peripheral patches that are equal in area, one connected to the central patch by a 150-meter corridor. To determine potential effects of patch shape, patches without corridors were either rectangular or squares with half a corridor on either side. We used pitfall traps to annually sample the ant community over five years. We specifically asked: (1) How do corridors affect the composition of ant communities? and (2) Do these effects change over time? We found that the number of ant species in our experimental landscapes increased over time with isolated patches containing more ant species than patches with corridors. Additionally, we found that the composition of ant communities diverged with connectivity and over time. We did not find evidence that patch shape affected any metrics of ant diversity. Taken together, these results suggest that habitat corridors impact ant communities via changes to patch connectivity, not patch shape.

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PLATFORM PRESENTATION:

Putative prophages of chytrid inhibiting bacterial isolates

Bueren, E.K.[1]*, *Snead, M.[1], Wax, N.[1], Haak, D.C.[2], Walke, J.B.[3], and Belden, L.K.[1]*

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[3] Department of Biology, Eastern Washington University, Cheney, WA

The global emergence of the fungal pathogen Batrachochytrium dendrobatidis (Bd), which causes the skin disease chytridiomycosis, has resulted in the decline of many amphibian species. The outcome of a Bd infection can be influenced by many variables, ranging from climate to the bacterial community living on the amphibian's skin. It is well known that host-associated bacterial communities, also known as microbiomes, influence the health of animals; for example, bacterial communities may prevent opportunistic infections via competitive exclusion or prime a host's immune system. Several bacterial species found on amphibian skins, such as Janthinobacterium lividum, or Pseudomonas spp., can inhibit the growth of Bd to various degrees. Additionally, bacterial genomes commonly contain prophages, integrated forms of a temperate bacteriophage (virus that infects bacteria). These prophages sometimes carry beneficial genes like toxins or auxiliary metabolic genes, and contribute to horizontal gene transfer between bacteria. It is possible that beneficial genes from a prophage could confer Bd-inhibition. If the phage is also able to infect and integrate into other, closely related strains, it could confer Bd-inhibition. To better understand the role prophage may play in Bd inhibition, a bioinformatic survey of prophages in 47 isolates from the amphibian skin microbiome was conducted. Putative prophage were compared within and across bacterial species for similarity, and functionally annotated for potentially beneficial genes that could be antifungal/antimicrobial or otherwise beneficial. Intriguingly, prophages across four hosts (J. lividum, Agrobacterium sp., Iodobacter sp.,, and an undetermined Achromobacter/Advenella sp.,) appear to encode a putative chitinase, which can be antifungal.

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CAPSTONE FLASH TALKS:

An interactive website on environmental justice within the New River Valley

Goodman, L.M[1]*, Panji, N.S.[2]*, *Kang, J.[3]*, **Risteca, P.[4]*, Sterling, C.[5]***

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[2] Department of Civil and Environmental Engineering, Virginia Tech
[3] Department of Geosciences, Virginia Tech
[4] Department of Biology, Virginia Tech
[5] Department of Biological Systems Engineering, Virginia Tech

In the roughly 350 years since European settlement, the New River Valley (NRV) has undergone substantial land use changes due to human activities. Such shifts in geography have inevitably altered the interactions between the NRV people and their surrounding environment, giving rise to several environmental justice (EJ) issues disproportionately affecting people of color and low-income communities. To address these, we have built an interactive website focused on EJ within the NRV to equip people with the information they need to voice their rights. The website has five key sections centered around the NRV: an introduction, air quality, water quality, land use, and EJ advocacy. In each section, we provide a high-level explanation of the science behind deteriorating environmental quality and how to evaluate it. It comes equipped with a compilation of EJ groups in the NRV that actively advocate for action against local sources of pollution. The website also acts as a hub for publicly available environmental data where users are led to various online resources with up-to-date environmental quality metrics and given a guide to navigating these resources. Apart from that, we provide a historical account of EJ issues in the NRV.

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CAPSTONE FLASH TALKS:

A Community-Science Driven Invasive Species Inventory and Management Guide for Brush Mountain

Coscia, J.T.[1]*, Upshur, I.F.[2]*, Howell, B.K.[3]*, Bone, N.[3]*

[1]School of Plant and Environmental Sciences, Virginia Tech
[2]Department of Biochemistry, Virginia Tech
[3]Department of Biological Sciences, Virginia Tech

In a collaborative effort with the Invasive Species Working group and the Town of Blacksburg Sustainability Chair, we organized and led a "BioBlitz"-style invasive species survey of Blacksburg's newly acquired Brush Mountain Property 3. The survey was conducted by community member volunteers using the iNaturalist app and open biodiversity database. We used this survey data to develop an R-based interactive dashboard that plots invasive species recorded in iNaturalist and displays their invasiveness scores and potential management options. This dashboard is designed to provide an up-to-date visualization of invasive species recorded in public parks throughout the Town of Blacksburg to inform future invasive species management decisions.

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CAPSTONE FLASH TALKS:

Weather or Not? Documenting the hardships and barriers of energy costs in off campus housing to identify local weatherization needs and opportunities to implement energy-saving strategies.

O'Brien, R.[1]*, Shea, B. D.[1]*, Duston, S.[2]*, *and Lim, T.[3]*

[1] Department of Fish and Wildlife, Virginia Tech
[2] Department of Forest Resources and Environmental Conservation, Virginia Tech
[3] School of Public and International Affairs, Virginia Tech

Weatherizing one's home helps to reduce the cost of utilities and improve personal health by protecting the interior of the home from environmental elements such as moisture, wind, cold temperatures in the winter, and heat in the summer. Vulnerable groups such as low-income families and students are often faced with financial hardship and may be disproportionately affected by high energy costs to which weatherization could be a great benefit. At Virginia Tech it has been well documented through University-wide surveys that students (especially graduate students) living off campus are experiencing financial hardship. Our capstone project aims to quantify the weatherization needs of off-campus student housing and identify some of the barriers to weatherization as well as factors which could help improve access, ability, and motivation to weatherize. Working in collaboration with Virginia Tech's Office of Sustainability, we collected data on living arrangements, energy cost expenditures, motivations to weatherize residences, and weatherization knowledge within the Virginia Tech community. This will be used to inform materials that can be used for future outreach efforts.

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CAPSTONE FLASH TALKS:

Learning to engage with values in science

Alfonso, C.[1]*, Brousseau, J.[2]*, O'Brien, C.[2]*, Wendler, A.[1]*, *Kovaka, K.[3], and Sewall, K.[1]*

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[2] Department of Forest Resources and Environmental Conservation, Virginia Tech
[3] Department of Philosophy, University of California, San Diego.

Our values play a role in the scientific questions we seek to answer and how we conduct research. For our IGC Capstone Project, we created an interactive, reflexive exploration of the role of values in science and facilitated the project during two sessions of the first-year IGC seminar to help other fellows articulate their core values and consider how these play a role in their own research. We adapted these sessions from Michigan State University's Toolbox Dialogue Initiative and piloted them in Spring 2022 with the first-year cohort. These sessions involved class discussions about values, ethical themes related to interdisciplinary research, and relevant case studies. Students also created a Values Statement that summarized their core values and the role of these values in their scientific work. We collected pre- and post-session survey data from the fellows to understand their perceptions on values and ethical considerations before and after the sessions and to assess changes in their perspectives due to the experience. We learned several lessons while leading these sessions, and feedback from IGC fellows who participated has informed how we revise this module for future seminars.

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CAPSTONE FLASH TALKS:

I Can SciComm: a grad student-led podcast on science communication

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Science communication is a fundamental step of the scientific process, yet access to training in such skills is inequitable across universities or organizations. Therefore, many scientists are limited in their ability to disseminate their work or discuss the importance of science more broadly. Here, we developed I Can SciComm, a freely available podcast that explores the best practices of science communication through interviews with experts from diverse disciplines. Invited guests included the Associate Director of the Center for Communicating Science at Virginia Tech, a Specialist in Natural Resources Policy at the Congressional Research Service, and a Professor in the Department of Biological Sciences at Texas Tech University. Additionally, we produced an introduction episode in which we collectively developed a definition of science communication as well as a conclusion episode discussing themes across our interviews, what we learned, and revisited our definition of science communication. Planning, recording, editing, and circulating each episode required teamwork at each step, exemplifying collaboration through ample idea exchange, conflict management, and revision prior to episode release. Episodes with invited guests were opportunities for engagement with experts on understanding best practices for communicating to distinct audiences. The series is meant to provide a foundational toolkit for individuals interested in enhancing their science communication skills. Beyond the production of our first season, we hope a new cohort of individuals continue the series and explore new topics that may serve the needs of scientists without, or limited by, access to training in science communication.

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Dynamically Coupled Hydrologic and Economic Models Using Systems Modeling Language (SysML) and Hetero-Functional Graph Theory (HFGT) to Create an Extensible Computational Framework

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The United Nation's 17 Goals for Sustainable Development including the protection of freshwater are intertwined and require global partnerships across nations and disciplines. Stakeholders who tackle these challenges rely on data and knowledge from the systems that influence modern societal challenges. Experts from distinct disciplines organize this information into process models that describe the behavior of individual systems to elucidate the impacts of stakeholder decisions. However, these systems are interdependent.

In the case of agriculturally-driven water pollution, associated hydrologic and economic process models capture meaningful information individually but must communicate with one another to predict the long-term and cascading impacts of the agricultural industry. Current coupling approaches either make use of existing, discipline-verified process models or mathematically link information from separate systems but do not attempt both simultaneously. Such approaches cannot reliably represent complex systems.

This project pioneers an extensible modeling framework that links information from systems that drive the environmental and economic health of the Occoquan region. Systems Modeling Language (SysML) and Hetero-functional Graph Theory (HFGT) will couple models of the hydrologic system of Northern Virginia—modeled in Hydrological Simulation Program-Fortran (HSPF)—and the regional economic system—modeled in the World Trade Model with Rectangular Choice of Technology (WTM-RCOT). This project will elucidate unclear dynamics within the complex hydro-economic system at both the county and regional levels of the Occoquan Watershed. Ultimately, the coupled model will educate city planners, developers, and farmers about the impact of their land use choices on water quality and facilitate informed stakeholder decision-making.

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Agroforestry with Refugees and Hosts in Northwestern Uganda

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Steep population increases in refugee-hosting northwestern Uganda are associated with regional deforestation, with important consequences including the disruption of local ecosystems, soil erosion and the loss of tree products such as fruits, medicine and fuelwood. Since 2018, World Agroforestry (CIFOR-ICRAF) has promoted tree planting with South Sudanese refugees and Ugandan hosts in the Imvepi and Rhino Camp refugee settlements of northwest Uganda for environmental restoration and human welfare purposes. Evaluative data on CIFOR-ICRAF's progress has been sparse. The objectives of this research are to study CIFOR-ICRAF's outputs related to 1) environmental restoration, 2) participant human welfare, and 3) to collect participant recommendations for future directions of CIFOR-ICRAF programming. A face-to-face questionnaire was conducted with 80 refugee and host community households. Refugee households with longer CIFOR-ICRAF involvement were found to have 22 more trees per plot than households with less involvement. Refugees and hosts alike are planting a variety of native and non-native tree species, contributing to biodiversity preservation. Increased duration of CIFOR-ICRAF involvement is strongly associated with reduced off-plot fuelwood harvesting, potentially lowering pressure on surrounding vegetation. Small improvements to household income demonstrate human welfare gains from tree planting. Women reportedly manage agroforestry activities in 76% of refugee and 42% of host national households. Participants recommended increasing agroforestry training, tree planting groups for women, and the incentivization of tree establishment. Programming impacts appear most hindered by low seedling survival rates. The results suggest that, despite challenges, CIFOR-ICRAF is contributing to landscape-level environmental restoration and human welfare improvements among participants.

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Characteristics of Success and Unsuccessful Strategies to Recruit Underrepresented Populations into Clinical Research

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Thirty years after the NIH Revitalization Act of 1993 requiring inclusion of women and minorities in clinical research, members of vulnerable populations continue to be underrepresented in research studies. While barriers to recruitment of these populations from an individual to an institutional level have become more clearly understood, there is considerable interest in designing recruitment strategies to overcome those barriers. Although most studies include detailed methodology of their recruitment processes, there is a significant gap in discerning which strategies are successful compared to others for enrollment and retention. Taking a systematic approach of existing literature, this work seeks to evaluate and synthesize evidence from recruitment and retention interventions to improve inclusion of vulnerable and underrepresented populations in research studies.

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Subsewershed Surveillance in Rural Central Appalachia Reveals Enteropathogen Signal is Influenced by Inflow and Infiltration

Darling, A.*[1]**, *Deck, M.*[1]*, Markham, C.*[1]*, Maldonado, G.*[1]*, Davis, B.*[1]*, Pruden, A.*[1]*, Taniuchi, M.*[2]*, Cohen, A.*[1]

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Despite the advantages of wastewater based surveillance (WBS) for monitoring community health, in the U.S. it has been used primarily in densely populated communities with relatively well-maintained and funded sewer infrastructure. Consequently, there is a lack of knowledge with regard to how WBS may be used in rural communities, and the potential of wastewater based epidemiology to better understand health outcomes and disparities. In this study, we initiated a year-long monthly wastewater monitoring campaign in a small, rural sewershed in Southwest Virginia with known infrastructural challenges, including sewer main leaks and groundwater and surface water infiltration and inflow (I&I). In addition to collecting wastewater treatment plant (WWTP) influent, we sampled 12 sewershed nodes at each branch line to the sewer conveyance system to assess pathogen signal, and potential signal loss due to I&I and sewer system design characteristics. TaqMan Array Card (TAC) qPCR was performed for simultaneous quantification of 54 enteric pathogen targets. After six months of data collection, Giardia lamblia and Adenovirus were present in 88% and 34% of WWTP influent samples respectively. Due to a 21% lower detection rate of pathogen signal at the influent as compared to downstream of a large residential facility, preliminary results point to the risk of underestimating pathogen circulation when sampling only WWTP influent in a system with persistent I&I.

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Will frugivores enable Appalachian plants to track climate change?

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Vertebrate-mediated seed dispersal is a key ecosystem process that governs plant species diversity and distribution in forests. However, global climate change is driving unprecedented biodiversity loss, shifts in species distributions, and disassembly of mutualistic interactions. More than half of the world's animal-dispersed plants may have already lost the ability to track climate change due to the loss of seed dispersers and many others face the risk of extinction in future scenarios. However, there is little empirical information on fruit-frugivore networks from most regions of high fleshy fruited plant diversity. My Ph.D. research aims to obtain a community-wide understanding of functional responses of fruit-frugivore interactions to climate change using trait-based assessments. Since plant and animal communities might respond differently to environmental changes in different forest types, I will collect data from temperate sites in the southern Appalachian mountains in North America and tropical sites in the eastern Himalaya in Asia along elevational and latitudinal gradients. I will first create extant fruit-frugivore interaction networks at each site-elevation combination through fruit tree watches, camera traps, and fecal samples. By incorporating traits such as morphology, nutrition, and dispersal effectiveness, I will then map the species distributions of key plant and animal species to predict novel interactions and habitat suitability in 50 years using climate envelope models. This research will provide insights into vulnerable and resilient members of the novel interaction networks and help determine if dispersers with certain traits might effectively facilitate climate tracking for certain plant species under future environmental changes.

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How sensitive are stream macroinvertebrates to variations in land use?

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Rapid global change continues to impact both past and present anthropogenic and environmental stressors on freshwater ecosystem functions and biodiversity in streams. Aquatic macroinvertebrates provide key ecosystem services and functions, making them ideal indicators of local and ecosystem-wide responses to environmental stressors. Their community structure is commonly assessed by studying their response to stressors and the subsequent remediation practices (e.g., best management practices). Yet, focusing on the taxonomic identity of macroinvertebrate communities may fail to inform the selection pressures driving biological responses. Integrating functional trait diversity into established assessment protocols allows for expanded quantification of biological responses to remediation efforts to reach biological uplift. However, understanding what types of traits show the greatest affinity to environmental changes is a priority. The objective of this study is to compare regional stream assessment protocols from the Chesapeake Bay Watershed, one of the most well-studied freshwater ecosystems in the world, with metrics that integrate a suite of traits weighted by density and biomass. We will assess a) influence of single-trait selection when multiple traits (e.g., filter-feeder) have been assigned to a grouping feature (e.g., FFG) for the same aquatic macroinvertebrate taxa, and b) quantify how biomass-weighted functional trait diversity responds across varying pasture landuse gradients with different remediation levels. We hypothesize that functional traits weighted by biomass will explain more variation across the land use and remediation gradients because they better represent energetic and ecological response to stressors compared to taxonomic diversity metrics alone.

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Why Do Birds Join Mixed Species Flocks?

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Many birds are known to flock with other bird species. This is typically to increase foraging success directly (via efficient food location) or indirectly (via entrusting predator vigilance to others). However, the large size yet low density flocks of the southeastern US pine savanna present a unique case for delineating these benefits, particularly in small, seasonally granivorous birds such as the Brown-headed Nuthatch (Sitta pusilla) (BHN). I measured BHN foraging time budgets and anti-predatory behavior at eight transects for three seasons at two sites in North Carolina, as well as a one season predator decoy playback experiment. My results show that BHN's reduce mixed flock recruitment during high food abundance. My also results reveal a correlation between predator observation rates and BHN mixed flock recruitment by site. BHN's at the less frequent predator site also froze in place more often (presumably predator vigilance) following predator call playback. These findings show that both predator abundance and food availability modulate BHN foraging strategies. However, vigilance plasticity from predation threat seems slight, and predator mediation may thus occur primarily across broader scales. Contrastingly, decisions based on food availability dictate significant and rapid changes in behavior, which follows given the annual and spatial variation in pine seed forage availability.

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Assessment of Bull-Run River Microbial Communities Using 16S Amplicon Sequencing

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Antimicrobial resistance (AMR) is widely acknowledged as one of the most serious public health challenges of the twenty-first century, threatening human health and well-being and causing hundreds of thousands of deaths each year globally. The epidemiology of AMR is influenced by human, animal, and environmental reservoirs, and there are many pathways for transmission both within and between human, animal, and environmental spaces including surface and groundwater. In this study, we assessed the microbial communities of a segment of the Bull-Run River using 16S amplicon sequencing on 14 samples taken from a segment of the River. We found a significant difference in the microbial communities of the river samples ($R = 0.822$; $p = 0.0003$), but as samples became physically separated due to geographic distance, their associated microbial communities did not necessarily become more dissimilar ($R = 0.406$, $p = 0.127$). *Flavobacterium* (12.27%), *Planktophila* (8.088%), *Leptothrix* (5.114%), *Parasegitibacter* (3.904%), *Methylotenera* (2.391%), *Siphonobacter* (2.266%), *Herbaspirillum* (2.152%), *Pedobacter* (0.669%), and *Acidovorax* (0.665%) are the genera that contributed the most to dissimilarity in the samples. The species most responsible for sample dissimilarity were: *frigidarium* (14.08%), *limnetica* (7.001%), *discophora* (3.54%), *luojiensis* (3.379%), and *versatilis* (2.07%). Thus, we observed that the microbial communities of the river differ due to the genera and species in each sample but not due to their spatial proximity. In the future, we aim to use shotgun metagenomics to study the AMR genes in each sample and the associated AMR bacteria.

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Tributary junction, what's your function? Stream confluences alter carbon and nutrient cycling in freshwater networks

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Stream confluences are ubiquitous interfaces in freshwater networks and serve as junctions of previously independent streams. The capacity for confluences to alter biological processes remains a knowledge gap in understanding the fate of carbon and nutrients across freshwater networks. To test how a confluence alters carbon and nutrient cycling, we estimated dissolved organic carbon (DOC) and phosphorus (as soluble reactive phosphorus (SRP) uptake in the reaches upstream and downstream of a confluence. We also measured DOC uptake in the water column throughout the confluence mixing zone to elucidate how and where carbon metabolism was altered downstream of the confluence. We hypothesized that biological processes would be enhanced at confluences due to the delivery and mixing of different carbon and nutrient sources. Surprisingly, we found that both DOC and SRP uptake were lower downstream of the confluence compared to upstream, indicating that biological uptake was suppressed downstream of the confluence. In the confluence mixing zone, water column DOC uptake was spatially variable with sites having DOC uptake both higher and lower than predictions made based on the mixing of upstream and tributary sources. Our results suggest that DOC and SRP uptake at confluences cannot be estimated from tributary DOC and SRP uptake alone and by ignoring mixing zone processes in our understanding of ecosystem function, water quality, and the fate of carbon and nutrients. throughout freshwater networks may suffer.

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Can acoustic monitoring give new insights to the spatial and temporal distribution of an invasive and a threatened amphibian?

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Amphibian species are threatened worldwide due to factors such as habitat loss, disease, and water availability. In the American Southwest, drought, climate change, and human modification of freshwater resources are leading to changes in the timing, duration, and spatial availability of temporary aquatic habitats. Additionally, American Bullfrogs (Lithobates catesbeianus) are an invasive species that prey on native amphibians. In southeastern Arizona, there is a distinct population of the Arizona treefrog (Hyla wrightorum) that has been listed as a conservation concern due to its small size, habitat loss, and predation by invasive species such as L. catesbeianus. Many aspects of the spatial and temporal distribution of these species' populations remain unknown, hindering efforts to understand their interactions. To address this knowledge gap, we asked: 1) Can acoustic monitoring reveal previously unknown breeding locations of H. wrightorum? 2) Where do populations of L. catesbeianus and H. wrightorum overlap? We deployed an array of acoustic recorders at 50 ponds over a 50 km2study region. We discovered 5 new breeding locations of H. wrightorum, and 1 site where both species occurred during the summer of 2021. Preliminary data analyses suggest little variation in duration of breeding among sites but do point to variation in the start date of breeding among sites. Our results provide an early look into the temporal and spatial distributions of two amphibian species.

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Flood pulse effects on fish catch in the Amazon River

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Fish catch in floodplain river systems is key to the livelihoods of millions of people worldwide. In these systems, fish catch is regulated by the flood pulse, a seasonal fluctuation in river water levels that determines the structure and function of large river ecosystems. However, the hydrological aspects of the flood pulse affecting fish catch are poorly understood. The main goal is to identify and quantify key hydrological effects on fish catch. I will integrate long-term, large-scale datasets of fish catch, river hydrology, and fish life-history traits within a statistical modeling approach. Here, I present a conceptual framework for this research using daily fishing landings and river water levels covering fishing locations over the Amazon River. I will measure hydrological metrics and fishing effort to identify the key factors affecting fish catch. I will be modeling fish catch responses to hydrological indices based on fish effort, and gear type over each fishing trip for each fishery boat. High variability in fish catches is expected in response to flood pulse effects, leading to a decrease in catch of fish taxa, especially the ones who depend on the flood to reproduce and recruit. These research results would be expected to identify key hydrological factors of each exploited fish taxa for adaptive management with better practices. In this context, knowing the hydrological effects on fish catch to create management strategies will help fishers better adapt to hydrological alterations induced by climate change.

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Urban male song sparrows show flexibility in aggression over sustained challenge

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Urbanization is altering habitats on a global scale, and animals must be flexible in their behavior in order to colonize and persist in these altered habitats. In several species of songbirds urban males are more aggressive than their rural counterparts. However, aggression is generally measured using a 10 min. simulated territorial challenge and we do not know how males modulate their aggression over longer periods. Many species show decreased aggression with sustained interaction, described in territorial birds as 'dear enemy' effects. To understand how urban song sparrows (Melospiza melodia) respond to sustained simulated territorial challenge compared to their rural counterparts we performed 30 min. simulated territorial intrusions on territorial males in urban (n=15) and rural (n=15) habitat. We recorded an individual's aggressive response (broadcast song, wing waves, soft song, and distance to speaker) to playback for the first and last 6 min of the challenge. Just as in prior studies, we found that urban birds are more aggressive than rural birds in the first 6 min of territorial challenge. However, urban birds became significantly less aggressive in the last 6 min of challenge compared to the first 6 min., such that they expressed levels of aggression similar to rural males, which maintained consistently lower levels of aggression at both timepoints. Urban male song sparrows have larger territories and fewer neighbors than rural males so these results could be consistent with faster habituation to neighbors or rapid modulation of aggression for other reasons.

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Zooplankton community structure is more variable over time than space, with implications for water quality management

***Wander, H.L.*[1]*,** *Lewis, A.S.*[1]*, Howard, D.W.*[1]*, Woelmer, W.M.*[1]*, Brown, B.L.*[1]*, and Carey, C.C.*[1]

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Zooplankton are integral components of freshwater lake and reservoir food webs. Because of their role as a food source for fish and their ability to rapidly graze down algal populations, zooplankton play a critical role in maintaining water quality. To avoid fish predation during the day, zooplankton may migrate both vertically or horizontally (Diel Vertical Migration or DVM and Diel Horizontal Migration or DHM, respectively). In DVM, zooplankton migrate to the bottom waters, whereas in DHM, zooplankton migrate to near-shore shallow habitat during the day to avoid predation. In both cases, zooplankton return to deep surface waters at night to feed where algal food is most abundant. While drivers of these migration behaviors are not fully understood, DHM is thought to be more favorable than DVM when bottom water oxygen concentrations are low, a common occurrence in reservoirs. Additionally, shifts in DVM and DHM behavior may be linked to changes in zooplankton community structure (i.e., community composition and density) and therefore could alter freshwater functioning.

To understand how zooplankton community structure changes over time, we conducted five independent 24-hour sampling campaigns during the summers of 2019-2021 in Beaverdam Reservoir, VA, USA, a secondary drinking water supply reservoir that experiences summer hypolimnetic anoxia. We collected paired vertical tows at deep and shallow sites throughout a 24-hour period to capture patterns in DVM and DHM, respectively. Our results show that zooplankton exhibit greater variability within 24-hours than they do among years or sites. Variability in zooplankton community structure is likely partially explained by zooplankton migration behavior, as spatial distribution changes among taxa as they respond to changing environmental conditions over both short and long-term scales. Our work implies that current zooplankton monitoring approaches which typically occur once a day around noon are likely underestimating much of the variability in zooplankton community structure. Importantly, this short-term variability in zooplankton densities can have implications on fish communities that feed on zooplankton, as well as algal biomass and water quality, as zooplankton grazing efficiency changes over the course of 24-hours. Ultimately, this work will further our understanding of how zooplankton communities control water quality and food web dynamics in the face of global change.

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Linking greenhouse gas concentrations and changing inundation regimes in wetlands

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Changing hydrology is regarded as an important driver of greenhouse gas (GHG) dynamics. Specifically, in small headwater wetlands, spatiotemporal variability in hydrologic flowpaths and resulting inputs and outputs of carbon sources are thought to influence GHG concentrations. How variable the hydrology-GHG relationship and the factors that control it remains an important knowledge gap. To explore the influence that hydrologic regimes have on GHG concentrations, we sampled 15 headwater wetlands and adjacent groundwater wells in the Delmarva Peninsula, Maryland over two years during varying hydrologic conditions. We analyzed the samples for dissolved carbon dioxide (CO2) and methane (CH4) as well as dissolved organic carbon (DOC), anions, and cations. We found that dissolved CH4 in wetland surface water (15uM) is, on average, higher than in groundwater (6uM). By contrast, groundwater (1,041uM) has higher CO2 concentrations than wetland surface water (315uM). Spatiotemporal variability in surface water, as determined by coefficients of variability (CVs), showed that surface water CH4 is more variable over time than CO2, with an average CV of 75% (37-140%) and 31% (10-50%), respectively. Spatial variability in GHG concentrations among wetlands also increased during drawdown periods, likely due to increased heterogeneity as wetlands become more hydrologically isolated from each other and from groundwater sources. Future work will incorporate high-frequency CO2 data which will allow us to improve our understanding of how inundation regime and hydrologic connections can influence GHG emissions in headwater wetlands at event scales. This integrated understanding will be crucial as we move into a future of increased climatic variability.

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A Triassic stem caecilian and the evolutionary and origins of living amphibians

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Living amphibians (Lissamphibia) include frogs, salamanders, and the limbless worm-like caecilians. The evolutionary origin of caecilians is estimated to occur over 300 million years ago, however the oldest-known caecilian fossils are about 183 million years old, indicating a missing fossil record during their early evolutionary history. The lack of caecilian fossils from the first half of their evolutionary history obscures the evolutionary steps leading to the extant caecilian body plan, and has led to controversy surrounding their evolutionary relationships to frogs and salamanders. Here we report the geologically oldest fossil caecilian from the Late Triassic epoch of Arizona (220 Million years ago), USA, extending the caecilian record by around 35 million years. These fossils illuminate the timing and pattern of early caecilian morphological and functional evolution, demonstrating a delayed acquisition of musculoskeletal features associated with fossoriality (burrowing) in living caecilians. The provenance of these fossils suggests the evolutionary origins of caecilians lies in the equatorial paleotropics of the Pangaean supercontinent, implying that living caecilian biogeography reflects conserved aspects of caecilian function and physiology, in combination with vicariance patterns driven by plate tectonics. These fossils reveal a combination of morphologies that are unique to caecilians alongside features that are shared with frogs, salamanders, strongly indicating that caecilians are closely related to these taxa, resolving the controversial evolutionary placement of caecilians.

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Causal inference to scope environmental impact assessment in multisector systems: the case of trans-border hydropower exports

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Decarbonization of the United States' electricity sector will require trillions of dollars of investment in generation and transmission infrastructure. The National Environmental Policy Act (NEPA) requires proponents of many major projects to complete environmental impact statements (EIS) that address reasonably foreseeable impacts, regardless of where these impacts occur. There has been controversy over the cause-effect relationships among electrical supply, electrical demand, apparent cost, and other variables given the complex interactions between them. Therefore, the range of environmental impacts attributable to new infrastructure projects is subject to frequent disagreements. In this work, we address increasing U.S. imports of Canadian hydropower in the setting of falling prices and surplus generation. There has been controversy as to whether new transmission capacity stimulates new generation capacity, and thus whether generation-side environmental and health impacts must be assessed in the scope of incremental transmission projects. We have developed a rich longitudinal database of variables related to generation capacity, export volume, retail prices, and climate over the period 1979 to 2021. We have applied a novel multivariable wide neural network machine learning methodology to evaluate alternative causal models for the evolution of the electricity system and the role of new transmission infrastructure. We find no evidence that transmission capacity stimulates generation capacity. Rather, generation capacity growth in Canada is triggered primarily by domestic price signals and climate parameters, with trans-border transmission capacity developed primarily to absorb excess generation potential. This work supports a relatively narrow scope for EIS related to trans-border transmission projects. More generally, this analysis demonstrates how causal inference methods may help build consensus around the appropriate scope of EIS for highly interconnected energy and infrastructure projects.

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Incidence of per-polyfluoroalkyl substances (PFAS) in private water supplies in Southwest Virginia

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Per- and polyfluoroalkyl substances (PFAS) are a family of contaminants of emerging concern due to their persistence in the environment and potential negative health impacts. Because drinking water is suspected to be a primary source of human PFAS exposure, the US Environmental Protection Agency (US EPA) has set aggressive health advisories (HA) for four PFAS species that apply to municipal water systems. Private drinking water supplies may be uniquely vulnerable to PFAS contamination as these systems often include limited treatment prior to use. The goal of this study was to examine the incidence of PFAS contamination in private drinking water supplies in two counties in Southwest Virginia (Floyd and Roanoke), and to examine the potential for reliance on citizen-science based strategies for sample collection in subsequent broader efforts. Samples for metals, bacteria, and PFAS analysis were collected by homeowners and experts at the drinking water point of use (POU) for comparison. At least one PFAS was detected in 76% of samples (n=60), with an average Σ PFAS concentration of 6.91 parts per trillion (ppt). PFOA and PFOS, which are currently included in EPA HA, were detected in 13% and 11% of samples, respectively. Although there were significant differences in total PFAS concentrations between expert and homeowner collected samples (Wilcoxon, alpha = 0.05), it is unclear whether this difference was due to contamination by the collector or the time of day of sampling.

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Growing Cover Crops for a Diverse Soil Microbiome

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[2] Forest Resources and Environmental Conservation, Virginia Tech, Blacksburg, VA

The agricultural and ecological benefits of cover crops are well documented. Furthermore, cover crop diversification (i.e., mixtures) has been shown to enhance these benefits within specific agro-ecosystems. However, recent work suggests that accounting for cover crop diversity alone only explains a small fraction of the variability observed in agroecological benefits. The soil microbiome, which is also known to mediate crop growth and ecosystem services, is a critical, yet poorly understood link between cover crops and ecosystem function. To understand how plant diversity pertaining to plant functional traits, influences the associated soil microbiome, we directly measured the diversity of soil microbiomes selected for by a broad range of cover crops exhibiting diverse plant functional traits (PFTs). Specifically, we grew individuals of twenty-nine different plant species for a six-week period in the greenhouse. At the end of the experiment, we quantified numerous PFTs and rhizosphere microbial communities were characterized via 16S rRNA amplicon sequencing. Our results suggested that plant species differed in their functional traits and soil microbiomes. The differences in alpha and beta diversity of soil microbiomes associated with different plant species can also be attributed to certain plant functional traits including biomass and C:N ratios as analyzed via multiple linear regression and redundancy analysis, respectively. Future work will include growing mixtures of winter cover crops to either maximize (heterogenous) or minimize (homogenous) the diversity in their PFTs and soil microbiomes to understand their resultant effects on ecosystem services including soil health parameters, weed suppression and cash crop (corn) yield.

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What did I order for lunch?

Turkey with Avocado	**Turkey cont.**	**Chicken Caesar Wrap**	**Caprese Focaccia (Vegetarian)**	**Hokie Wrap (Vegetarian):**	**Veggie Wrap (Vegan)**	**Spring Salad (Vegan, GF)**
Alfonso	Jain	Abadian	Amaya	Benami	Badgley	Duston
Alves Pereira	Jones	Agarwal	Belden	Brennan	Brousseau	Hensley
Barney	Kailing	Brown	Bone	Castello	Bueren	Hymel
Benfield	Kligman	Carey	Borba	Daniel	Fossett	Johnson
Burt	Lin	Chaves	Bretz	Gohlke	Islam	Mayer
Castaneda Guzman	López Lloreda	Draghi	Cunha	Goodman	Kuchinsky	Russell
Chen	McGlothlin	Holloway	Foffa	Hunter	Lewis	
Coscia	McLaughlin	Hopkins	Hotchkiss	Lahondere	Riddle	
Czuba	McMillian	McNeill	Isaacman-VanWertz	Langwig	Snyder	
Darling	Nyboer	Mims	Lofton	O'Brien	Stocker	
Entrekin	Reid	Mouser	Moore	Olsson	Vikesland	
Escobar	Richards	O'Malley	Moran	Pototsky		
Frimpong	Scott	Okeshola	O'Brien	Schoenle		
Gazar	Sewall	Panji	Parker	Tithi		
Govenor	Silknetter	Plont	Re			
Haak	Smith	Reed	VanDiest			
Harris	Stewart	Sabat-Bonilla	Wendler			
Hawley	Thompson	Schenk				
Hohweiler	Upshur	Shea				
Howard	Walters					
Howell	Wander					
Hull	Werth					
Hultin	Xia					
	Zielske					

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KEYNOTE SPEAKER:

Laura Schoenle
Associate Director,
Office of Undergraduate Biology,
Cornell University

Keynote: *Centering Culture & Mentorship in Research*

Participation in research can be a transformative experience. At their best, research experiences shape career trajectories, teach professional skills, and help students develop a sense of belonging and identity in their field of interest. The positive impacts of a research experience strongly rely on the lab environment, research culture, and mentorship. We will discuss evidence-based strategies to intentionally build a culture of inclusion, strong mentorship, and research excellence scaling from a single lab to a broader community of practice.

About Dr. Schoenle:

Laura joined the Office of Undergraduate Biology (OUB) at Cornell in October 2018. In her position Laura develops, implements, and assesses programs that facilitate an interest in and access to undergraduate research for Cornell's ~1300 undergraduate students. She also coordinates the Biological Sciences Honors Program and leads OUB efforts to educate and guide students planning to pursue graduate school. And, like all OUB professional staff advisors, Laura provides both academic and career advising as well as offer general support for the holistic development, well-being and success for all their biological sciences students. Laura brings a wealth of experiences in education, life sciences, and research to the position. She has demonstrated an enthusiasm for supporting diversity and inclusion efforts in the sciences.

Following completion of her B.S. in Animal Science from Cornell in 2006 and M.Ed. from University of Arizona in 2009, Laura taught high school biology and environmental science in Tucson, AZ. Laura is also an ecophysiologist and studied how wildlife cope with environmental challenges. Laura is an alumnus of the Interfaces of Global Change Interdisciplinary Graduate Program, and she completed her Ph.D. in Biological Sciences at Virginia Tech and postdoctoral research at the University of South Florida and Hamilton College.

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