IGC Graduate Research Symposium

April 22, 2022

Graduate Life Center Multipurpose Room

- AGENDA -

8:00 – 8:50 Poster setup with coffee & refreshments

8:55 – 9:00 **Welcome,** by Dr. Bill Hopkins

9:00 – 10:00 **IGC Platform Presentations Session 1**

Moderator: **Brenen Wynd**

9:00 - 9:15 **Do herbivore-induced plant volatiles affect insectivorous bat activity in agricultural fields?**, by Lauren Maynard (BIOL)

9:15 - 9:30 **Using big data to test the effects of spatial protection in remote island shark sanctuaries**, by Brenden Shea (FWC)

9:30 - 9:45 **Novel low-cost concentrating inlet for detection of atmospheric reactive organic gases in small sample flows**, by Namrata Shanmukh Panji (CEE)

9:45 - 10:00 **How does urbanization impact female song sparrows? A comparison of physiological and behavioral recovery from disturbance**, by Sam Lane (BIOL)

10:00 – 11:15 **Poster Viewing Session 1** and coffee break

Observations in deep time: Teaching phylogenetic natural history with iNaturalist, by Nic Bone and Bailey Howell (BIOL)

How equitable is adaptation planning and implementation? A review of climate action and adaptation plans across the US, by Jennifer Brousseau (FREC)

Warming up mutualisms: a case study of an ant–dispersed plant, *Sanguinaria canadensis*, by Melissa Burt (BIOL)

Floristics of Virginia's piedmont grasslands, by Jordan Coscia (SPES)

Horsenettle (*Solanum carolinense*) fruit bacterial communities are not variable across fine spatial scales, by Ariel Heminger (SPES)

Sex-biased infections and mortality in a multi-host fungal pathogen of bats, by Macy Kailing (BIOL)

Brown-headed nuthatch foraging responses to predator presence, by Noah McNeill (BIOL)

Unraveling migration patterns of catfish in the Amazon, by Luciana Pereira (FWC)

Use of pycnophylactic interpolation to determine the number of households in redlined districts in Roanoke City Virginia that lack complete plumbing, by Charles Sterling (BSE)

Differences in arthropod communities associated with urbanization, by Isaac VanDiest (BIOL)

Linkages between water transit times and stream solute concentrations in forested headwater catchments, by Tyler Weiglein (FREC)

Contrasting ecosystems along Panama's coasts reveal variation between phage communities, by Alaina Weinheimer (BIOL)

11:15 – 12:00 **IGC Platform Presentations Session 2**

Moderator: **Alaina Weinheimer**

11:15 - 11:30 **Characterization of prophages in bacterial genomes from the honey bee (*Apis mellifera*) gut microbiome**, by Emma Bueren (BIOL)

11:30 - 11:45 **Elusive pathways to adaptation? Perceptions of the catalysts and constraints to climate workshop outcomes**, by Caleb O'Brien (FREC)

11:45 - 12:00 **Community stability in stream networks: Disentangling the roles of dispersal mode and network position**, by Sara Cathey (BIOL)

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12:00 – 1:00 Lunch break

1:00 – 1:45 **IGC Platform Presentations Session 3**

Moderator: **Amanda Hensley**

1:00 - 1:15 **Inert fibers and soil microorganisms promote streambank soil resistance to fluvial erosion**, by Daniel Smith (BSE)

1:15 - 1:30 **Anoxia decreases carbon sequestration over multi-annual timescales in two freshwater reservoirs**, by Abby Lewis (BIOL)

1:30 - 1:45 **Management practices influence the mitigation potential of Southeastern U.S. forests under climate change**, by Joshua Rady (FREC)

1:45 – 2:30 **IGC Capstone Project Presentations**

Moderator: **Korin Jones**

1:45 - 2:00 **Rubbing salt in wounded ecosystems: An IGC Capstone review of zootic responses to anthropogenic salinization**, Abigail Belvin (ENTO), Joshua Mouser (FWC), Amanda Pennino (FREC) and Stephen Plont (SPES)

2:00 - 2:15 **Paleontological educational modules: Hands-on activities for K-12 students achieve Virginia Standards of Learning related to global change**, by Devin Hoffman and Ben Kligman (GEOS)

2:15 - 2:30 **In Flipped Science Fair, children judge graduate posters and see themselves as scientists**, by Emma Bueren (BIOL), Amanda Hensley (TBMH), Abby Lewis (BIOL), Grace O'Malley (BIOL), and Heather Wander (BIOL)

2:30 – 3:45 **Poster Viewing Session 2** and coffee break

How does stream connectivity drive carbon dynamics?, by Kristen Bretz (BIOL)

Drinking water contamination and associated health outcomes in rural Appalachia: A systematic review and meta-analysis, by Amanda Darling (CEE)

Plant attributes and soil organic carbon stabilization: getting to the root of it, by Stephanie Duston (FREC)

Cumulative effects of stream restoration and watershed characteristics on watershed-scale nitrate removal, by Luke Goodman (BSE)

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Newt bacterial skin communities recover to natural composition after antibiotic exposure in the presence of environmental bacteria, by Korin Jones (BIOL)

Nitrate limitation in the early Neoproterozoic oceans delayed the rise of eukaryotes, by Junyao Kang (GEOS)

Redundant or complementary? Identifying patterns of multifaceted frog and toad biodiversity in Virginia, USA, by Chloe Moore (BIOL)

Landowner perspectives on allowing private lands research, by Becca O'Brien (FWC)

Patterns of genetic structure in freshwater invertebrates are scaled by biological and geographic drivers, by Sam Silknetter (BIOL)

Mosquito sugar-feeding: Using DNA barcoding to determine mosquito plant diet, by Forde Upshur (BioChem)

Data frequency affects water temperature forecast skill in a eutrophic reservoir, by Heather Wander (BIOL)

3:45 – 4:45 **Keynote Presentation,** by Dwight Bigler

4:45 – 6:00 **Reception and Platform Award Announcements**

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2022 IGC Symposium Presentation Abstracts

Capstone Project Presentations

1. **Paleontological educational modules: Hands-on activities for K-12 students achieve Virginia Standards of Learning related to global change**

Hoffman, D. K.[1]*, and Kligman, B. T.[1]*
[1] Department of Geosciences, Virginia Tech

Engaging educational material is crucial for successful understanding of global change issues for K-12 students. Inspired by our experiences using 3D printed fossil replicas in science outreach events at Virginia Tech and Petrified Forest National Park and informed by input from science educators like Mariah Green from the Virginia Tech Museum of Geosciences, we undertook an IGC capstone project focused on using 3D printed fossils as accessible hands-on learning tools. Two activity kits were designed including: [1] using 3D printed fossils from the age of dinosaurs in Virginia satisfying grade 3 Virginia Science Standards of Learning focused on understanding fossils, ecosystems, environmental change, and food webs; and [2] using 3D printed extant and extinct tetrapod limbs to satisfy high school biology Virginia Standards of Learning focused on understanding evolution, homology, and the fossil record. Our activities act to serve K-12 students through highlighting required learning concepts from the Virginia Standards of Learning, and more importantly provide an engaging opportunity to learn about concepts of global change from a deep-time perspective. A powerful aspect of these kits is the transferrable nature of 3D fossil data - 3D models used in these kits can be printed on any standard 3D printer, allowing for digital transfer and remote replication of these activity kits at any educational institution with 3D printing technology. We intend to carry forward the frameworks of this Capstone Project to create similar hands-on educational activities in our post-graduate careers.

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2. **Rubbing salt in wounded ecosystems: An IGC Capstone review of zootic responses to anthropogenic salinization**

***Joshua B. Mouser[1] *, Abigail C. Belvin[2]*, Amanda Pennino[3]*, Stephen Plont[4]**, *Christopher D. Robinson[7], Lucy B. Smith[8], Jyoti Thapa[9], Carl E. Zipper[10], Paul L. Angermeier[4, 11], Sally A. Entrekin[3], Richard H. Walker*[1,2]*
[1] U.S. Geological Survey, Eastern Ecological Science Center at the Leetown Research Laboratory, Kearneysville, West Virginia, USA.
[2] Current affiliation: Department of Biology and Chemistry, Upper Iowa University, 605 Washington Street, P.O. Box 1857, Fayette, IA 52142, USA.
[3] Department of Entomology, Virginia Polytechnic Institute and State University, Blacksburg, Virginia, USA.

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[4] Department of Fish and Wildlife Conservation, Virginia Polytechnic Institute and State University, Blacksburg, Virginia, USA.
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[6] Department of Biological Sciences, Virginia Polytechnic Institute and State University, Blacksburg, Virginia, USA.
[7] Department of Biology, University of Virginia, Charlottesville, Virginia, USA.
[8] Virginia Department of Environmental Quality, Salem, Virginia, USA.
[9] Hollins University, Roanoke, Virginia, USA.
[10] School of Plant and Environmental Sciences. Virginia Polytechnic Institute and State University, Blacksburg, Virginia, USA.
[11] U.S. Geological Survey, Virginia Cooperative Fish and Wildlife Research Unit, Virginia Polytechnic Institute and State University, Blacksburg, VA, USA.

Anthropogenic salinization of freshwater habitats is a major component of global change that alters biological communities and impairs ecosystem services. For our capstone project, we worked with an interdisciplinary group of scientists from different academic institutions to better understand global salinization effects on freshwater biota. We synthesized 570 journal articles characterizing 5735 responses of freshwater mollusks, macro-crustaceans, zooplankton, other non-arthropod invertebrates, insects, fishes, and amphibians to salinization. Organismal responses to salinization most commonly focused on aquatic macroinvertebrates (31% of responses) and fishes (21% of responses). Responses were recorded primarily in temperate climates in North America (37% of articles) and Europe/Russia (25% of articles). Key anthropogenic sources of salinization were urbanization or mixed land use, as well as and/or road salts, and the most common ions studied included Cl^- and Na^+. Negative responses to salinization were most common for all organismal groups reviewed. Our review identified key knowledge gaps regarding freshwater animal responses to salinization and suggests additional management of salinization is warranted. This project allowed us to collaborate across departments as part of a team led by USGS partners and apply our research specialties towards a collaborative outcome. Throughout this capstone project, we strengthened skills in scientific writing, data manipulation and visualization, and utilized interdisciplinary expertise to interpret data from different organisms. We also strengthened skills that benefit us working at the science/policy interface on topics with global environmental significance. More quantitative taxon-specific sensitivities to salinization will be assessed using this comprehensive database.

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3. In Flipped Science Fair, children judge graduate posters and see themselves as scientists

Bueren, E. K.[1], Hensley, A. A.[2], Lewis, A. S. L.[1], O'Malley, G.[1], Wander, H. L.[1]
[1] Department of Biological Sciences, Virginia Tech
[2] Translational Biology, Medicine, and Health Program, Virginia Tech

This winter, five IGC fellows collaborated with several other VT graduate students and the Roanoke City Public Libraries to host a Flipped Science Fair, with twin goals of science outreach and graduate training. At the fair, 28 graduate students presented posters about their research, and elementary students (ages 8–10) were invited to serve as judges. We specifically reached out to students from the city of Roanoke, VA, USA, where 15 out of 17 elementary schools receive support from Title I (allocated to schools with low-income students). These students often face barriers to entering science fields, including a lack of self-identification as potential scientists. We based this event on the

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premise that actively requesting and valuing student opinions is critical in empowering children to develop a science identity of their own. While judging posters, children learned about a wide range of leading-edge research occurring at Virginia Tech and had meaningful interactions with professional scientists in small-group settings. For graduate students, this program provided an opportunity to practice communicating their research to a new audience. To prepare graduate students for this challenge and further advance the educational goals of the project, we held an additional workshop prior to the Flipped Fair event; graduate students received training in communicating science to children and discussed diversity, equity, and inclusion considerations. Ultimately, the success of this event highlights how breaking down traditional hierarchies in science communication and valuing non-expert opinions can enhance both outreach and educational goals.

PLATFORM PRESENTATIONS:

1. Characterization of prophages in bacterial genomes from the honey bee (*Apis mellifera)* Gut Microbiome

Bueren, Emma K.*[*1], *Alaina R. Weinheimer[1], Frank O. Aylward[1], Bryan B. Hsu[1], David C. Haak[2], and Lisa K. Belden[1]*
[1] Department of Biological Sciences, Virginia Tech, Blacksburg, VA, USA
[2] School of Plant and Environmental Sciences, Virginia Tech, Blacksburg, VA, USA

Honey bees (*Apis mellifera)* are critical pollinators of crop plants around the globe and have been suffering from increasing colony losses in many regions. A variety of pathogens, in combination with environmental factors, are likely contributing to these losses. The gut microbiome can be very important in host immune defense for both vertebrates and invertebrates, including honey bees. The presence of prophages (lysogenic bacteriophages integrated into the bacterial genome) in the honey bee gut may impact both the structure and function of the gut community, as they can confer protection from other phage species, as well as encode additional metabolic pathways and toxins that are useful to their bacterial hosts. Therefore, to understand how prophages affect their bacterial hosts, which in turn influence host health, honey bee prophages need to be identified and characterized. Using 179 publicly available honey bee gut-associated bacterial genomes (including two bacterial pathogens), a total of 304 putative prophage regions were predicted. Among core gut bacteria, the number of prophages per genome ranged from 0 – 5 and prophage composition of the genomes ranged from 0 – 13%. *Snodgrassella alvi* had the highest median number of prophages, while *Lactobacillus melliventris* had the highest median prophage composition. The pathogen *Paenibacillus larvae* had a higher median number of prophages than the pathogen *Melissococcus plutonius* or any of the core bacteria. This initial genome survey suggests that prophages within the honey bee gut may interact with and potentially modulate specific members of the gut bacterial community.

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2. **Community stability in stream networks: Disentangling the roles of dispersal mode and network position**

***Cathey, S.E.*[*1]*,** *Swan, C.[2], Anderson, K.[3], Sokol, E.[4], and Brown, B.L.[1]*
[1] Department of Biological Sciences, Virginia Tech;
[2] Department of Geography and Environmental Systems, University of Maryland Baltimore County;
[3] Department of Biological Sciences, University of California, Riverside;
[4] National Ecological Observatory Network, Battelle

Freshwater systems face numerous threats from global change. Determining the factors that influence the assembly and stability of freshwater communities is crucial for managing and restoring these systems. Community assembly may vary across stream networks due to differences in environmental filtering and regional processes, such as dispersal. Stream insect dispersal varies by mode, and this variability may affect the recovery of streams at the local and network scale. To examine the effect of different dispersal modes on community assembly and stability, we conducted a field experiment using streamside flumes at Coweeta Hydrologic Lab. We built 18 flumes and divided them into four channels. Each channel received one dispersal treatment: open to drift and aerial dispersal (control), aquatic drift only, aerial flight only, and no drift and aerial dispersal. Following two initial sampling events, we applied a disturbance treatment across all of the flumes by raking the stream sediments and then continued to sample monthly. Preliminary data support two of our predictions: communities more central in the network are more stable than headwaters, and channels that received drift dispersal recovered more quickly from the disturbance. These results confirm community assembly and stability vary with network location, and that multiple modes of dispersal contribute to assembly of benthic communities. Understanding these drivers of assembly can improve restoration and management strategies in river networks by accounting for network-position-specific effects.

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3. **How does urbanization impact female song sparrows? A comparison of physiological and behavioral recovery from disturbance**

***Lane, Samuel J.*[*1]*; *VanDiest, Isaac, J.[1]; Fossett, Taylor E.[1]; Sewall, Kendra B.[1,2]*
[1]Virginia Tech, Department of Biological Sciences, 1405 Perry Street, Blacksburg, Virginia, 24061;
[2]Virginia Tech, Department of Biological Sciences and School of Neuroscience, 1405 Perry Street, Blacksburg, Virginia, 24061

Urban habitats often present animals with chronic, potentially life-threatening disturbances. Organisms employ behavioral strategies and physiological mechanisms, such as the glucocorticoid stress response, to cope with these stressful environments. However, there is no consensus on how urbanization affects songbird's glucocorticoid stress response. One reason for the disparate conclusions may be that most studies focus on a subset of individuals, males. Females, in contrast, may carry a higher allostatic load during reproduction and must decrease their mobility while incubating eggs, which could expose them to more stressors than free-flying males. If urban female songbirds express altered behavioral and physiological coping strategies to urban habitats, we predicted they would have lower baseline and stress induced glucocorticoids compared to rural females. Additionally, we predicted they would have significantly faster behavioral recovery times following disturbance. To test these predictions, we captured 26 urban and 14 rural female song sparrows (Melospiza melodia) during incubation or brooding. We collected baseline and stress induced blood samples and measured return to parental behaviors using a radio frequency

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identification system installed at the nest. We found that urban females had significantly lower baseline and stress induced glucocorticoids but had no difference in behavioral recovery times, relative to rural females. Our hormone results suggest urban females have a dampened physiological stress response that could reflect stress resistance, which may protect them from chronic exposure to glucocorticoids. Given that rural females express similar behavioral recovery times, this altered physiological response could play a role in maintaining parental care in urban habitats.

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4. Do herbivore-induced plant volatiles affect insectivorous bat activity in agricultural fields?

***Maynard, L.D.*[*1], ***Ford, W.M.[2], Parker, J.D.[3], Whitehead, S.R.[1]
[1] Department of Biological Sciences, Virginia Tech, Blacksburg, VA
[2] US Geological Survey, Virginia Cooperative Fish and Wildlife Research Unit, Blacksburg, Virginia
[3] Smithsonian Environmental Research Center, Edgewater, MD

Bats are important pest control agents in agricultural systems worldwide. Tracking insect abundance spatially and temporally, bats can detect insect fluctuations and outbreaks. Yet, the underlying mechanisms that drive these foraging behaviors are unclear. It is well documented that plants respond to herbivore damage by emitting herbivore–induced plant volatiles (HIPVs), which influence many tri-trophic interactions. Notably, HIPVs can attract invertebrate and avian natural enemies that use the chemical cues to locate insect prey, but it is unknown if HIPVs are used by carnivorous mammals. Using a model crop system, soybean (*Glycine max*), in the mid-Atlantic US, our study asked three questions: 1) Which bat species are active in soybean fields?; 2) Is insectivorous bat activity affected by naturally occurring and/or synthetic soybean HIPVs; and 3) If so, which species are affected? Across soybean fields in the mid-Atlantic US, we created paired plots that were either HIPV plots (damaged plants or synthetic dispensers) or control plots (undamaged plants or empty dispensers) and measured bat activity using ultrasonic recorders. As anticipated, the big brown/silver-haired bat (*Eptesicus fuscus/Lasionycteris noctivagans*) was the most active species group on the landscape. Yet, our results do not support our hypothesis that bats use soybean HIPVs, as bat activity did not significantly differ between control and HIPV plots. However, the relationships among plants, herbivores, and natural enemies are extremely variable and context-dependent, and we hope this initial study on bats and HIPVs may serve as a roadmap for developing future bat–plant research.

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5. Anoxia decreases carbon sequestration over multi-annual timescales in two freshwater reservoirs

***Lewis, Abigail S. L.*[*1], ***B. R. Niederlehner[1], Arpita Das[1], Nicholas W. Hammond[2], Madeline E. Schreiber[2], Cayelan C. Carey[1]
[1] Department of Biology, Virginia Tech, Blacksburg, VA, USA
[2] Department of Geosciences, Virginia Tech, Blacksburg, VA, USA

Earth's climate is regulated by complex interplay between uptake and release of greenhouse gases. Freshwater lakes and reservoirs play a disproportionate role in these cycles, sequestering more carbon than ocean sediments each year. However, it remains unknown how global declines in bottom-water oxygen concentrations may impact carbon sequestration in freshwater sediments. In particular, associations between iron (Fe) and organic carbon (OC) are hypothesized to play an

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important role in aquatic carbon sequestration, but Fe-bound OC (Fe-OC) complexes may be sensitive to changes in oxygen concentrations in overlying water. Here, we used whole-ecosystem experiments to test the sensitivity of Fe-OC to changing oxygen levels in two freshwater reservoirs: Falling Creek (FCR) and Beaverdam (BVR; Roanoke, VA, USA). FCR is equipped with a bottom-water oxygenation system that has been operated on a variable schedule for nine years, maintaining primarily oxic conditions from 2013–2019 and low-oxygen conditions from 2020–2021. BVR serves as an unoxygenated reference reservoir and exhibits hypolimnetic anoxia from May to October each year. In 2019, Fe-OC concentrations were significantly higher in FCR (μ = 36% of sediment OC) than in BVR (μ = 31%; $p = 0.03$). However, after two years of low-oxygen conditions in FCR, Fe-OC concentrations decreased significantly ($p < 0.001$) and no longer differed from the unoxygenated reference reservoir ($p = 0.259$). These results suggest that global declines in oxygen concentrations can decrease carbon sequestration, providing a positive feedback to global climate change.

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6. Elusive Pathways to Adaptation? Perceptions of the Catalysts and Constraints to Climate Workshop Outcomes

O'Brien, Caleb*[1]; *Stern, Marc J.*[1]; *Brousseau, Jennifer*[1]; *Hansen, Lara J.*[2]
[1] Dept. of Forest Resources and Environmental Conservation, Virginia Tech;
[2] EcoAdapt

Groups in the United States are increasingly relying on place-based climate adaptation workshops to aid their efforts to prepare for—and cope with—climate change. Adaptation workshops vary widely in their duration, structure, and scope, and there is relatively limited empirical evidence about the drivers of participation in these workshops and their impact on implementation of adaptation strategies. To begin addressing this gap, we sought to understand participant perceptions of the outcomes of adaptation workshops and the catalysts and constraints of those outcomes across a wide range of locations and formats. We surveyed participants in 33 place-based adaptation workshops that occurred between 2017 and 2020 in the United States. Each workshop included multiple stakeholder groups and was attended by at least 10 participants. We found that participants generally believe the events they attended fulfilled their learning and relational goals. However, they were less likely to identify direct connections between the workshop and meaningful climate action. Persistent constraints related to resource availability, leadership, and political/collaborative challenges stymied action. Planning, learning, and knowledge-sharing outcomes were frequently linked to workshops, whereas participants were less likely to attribute projects and initiatives to workshops. Projects and initiatives linked to workshops tended to be "low-hanging fruit." Elements including the quality of the facilitator, learning during the workshop, pre-existing relationships between attendees, relationships enhanced during the workshop, and realistic strategies developed during the workshop all positively influenced outcomes. These findings could help facilitators design events that better support desired outcomes and address lingering obstacles to action.

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7. Novel Low-Cost Concentrating Inlet for Detection of Atmospheric Reactive Organic Gases in Small Sample Flows

***Panji, Namrata Shanmukh*[*1]**, *Gabriel Isaacman-VanWertz*[1]
[1] Department of Civil and Environmental Engineering, Virginia Tech, Blacksburg, USA

Every day, there are thousands of different volatile organic compounds (VOCs) emitted into the atmosphere by biogenic and anthropogenic sources. Despite being present in the sub-ppt to sub-ppb concentrations, they carry a wide range of impacts on air quality, radiative forcing, and human health. These compounds, especially terpenes emitted by trees, contribute significantly to organic aerosols, ozone production and loss, and oxidant removal. Measuring reactive gases at these concentrations requires expensive and complex instrumentation due to the need for very low levels of detection which has been particularly limiting for the development of reliable low-cost instrumentation. Here, we present a novel inlet with the ability to concentrate organic gases in small sample flows (up to 5 sccm), and consequently provide improved limits of detection. Inert gases are selectively removed from the sample stream by selective permeation through a semi-permeable membrane, leaving organic gases concentrated into a smaller flow to any detector. We demonstrate enrichment by a factor of several for major reactive atmospheric gases: isoprene (C_5H_8), monoterpenes ($C_{10}H_{16}$, specifically α-pinene), and alkanes (methane, propane, butane, pentane, and cyclohexane). We estimate that enrichment by an order of magnitude or more is possible at sccm-level flows for substantially reduced costs.

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8. Management Practices Influence the Mitigation Potential of Southeastern U.S. Forests Under Climate Change

***Rady, J.M.* [*1]**, *Thomas, R.Q.*[1]
[1]Depart. of Forest Resources and Environmental Conservation, Virginia Tech

Climate change mitigation plans rely on forests as a means to capture carbon, store it, and to supply bioenergy alternatives to fossil fuels. Yet we know little about how climate change will effect managed forests and whether the management practices in those forests will have implications for climate feedbacks and mitigation potential. To address this uncertainty we implemented realistic forest management practices in the CESM CLM-FATES earth system model through the development of the Vegetation Management Module. We used this to perform simulations of the Southeastern United States' forests with varying degrees of management under possible climates for the next 100 years. Our results showed that the details of forest management strongly impacts the yield of wood products over the next century. Failing to represent the full suite of management behaviors in ESM projections has the risk of underestimating timber yields and overestimating the area of land necessary to meet economic demands and mitigation goals.

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9. Inert Fibers and Soil Microorganisms Promote Streambank Soil Resistance to Fluvial Erosion

***Smith, D.S.*[*1]** *and Wynn-Thompson, T.M.*[1]
[1] Biological Systems Engineering Department, Virginia Tech

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Climate change may exacerbate processes such as stream channel migration in part due to changes in water temperature and storm frequency/intensity. Streambank erodibility can have significant impacts on channel morphology, so it is not possible to effectively model changes in channel form without first understanding the components/processes that drive streambank erosion. The goal of this experiment was to determine the relative contribution of different root mechanisms and soil microorganisms on soil resistance to fluvial erosion. Soil treatments were created representing: 1) no roots (NR, control); 2) no roots amended with organic matter (NR+OM); 3) flexible synthetic roots (FSR); 4) flexible synthetic roots+OM (FSR+OM); 5) rigid synthetic roots (RSR); 6) rigid synthetic roots+OM (RSR+OM); 7) live roots (LR; switchgrass [*Panicum virgatum*]); and 8) live roots+OM (LR+OM). The samples matured in a greenhouse prior to flume erosion testing; three flume walls were used to represent unvegetated, herbaceous rooted, and woody rooted streambanks. FSR and RSR reduced erosion rates by 42% and 47% (median values) compared to NR, though the effect was not significant. Adding OM had a greater effect; NR+OM significantly reduced erosion rates by 63% when compared to NR. The erosion rate reductions of live rooted (LR, LR+OM; 93% - 96%) and synthetic rooted + OM treatments (FSR+OM, RSR+OM; 92% - 98%) were identical. This work is applicable to practitioners and researchers alike and highlights the need to critically assess the roots and OM inputs of vegetation species of interest when evaluating how they may influence stream channel migration overtime.

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10. Using Big Data to test the effects of spatial protection in remote island shark sanctuaries

Shea, Brendan D. *[1,2], *Austin J. Gallagher*[2], *Lindsay K. Bomgardner*[1], *Francesco Ferretti*[1]
[1] Department of Fish & Wildlife Conservation, Virginia Tech, Blacksburg, VA, USA
[2] Beneath the Waves, Herndon, VA, USA

Sharks were historically abundant throughout oceanic regions; however, today many populations are threatened with extinction. Recent conservation efforts include the creation of large-scale marine protected areas (LMPAs), with one of the greatest expectations of LMPAs being the potential to conserve highly migratory species like sharks. In the last 15 years, a total of 17 nations or territories have established 'shark sanctuaries', whereby the targeting and retention of sharks is prohibited within territorial waters. Yet, the conservation impacts of such sanctuaries remain unclear. Migratory species may spend less time in protected areas, and furthermore, while targeting sharks is prohibited, commercial fishing continues in many sanctuaries. While sharks captured by fisheries operating in sanctuaries are mandated to be released, many sharks succumb to capture stress or post-release mortality, particularly in longline fisheries. We used big data to model longline fishing effort and shark catch to generate estimates of annual catch and mortality in eight shark sanctuaries. We developed a predictive model which estimates the number of longline hooks deployed using satellite-derived vessel positioning data, then generated standardized catch-per-unit-effort rates for 11 species or species groups using fisheries observer data, and finally estimated shark catch and morality using species-specific capture and post-release mortality rates gleaned from the literature. Our results suggest that longline bycatch remains a significant yet undercounted source of mortality for sharks within sanctuaries. Given the data gaps in regional stock assessments for many pelagic species, we discuss the implications of our findings for stock management across the wider fishing region.

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POSTER PRESENTATIONS:

Session 1

10:00 - 11:15 AM

1. **Observations in Deep Time: Teaching Phylogenetic Natural History with iNaturalist**

Nic Bone*[1], Bailey Howell*[1]
[1] Biological Sciences, Virginia Tech

Using citizen science initiatives such as iNaturalist provides benefits to both scientists and the community. This makes community members feel more connected to the natural world, and using these resources as a data source for teaching gives students' agency in both data collection and analysis. Here we present a tool that uses iNaturalist data collected by students to generate a phylogeny. The tool allows students to quantify the amount of biodiversity they viewed on a single hike, or ask if there is phylogenetic signal in the traits of species they saw in Heritage Park. A variety of evolutionary and ecological questions can be asked and answered with the framework presented here, allowing the students to explore what is most interesting to them. After using the activity with Virginia Tech undergraduate students in Quantitative Evolutionary Biology this spring, we present recommendations for when and how to use the tools developed here in both teaching and outreach to achieve particular learning objectives.

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2. **How Equitable is Adaptation Planning and Implementation? A Review of Climate Action and Adaptation Plans Across the US**

***Brousseau, Jennifer*[1]**, *Malia Pownall[1], Tyler Whitford[2], Barbara Belsito[2] and Marc Stern[1]]*
[1] Forest Resources and Environmental Conservation Department, Virginia Tech, Blacksburg, VA, USA
[2] Center for Leadership in Global Sustainability, Virginia Tech, Blacksburg, VA, USA

As communities adapt to climate change, they must also address the disproportionate impacts facing frontline communities. Even with increased focus on considering equity in adaptation efforts, it's less clear how communities plan to do this. Earlier research sought to understand how cities incorporate equity in their resilience plans, but their work was narrowly focused and failed to examine how proposed strategies are implemented. This study attempts to improve our understanding of how equity is considered in adaptation planning and implementation through a literature review of climate action and adaptation plans in the US. We reviewed each plan using a three-pronged framework of distributional, recognitional and procedural equity to identify examples of equitable adaptation strategies and any other considerations of equity. Initial findings show considerable variation in the extent to which equity is considered, with a stronger focus on distributional equity than procedural and recognitional. We have also found that many communities

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address equity at a broad level, failing to describe how they intend to implement proposed strategies. We will conduct follow-up interviews in spring 2022 with a sample of communities that addressed equity considerably and those that addressed the concepts more broadly. We will use these interviews to understand how plans are being implemented, the constraints these communities are facing and how frontline communities are being impacted. We hope that our findings will help inform more equitable adaptation planning and identify areas for improvement.

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3. Warming up mutualisms: a case study of an ant–dispersed plant, *Sanguinaria canadensis*

Burt, M.A.*[1], Nelson, A.S.[1], Kwit, C.[2], and Whitehead, S.R.[1]*
[1] Dept. of Biological Sciences, Virginia Tech; [2] Dept. of Forestry, Wildlife and Fisheries, University of Tennessee

Diverging responses of interacting species to warming may result in the breakdown of mutualisms with anthropogenic climate change. Since species interactions are important to the function of ecosystems, it is critical that we understand these effects. We used a greenhouse experiment to test how warming affects the seed dispersal mutualism between *Aphaenogaster rudis* (Winnow Ant) and *Sanguinaria canadensis* (Bloodroot). With our experiment we asked: (1) How do ant-dispersed plants and their ant mutualists individually respond to warming? and (2) What is the effect of warming on the quantity and quality of the seed dispersal services provided by ants? We found that colony and worker survival did not differ between warmed and ambient conditions. However, colonies in ambient conditions consumed ~62% more mealworms over the course of the experiment than colonies in warmed conditions. Similarly, we found that ambient colonies removed more seeds during the first six hours of seed placement, although these differences had disappeared by 24 hours. Taken together these results suggest that ants participating in seed dispersal mutualisms may respond to warming through changes to their activity rates, but perhaps not through impacts on survival. Future field-based studies would provide greater insights into the consequences of this on seed fate. Given that ants influence plant distributions through seed dispersal in terrestrial ecosystems throughout the world, a greater understanding of the impacts of warming on this seed dispersal mutualism may be critical to understanding the impacts of warming on ecosystems.

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4. Floristics of Virginia's Piedmont Grasslands

Coscia, Jordan T.*[1], J. Berton C. Harris[2], Devin Floyd[3], Michael Beall[1], Jared Gorrell[1], Drew Chaney[3], Ezra Staengl[3], J. Leighton Reid[1]*
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Temperate and subtropical grasslands are among the most globally threatened biomes, and increased recognition of their biodiversity and functional value is needed to promote their conservation and restoration. The temperate grasslands of Virginia's Piedmont exemplify this plight. Piedmont grasslands have lost over 90% of their historic range, and those that remain face continued habitat loss, the disruption of natural disturbance regimes, and invasive species pressure. To conserve the remaining Piedmont grasslands, we need to recognize their natural extent, characterize distinct grassland floristic community subtypes, and identify the disturbance regimes and edaphic

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factors that drive their persistence. To discern if Piedmont grassland communities have distinct subtypes driven by variation in edaphic characteristics, we surveyed plant communities and collected soil samples using modified Whittaker plots in 135 remnant and semi-natural grassland fragments across the northern and central Virginia Piedmont.

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5. Horsenettle (*Solanum carolinense*) fruit bacterial communities are not variable across fine spatial scales

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[2]Global Change Center, Virginia Tech, Blacksburg, VA, USA
[3]Department of Biological Sciences, Virginia Tech, Blacksburg, VA, USA

Fruit house microbial communities are unique from the rest of the plant. While symbiotic microbial communities complete important functions for their hosts, the fruit microbiome is often understudied compared to other plant organs. Fruits are reproductive tissues that house, protect, and facilitate the dispersal of seeds, and thus they are directly tied to plant fitness. Fruit microbial communities may, therefore, also impact plant fitness. It is important that these interactions are studied especially now that global changes threatens to disrupt these interactions. In this study, we assessed how bacterial communities associated with the fruit of *Solanum carolinense*, a native herbaceous perennial weed, vary at fine spatial scales (< 0.5 km). A majority of the studies conducted on plant microbial communities have been done at large spatial scales and have observed microbial community variation across these large spatial scales. However, both the environment and pollinators play a role in shaping plant microbial communities and likely have impacts on the plant microbiome at fine scales. We collected fruit samples from eight sampling locations, ranging from 2 to 450 m apart, and assessed the fruit bacterial communities using 16S rRNA gene amplicon sequencing. Overall, we found no differences in observed richness or microbial community composition among sampling locations. Bacterial community structure of fruits collected near one another were not more different than those that were farther apart at the scales we examined. These fine spatial scales are important to obligate out-crossing plant species such as *S. carolinense* because they are ecologically relevant to pollinators. Thus, our results could imply that pollinators serve to homogenize fruit bacterial communities across these smaller scales.

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6. Sex-biased infections and mortality in a multi-host fungal pathogen of bats

Kailing, Macy J.*[1]*, *Joseph R. Hoyt[1], J. Paul White[2], Heather M. Kaarakka[2], Jennifer A. Redell[2], John E. DePue[3], William H. Scullon[3], Katy L. Parise[4], Jeffrey T. Foster[4], A. Marm Kilpatrick[5], Kate E. Langwig[1]*
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[2] Wisconsin Department of Natural Resources, Bureau of Natural Heritage Conservation;
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[4] Center for Microbial Genetics and Genomics, Northern Arizona University;
[5] Department of Ecology and Evolutionary Biology, University of California Santa Cruz

Emerging infectious diseases are a key threat to wildlife and understanding disease dynamics within populations is fundamental for the conservation of impacted species. Intersex differences in infection

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are widely observed across disease systems and may have consequences for host population recovery. We explored sex-biased infections of bat species impacted by an emerging fungal disease, white-nose syndrome, and evaluated disease-associated differences in mortality between sexes and potential effects on population structure. We collected fungal swabs, morphometrics, and environmental data from five species of hibernating bats at 43 sites spanning the eastern and midwestern U.S. to characterize infections and host traits over the course of an annual outbreak. We also used RFID systems at hibernacula and PIT-tagged bats to determine the role of sex-based activity patterns in shaping intersex infection patterns. We found females suffered from more severe infections than male conspecifics when there was a clear sex-bias. In addition, we found females were less likely than males to be recaptured overwinter and accounted for a smaller proportion of populations over time. Notably, female-biased infections were evident by early hibernation, suggesting that sex-based dynamics prior to hibernation may play an important role in shaping WNS outbreaks. Higher fall activity in male bats compared to female bats may enable males to reduce infections relative to female bats. Higher impacts in female bats may have cascading effects on bat populations and extend the consequences of WNS beyond the hibernation season, such as limiting recruitment and increasing the risk of Allee effects.

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7. Brown-headed Nuthatch Foraging Responses to Predator Presence

McNeill, Noah[1]* *and Walters, J.R.[1]*
[1]Department of Biological Sciences, Virginia Tech

Birds typically join mixed species flocks in order to garner foraging or anti-predation benefits. However, the large size yet low density flocks of the southeastern US pine savanna present a unique case for delineating these drivers, particularly in small, seasonally granivorous birds such as the Brown-headed Nuthatch (*Sitta pusilla*). In order to test for anti-predatory benefits in these flocks, I have surveyed eight transects for mixed flocks and potential flock predators for the past three years, and conducted a predator decoy playback experiment at two sites in North Carolina. My results reveal a correlation between predator observation rates and nuthatch mixed flock recruitment, with my Sandhills site containing more predators and higher mixed flocking rates. Furthermore, nuthatches at the Lejeune site recruited to mixed flocks more often in transects which received the predator decoy treatment, though not at substantially different rates from the previous year. Nuthatches at Lejeune also froze in place more often following predator playback. These findings show that predator abundance likely modulates nuthatch strategies of flock recruitment and predator vigilance, though it may not be a primary driver of nuthatch behaviors. More demonstrative of nuthatch foraging and flocking decisions are annual and spatial variation in pine seed forage availability, which are highly predicated on the region's shifting weather and climate patterns.

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8. Unraveling migration patterns of catfish in the Amazon

Pereira, L.A*[1]; *Castello, L.[1]; Hallerman, E.[1]*
[1] Dept. of Fish and Wildlife Conservation, Virginia Tech

Most fish movements in Neotropical river-floodplains coincide with the flood pulse, which is the predictable annual flooding of large rivers. We are studying the migration of a species of catfish in

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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 question: 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., their 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 will provide the profiles of Strontium isotopes, which will reveal migration patterns along with the life of individuals. These results will be used to inform stakeholders on the migration patterns and critical habitats used by the species to avoid overfishing and to guide the construction of the dams. Thus, this research will produce the knowledge necessary to develop new science-based fisheries policies to sustainably manage and conserve this catfish.

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9. Use of Pycnophylactic Interpolation to Determine the Number of Households in Redlined Districts in Roanoke City Virginia that Lack Complete Plumbing

Sterling, C.*[*1]*, *Pingel, T.[2], Winling, L.[3]*
[1] Department of Biological Systems Engineering, Virginia Tech; [2] Department of Geography, Virginia Tech; [3] Department of History, Virginia Tech

The US Home Owners's Loan Corporation (HOLC) implemented redlining in the 1930s with the ostensible purpose of assessing risks associated with extending loans. However, it evolved into de jure segregation as minority communities were more likely to be redlined and designated high risk. Examinations of patterns of health disparities suggest the impacts of redlining on minority communities are still apparent today. Although access to high quality household water is of increasing concern to many minority communities in the United States, no previous research has examined the impacts of redlining on water infrastructure development. Digitized HOLC maps available through the Mapping Inequality Project (University of Richmond) and historical Census Bureau data available from the University of Minnesota were compared to quantify the number of individuals lacking complete plumbing in redlined versus more highly rated neighborhoods. To account for the incongruent geographies of the two sets of data (i.e. Census blocks vs digitized HOLC neighborhood polygons) in ArcGIS Pro, pycnophylactic interpolation was explored as a strategy to estimate numbers for individuals in redlined districts. Initial results applying pycnophylactic interpolation to the City of Roanoke suggest that an average of 1.42 households in redlined areas lacked plumbing, An average of 0 households in greenlined neighborhoods lacked plumbing.There is potential for this method to be applied to 200+ cities to estimate households lacking plumbing in different neighborhoods for the Census years 1950-2010. Following national application, Geographically Weighted Regression can assess the relationship between redlined districts and number of persons lacking plumbing.

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10. Differences in Arthropod Communities Associated with Urbanization

IJ VanDiest*[*1]*, *SJ Lane[1] KB Sewall[1]*
[1]Virginia Tech Department of Biological Sciences

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Arthropod populations have declined rapidly in the last century and a half. A decrease in arthropods is concerning as they often occupy the lower trophic levels of ecosystems, and higher trophic level organisms depend upon them as a food source. Arthropod decline is often the result of land use change, but we know relatively little about how urbanization influences arthropod communities and the predators that depend upon them. A first step toward understanding the effects of urbanization on trophic cascades is to compare arthropod communities between urban and rural habitats. Therefore, we completed arthropod vacuum sampling transects across three urban and three rural long-term study sites on and near Virginia Tech and compared biomass, abundance (total and by order), relative abundance of eight orders, and community structure based on trophic level. We found our rural sites had higher arthropod biomass and abundance across the eight orders we targeted when compared to urban sites. Additionally, rural areas had higher relative abundance of orders that contain higher trophic level species, while urban areas had higher relative abundance of orders that typically are at lower trophic levels. Our rural areas also had a higher Simpson's diversity index compared to urban sites. These findings suggest that urbanization plays a significant role in structuring arthropod communities by reducing abundance, biomass, and diversity. Future work will study the consequences these findings have on individuals in higher trophic levels, namely avian predators.

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11. Linkages between water transit times and stream solute concentrations in forested headwater catchments

Weiglein, T.L.[1]*, *Strahm, B.D.[1], and McGuire, K.J.[1,2]*
[1] Department of Forest Resources and Environmental Conservation, Virginia Tech
[2] Virginia Water Resources Research Center

Forested headwater catchments (watersheds) are an important source of drinking water, providing an estimated 50% of total surface water yield in the conterminous U.S. Water quality in the streams draining these catchments is in part determined by the concentration of various solutes. As such, proper management of our drinking water resources requires an understanding of what controls stream solute concentrations in these forested headwater catchments. Previous work primarily conducted in agricultural catchments has shown that water transit times (how long it takes water to move through a watershed) have a major effect on solute concentrations. The extent to which a similar relationship exists in forested headwater catchments has been less extensively studied, especially for certain solutes such as nitrate. My dissertation research seeks to fill this knowledge gap by leveraging data from several forested catchments in the U.S. Ultimately, this work will improve our understanding of how forested headwater catchments function, allowing better management of our drinking water resources.

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12. Contrasting ecosystems along Panama's coasts reveal variation between phage communities

Alaina R. Weinheimer[1]*, *Jarrod J. Scott[2], Matthieu Leray[2], Frank O. Aylward[1,3]*
[1] Department of Biological Sciences, Virginia Tech, Blacksburg, VA, USA
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Dominating the seas, bacteriophages (viruses of bacteria) are critical components of marine ecosystems. Bacteriophage (phage) infections release roughly 25% of carbon in some regions of the ocean per day, preventing carbon from moving up the food chain or sinking to the bottom of the sea. Despite their significance, their evolution and drivers of their diversity remain open questions. The contrasting, tropical ecosystems of Panama's coasts present a unique opportunity to unravel both global and local factors shaping phage communities. The Isthmus of Panama closed just millions of years ago; the Western Atlantic ocean became nutrient-poor, while the Eastern Pacific ocean remained nutrient-rich. While the impacts of the isthmus formation has been explored for animals and plants, the impacts on marine viruses remain unknown. Here, we examine patterns in phage diversity between the Eastern Pacific (EP) and Western Atlantic (WA) coasts of Panama. We use metagenomes of seawater collected in mangroves and coral reefs on both coasts. Our analyses have revealed striking differences between the oceans, with less than 2.3% of phages present in both oceans. Locally, phage communities were more similar between mangroves and reefs in the WA than in the EP, potentially reflecting their close proximity in the WA versus their distance in the EP. Taken together, our work provides a foundational account of phage diversity along Panama's coasts, revealing candidate factors that shape phage community composition, as well as, providing a starting point to characterize the impact of bacteriophages on carbon cycling in marine ecosystems surrounding Panama.

POSTER PRESENTATIONS

Session 2

2:30 - 3:45 PM

13. How does stream connectivity drive carbon dynamics?

Bretz, Kristen A.*[1]*, Natalie Murphy*[2]*, B.R. Niederlehner*[1]*, and Erin R. Hotchkiss*[1]*
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[2] Department of Biochemistry, Virginia Tech

Intermittent streams are increasingly common in the southeastern US as dry periods become longer and more frequent. Stream intermittency disrupts carbon cycling and transport; however, we have few estimates of how the extent of surface water connectivity quantitatively affects carbon emissions and transport. We took high-frequency dissolved CO_2 sensor measurements from the outlet as we tracked surface water presence along the entire stream. CO_2 concentrations at the outlet increased as surface water connectivity decreased, from around 125 mmol m^{-3} when greater than 50% of the stream is surface connected to over 360 mmol m^{-3} when only 25-40% connected. We sampled monthly CO_2 and CH_4 concentrations in several persistent pools to assess if concentrations at the

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outlet were consistent with those of upstream surface water pockets as stream connectivity changed. Stream pool CO_2 and CH_4 were spatially and temporally heterogeneous. Upstream pool CO_2 was frequently lower and less variable, around 200 mmol m^{-3}, than at the outlet where concentrations were nearly 500 mmol m-3. CH_4 concentrations were boosted at more downstream pools when the stream was surface-disconnected (up to 1 mmol m^{-3} compared to less than 0.25 mmol m^{-3} when connected) while low and more stable in more upstream pools (always under 0.25 mmol m^{-3}) . Ongoing work will integrate stream dissolved organic matter and discharge measurements with dissolved CO_2 and CH_4 to better quantify the effects of stream intermittency on carbon transport and emissions.

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14. Drinking water contamination and associated health outcomes in rural Appalachia: A systematic review and meta-analysis

Darling, Amanda*[1,3], *Hannah Patton[2], Md Rasheduzzaman[3], Rachel Guevara[4], Joshua McCray[4], Elizabeth Rogawski McQuade[5] (TBC), Leigh-Anne Krometis[2], & Alasdair Cohen[1,3]*

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[3] Department of Population Health Sciences & the Public Health Program, Virginia Polytechnic Institute & State University (Virginia Tech), Blacksburg, VA, USA;
[4] Department of Natural Sciences, University of Virginia's College at Wise, Wise, VA;
[5]Rollins School of Public Health, Emory University, Atlanta, GA

Of the ~2 million Americans who still lack reliable access to safe drinking water, many live in low-income rural areas in Appalachia. Limited evidence suggests health-related impacts associated with contaminated water may be disproportionately common in Appalachia. Aside from some noteworthy media coverage of high-profile water contamination incidents in the region, data on the nature and extent of drinking water contamination in Appalachia is limited. We conducted a systematic review to comprehensively evaluate and synthesize published research findings on drinking water contamination and associated health outcomes in the Appalachian region. We pre-specified and pre-registered our study protocol, limiting eligibility to studies that collected primary data . We searched four databases to identify eligible papers (PubMed, EMBASE, Web of Science, and the Cochrane Library) published over a 20-year period from January 1, 2000 and December 31, 2019. We identified 3,452 records for screening; of these, 85 papers met our eligibility criteria and reported sufficient data for extraction. We calculated summary statistics of reported results for microbial and chemical parameters using sample size-based weights and conducted various sensitivity analyses, as well as risk of bias and meta-regression analyses. Of the five subregions in the Appalachian region, we identified only five eligible studies from Central Appalachia (6%). Only 32% of the eligible papers (n=27) specifically addressed health outcomes associated with exposures to contaminated drinking water sources. Frequently measured drinking water exposure outcomes included heavy metals and fecal indicator bacteria, while only a few studies used epidemiologic methods to assess associations between such exposures and health outcome data. Our results indicate that more epidemiologic-based research is needed to better understand the nature and extent of contaminated drinking water and associated health outcomes in rural regions of Appalachia, particularly in Central Appalachia.

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15. Plant attributes and soil organic carbon stabilization: getting to the root of it

Duston, Stephanie*[1]*, Brian Badgley[2], Brian Strahm[1], Jacob Barney[2], John Seiler[1], Rachel Reid[3]*
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[2] School of Plant and Environmental Sciences, Virginia Tech
[3] Department of Geosciences, Virginia Tech

Soil organic carbon (SOC) is a critical component in ecosystems, being involved in nutrient supply and cycling, water infiltration and holding capacity, aggregate stability, and enhancing microbial activity and biodiversity. Efforts to sequester carbon in soil to mitigate climate change or build carbon to improve soil health for management and reclamation are current areas of interest. Challenges arise when attempting to quantify belowground fluxes, residence times, and mechanisms of SOC stabilization and destabilization. This is due to the complex mixture of organic compounds in different stages of decomposition, which further vary due to differences in ecosystem function, plant habitat, macro and microfauna, and climate. The objective of this portion of my research was to evaluate ground cover crops and post-mining forest reclamation plant species in their capacity to build SOC and cultivate a microbial community with functional attributes consistent with long-term SOC stabilization. A diverse mix of 30 ground covers were grown in a greenhouse over a 10-week period and labeled with 13C (13 Carbon isotope) in order to: (i) quantify plant derived carbon in soil based on plant species, (ii) to characterize carbon distribution patterns in different revegetation choices in order to make inferences about the long-term fate of SOM, and (iii) characterize the microbial community that are recruited by different plants. I hypothesize that root traits (e.g. length, area, proportion of fine to coarse roots) are a key factor for determining the amount and distribution of carbon in soil. Also that belowground plant traits foster the development of different microbial communities which in turn affect stabilization of soil carbon associated with minerals.

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16. Cumulative Effects of Stream Restoration and Watershed Characteristics on Watershed-Scale Nitrate Removal

Goodman, L.M.*[1]*, Federman, C.[2], Scott, D.T.[1], Kruse Daniels, N.[3], Hester, E.T.[4]*
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[2]Dept. of Civil and Environmental Engineering, Virginia Tech
[3]George V. Voinovich School of Leadership and Public Service, Ohio University

Stream restoration is increasingly implemented as a solution for eutrophication, particularly in the Chesapeake Bay; however, the cumulative effects of stream restoration projects on watershed-scale nutrient removal is poorly understood. We developed a HEC-RAS model coupled with an auxiliary R script that simulates floodplain, hyporheic, and Stage 0 stream restoration projects within a generic 4th-order watershed in the Eastern US. We also performed a systematic literature review and data synthesis on the effects of different restoration practices and watershed-scale controlling factors on denitrification rates. Using a random forest statistical approach, preliminary results indicate that mean annual streamflow, nitrate concentration, hydrologic condition (i.e., baseflow or stormflow conditions), and stream order are influential variables for denitrification rates. Initial model results showed an 83% reduction in downstream nitrate loading under baseflow conditions when all streams within the watershed underwent hyporheic restoration. The relationship was exponential in 1st- and 2nd-order streams and linear in 3rd- and 4th-order streams, which indicates that restoration location within a watershed is important in determining its effect on nitrate removal. Preliminary findings from floodplain and Stage 0 models suggest that Stage 0 restorations lead to greater nitrate

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removal due to increased hydrologic connectivity even during small, sub-annual storm events. Our preliminary results also indicate that stream restoration can be an effective tool for nitrate removal, particularly when applied in low-order streams; however, its effectiveness relies on the location and type of restoration projects, percentage of watershed network restored, and watershed characteristics.

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17. Newt bacterial skin communities recover to natural composition after antibiotic exposure in the presence of environmental bacteria

Jones, *Korin R.*[*1], *Matthew H. Becker[1,2], Jenifer B. Walke[1,3], Lisa K. Belden[1]*
[1]Department of Biological Sciences, Virginia Tech, Blacksburg, VA, USA
[2]Department of Biology and Chemistry, Liberty University, Lynchburg, VA, USA
[3]Department of Biology, Eastern Washington University, Cheney, WA, USA
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Host associated microbial communities, also known as microbiomes, can influence their host in a variety of ways. Facets of microbiome function have been demonstrated across a variety of systems, however we still lack a complete understanding of the mechanisms behind the assembly and stability of these communities. Among the proposed factors influencing microbiome composition, environmental source pools appear to be of high importance. Understanding the importance of environmental source pools will continue to increase in importance as climate change and human impacts begin to shift the composition of environmental bacterial communities. Here, we evaluated the ability of the eastern newt skin microbiome to recover from an antibiotic disturbance in the presence of natural environmental bacteria. Wild-caught newts were repeatedly sampled in outdoor mesocosms over a 28 day period following antibiotic treatment. Our results show that the skin communities recovered within this period to a state similar to that of untreated newts based on taxa relative abundance, but not in terms of the presence/absence of taxa. In addition, despite similar relative abundances, total bacterial abundance remained lower in our antibiotic treated communities over the duration of the experiment. Microbes associated with the environment quickly colonized newt microbiomes immediately following antibiotic treatment, but these differences faded over the course of the experiment. Together these data highlight the ecological resilience of the newt skin microbiome and the influence of environmental source pools in microbiome recovery.

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18. Nitrate limitation in the early Neoproterozoic oceans delayed the rise of eukaryotes

***Kang, Junyao**[*1],* *Benjamin Gill [1], Rachel Reid [1], Feifei Zhang [2], Shuhai Xiao[1]*
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Connecting the “Boring Billion” and “Snowball Earth” events, the Tonian Period (1000–720 million years ago) marks a critical transition in Earth history. Recent paleobiological studies have shown that major eukaryotic evolutionary divergences and innovations occurred in the Tonian Period. Previous studies suggest that these events may have been driven by the transition from sulfidic (hydrogen-sulfide-rich and no-oxygen) to ferruginous (ferrous-iron-rich and no-oxygen) mid-depth seawaters during the Tonian, which possibly created more favorable environmental conditions for the

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diversification of eukaryotes. To improve our understanding of Tonian oceanic conditions, we carried out a systematic investigation of shallow-water carbonates of the Huaibei Group in North China. New rare earth element and iron geochemical data from the Huaibei carbonates suggest that ferruginous conditions possibly expanded into shallow waters, which would have had an impact on the major nutrients (nitrogen and phosphorus) cycles within the basin. It has been suggested that widespread ferruginous conditions may lead to phosphorus limitation in the ocean. In this study, we focus on the unexplored nitrogen cycle. Nitrogen isotope composition of carbonate samples ($\delta^{15}N_{bulk}$) from the Huaibei Group show relatively low $\delta^{15}N_{bulk}$ values (mean 2.27 ‰) throughout the entire Huaibei Group. Low $\delta^{15}N_{bulk}$ of the Huaibei Group is interpreted as evidence for significant removal of nitrate from ferruginous shallow seawaters, leading to an ammonia-dominant ecosystem, where prokaryotes can outcompete eukaryotes. Our study revealed a more complex early Tonian marine environment than the existing ferruginous-driven hypothesis. On the one hand, the transition to ferruginous seawaters removed toxic hydrogen sulfide. On the other hand, ferruginous conditions expanded into shallow waters, causing phosphorus and nitrate limitation. The new $\delta^{15}N_{bulk}$ data are further compiled with existing data to examine the evolution of the nitrogen cycle when eukaryotes started to diversify and then become ecological dominance. The compiled dataset indicates that nitrate availability increased around about 800 to 700 million years ago. We suggest that higher nitrate availability may have played an important role in facilitating eukaryote diversification in the late Tonian Period.

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19. Redundant or complementary? Identifying patterns of multifaceted frog and toad biodiversity in Virginia, USA

Moore, C.E.*[1]* *and Mims, M.C.*[1]
[1]Department of Biological Sciences, Virginia Tech

At its core, biodiversity describes variation among organisms. It is often quantified as species richness, with a high number of co-occurring species designating biodiversity 'hotspots'. However, other biodiversity facets, including life history and phylogenetic diversity, may occur parallel or independent to species richness. Considering multiple facets may be vital to understand the distribution of biodiversity's functional and adaptive components, particularly if they do not co-occur. We characterized spatial patterns and environmental drivers of species richness, life history diversity, and phylogenetic diversity of anurans (frogs and toads) in Virginia, United States. We built species distribution models (SDMs) to estimate the range of the 27 native anurans using publically available occurrence and environmental data. The predicted ranges were used to determine species' presence within HydroBASIN level 12 watersheds (~130 km^2). We quantified species richness by summing present species in all watersheds. Life history and phylogenetic diversity were quantified as the functional dispersion and mean pairwise distance, respectively, of present species. Finally, we compared spatial patterns among and potential drivers of biodiversity facets to quantify regional redundancy and complementarity. Life history and phylogenetic diversity were most correlated, whereas species richness and life history diversity had no significant correlation. Richness increased with latitude, but life history and phylogenetic diversity showed no latitudinal or longitudinal trends. The evidence suggests complementarity in metrics and highlights the importance of considering multiple facets when quantifying anuran diversity. Measuring multifaceted biodiversity improves our understanding of why anurans occur where they do and can help inform comprehensive and multidimensional conservation.

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20. Landowner Perspectives on Allowing Private Lands Research

***O'Brien, Rebecca*[*1]**, *Ashley Dayer[1], and Bill Hopkins[1]*
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Over half the landmass of the United States is privately owned and gaining access to these lands can be difficult. In this study, we sought to better understand why landowners allow access to their property through a study of landowners in the Copper Creek watershed in Southwest Virginia. Using both a mail survey (n=231) and in-person interviews (n=37), we measured a suite of landowner attitudes, beliefs, and behaviors and assessed how well these traits predicted landowner willingness to allow research on their property. Our results suggest that landowners are more likely to consider allowing research if they are interested in learning about the research taking place on their property and if they have positive attitudes towards conservation. In contrast, concerns about participation leading to restrictions on free use of their property is a strong predictor of landowners declining to consider participation. From our follow-up interviews, we also found that landowners who agree to participate in research have a strong sense of place, and are encouraged to participate by both social and personal norms. This insight can be used to inform landowner contacts and tailor landowner engagement in conservation research projects.

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21. Patterns of Genetic Structure in Freshwater Invertebrates are Scaled by Biological and Geographic Drivers

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[3]School of Natural Resources and the Environment, University of Arizona, Tucson, AZ, USA
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Molecular tools allow for investigations of genetic structure and diversity of populations, offering insights into ecological and evolutionary processes in freshwater ecosystems and beyond. Yet, the spatial scale at which population genetic structure emerges may vary among species, as do the biological factors that influence it. This leads to the question: What is the scale at which population genetic structure is detected in streams, and how is it influenced by species traits? To answer this question, we used a systematic literature search to identify microsatellite genetic datasets for aquatic invertebrates. From this pool of relevant studies (N = 48) and controlling for stream network topology and sampling design, we determined the minimum geographic distance at which genetic structure emerges for each taxa per study using a standardized measure of differentiation comparable among taxa (F_{ST}'). We then evaluated correlations between species traits and F_{ST}' in a multivariate framework. Preliminary results suggest that traits related to organism dispersal (both mode and strength) and drift are strong predictors of the scale at which genetic structure emerges. Identifying the scales at which genetic structure is detectable can help design effective genetic studies and can provide baseline knowledge required to understand how biological and spatial factors interact to structure genetic diversity among diverse organisms.

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22. Mosquito Sugar-Feeding: Using DNA Barcoding to Determine Mosquito Plant Diet

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Mosquitoes are the deadliest animals on Earth due to the numerous pathogens they transmit to humans. While most of the research effort is concentrated on mosquito-host interactions, an essential part of their biology is often neglected: sugar feeding. Sugar feeding is vital for a mosquito's biology, affecting life longevity, metabolic activity, and reproductive success. Understanding more about this crucial process can contribute to the development of novel vector control strategies and mitigate the spread of mosquito disease. Knowing the plant species that mosquitoes are attracted to and feed on can be used to create and optimize effective baits and traps. Using a plant DNA barcoding technique, we extracted plant DNA from the guts of mosquitoes that were captured from trap sites in the residential Blacksburg area. Using PCR and Sanger sequencing, we then identified several plant species as potential plant hosts for local mosquito species. Using these results, candidate host plants can be screened for mosquito attraction and used for bait development and population control.

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23. Data frequency affects water temperature forecast skill in a eutrophic reservoir

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Freshwater lakes and reservoirs are increasingly susceptible to global change. Both anthropogenic and climate-induced changes have resulted in increased frequency of algal blooms, and decreasing dissolved oxygen concentrations in deeper waters. Additionally, nutrient inputs to waterbodies via agricultural and land use practice results in increased algae growth. As algae die and sink, decomposition results in low oxygen concentrations in the bottom waters of waterbodies. Given the importance of oxygen for many freshwater ecological processes, predicting conditions that would favor algal bloom formation, such as short-term changes in water temperature, can aid in understanding the role that climate change has on waterbodies. We used in-situ sensors, manually collected data, and a calibrated water quality ecosystem model to generate water temperature forecasts using FLARE (Forecasting Lake And Reservoir Ecosystems), an open-source forecasting system. We tested the effect of data collection frequency (daily, weekly, fortnightly and monthly) used to forecast water temperature 35-days ahead throughout the year. We found that forecast skill, calculated as the difference between observed and forecasted water temperature, is variable depending on season and data assimilation frequency. However, we found little difference between forecast skill between daily and weekly assimilation aggregated across seasons. Compared to daily and weekly data assimilation, fortnightly and monthly assimilation resulted in lower forecast skill across seasons. Forecasts are useful tools for understanding how freshwater ecosystems respond to short-term weather events, therefore, improving forecast skill is integral for managing and preserving waterbodies in a changing climate.

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