Faculty Mentors, Project Titles, and Descriptions
Department of Biology
Fall Research Semester

Students: What to do?

1. Review the list of projects below
2. Identify at least 3 projects that you would be interested in participating in.
3. Fill out the Research Semester application form
4. Submit this application along with the required supplemental information by the end of March.

Faculty Mentor	Title of Project	Contact Information
Ahn, Changwoo Professor Department of Environmental Science and Policy	**The Dirt Project**	Changwoo Ahn cahn@gmu.edu
Ascoli, Giorgio Professor, Molecular Neuroscience, Volgenau School of Engineering	**Hippocampome Project** **NeuroMorpho.Org**	Giorgio Ascoli ascoli@gmu.edu http://krasnow1.gmu.edu/cn3/ascoli/
Baranova, Ancha Professor, School of Systems Biology; Director, Study of Chronic Metabolic Diseases	**Molecular Pathways Involved in the Pathogenesis of Non-Alcoholic Fatty Liver Disease and Other Obesity Related Pathologies** **Clinical Data Analysis in Metabolic Disease** **Metabolomics of chronic diseases**	Ancha Baranova abaranov@gmu.edu Hospital on Gallows Road
Blackwell, Kim L. (Avrama) Professor, Molecular Neuroscience, Volgenau School of Engineering	**Signaling Pathways Involved in Striatal Synaptic Plasticity**	Avrama Blackwell kblackw1@gmu.edu
Chiari, Ylenia, Assistant Professor, Department of Biology	**Conservation genetics of Kemp's ridley sea turtle** **Sensorial ecology and evolution of coloration in geckos** **Shell shape variation within and among species of Galapagos tortoises**	Ylenia Chiari ychairi@gmu.edu

Crerar, Lorelei Assistant Professor, Department of Biology	**Ancient DNA Analysis and Sirenian Phylogeny**	Lorelei Crerar lcrerar@gmu.edu
De Mutsert, Kim Assistant Professor, Environmental Science & Policy	**Using eDNA to help determine river herring spawning population size**	Kim de Mutsert kdemutse@gmu.edu
Forkner, Rebecca Associate Professor, Department of Biology	**Bumblebee epidemiology – Pathogens and flower use in declining pollinator species** **Insect Driven Changes in Autumn Phenology**	Rebecca Forkner rforkner@gmu.edu
Fowler, Amy Assistant Professor, Environmental Science and Policy	**Impacts of Salinity on invertebrate and vertebrate community composition in the Potomac River, VA**	Amy Fowler Afowler6@gmu.edu
Frankenfeld, Cara Assistant Professor, Global & Community Health, College of Health & Human Services	**Nutrition and Environmental Risk Factors for Human Health Conditions**	Cara Frankenfeld cfranken@gmu.edu
Freeman, Elizabeth **Associate Professor** **School of Integrative studies**	**Coming soon** **https://integrative.gmu.edu/people/efreeman** **Wildlife conservation, behavioral endocrinology, behavioral ecology**	Elizabeth Freeman efreeman@gmu.edu
Gallo, Sina Assistant Professor, Department of Nutrition and Food Studies	**https://chhs.gmu.edu/profile/view/6780**	Sina Gallo sgallo2@gmu.edu
Gillevet, Patrick Professor, Department of Biology Director, MicroBiome Analysis Center	**Metabiome of Human Disease** **Microbial Ecology of Environmental Disease** **Phylogenomics and Population Genetics**	Patrick Gillevet pgilleve@gmu.edu
Glaberman, Scott Associate Professor, Environmental Science & Policy	**Coming soon**	Scott Glaberman sglaberm@gmu.edu
Grant, Geraldine M. Associate Professor, Department of Biology	**Mechanisms of Idiopathic Pulmonary Fibrosis**	Geraldine M Grant ggrant1@gmu.edu
Hakami, Ramin Associate Professor, School of Systems Biology	**Exosome-mediated intercellular communication during bacterial infections.** **Host signaling during infection with biodefense bacterial agents.**	Ramin Hakami rhakami@gmu.edu

Hoemann, Caroline Professor Bioengineering	**Coming soon** **https://bioengineering.gmu.edu/profile/view/443811**	Caroline Hoemann choemann@gmu.edu
Jones, R.C. Professor, Department of Environmental Science and Policy	**Water Quality and Aquatic Ecology in The Tidal Potomac River and its Local Tributaries**	R Christian Jones rcjones@gmu.edu
Kabbani, Nadine Associate Professor, School of Systems Biology	**Axon Growth and Regeneration in the Brain**	Nadine Kabbani nkabbani@gmu.edu
Kehn-Hall, Kylene Associate Professor, National Center for Biodefense & Infectious Diseases, School of Systems Biology	**Novel Therapeutics for Viral Infections** **Altered Signaling Pathways in Virally Infected Cells**	Kylene Kehn-Hall kkehnhal@gmu.edu
Lim, HC Assistant Professor Department of Biology	**Analysis of gut metagenomic sequences of a primarily herbivorous waterfowl** **Genomic study of tropical birds**	Haw Chuan Lim hlim22@gmu.edu
Luther, David Associate Professor, Department of Biology	**The Evolution of Acoustic Competition in Songbirds** **Assessing the effectiveness of conservation actions for endangered species**	David Luther dluther@gmu.edu
Dr Claudius Mueller Research Assistant Professor SSB	**Deciphering the communication between tumor cells and sub-populations**	Claudius Mueller cmuelle1@gmu.edu
Olmo, Valerie Assistant Professor, Department of Biology	**Environmental factors and vertebrate development**	Valerie Olmo volmo@gmu.edu
Paige, Mikell Associate Professor, Department of Chemistry & Biochemistry	**Targeting the Leukotriene A4 Hydrolase Enzyme for the Treatment of Emphysema.** **Targeting IL-1B:IL-1RAcP:IL-1R1 Complex for Treating Osteoarthritis and other Inflammatory Diseases** **Design and Synthesis of Inhibitors of Metabolic Targets for the Treatment of Lung Cancer**	Mikell Paige mpaige3@gmu.edu
Peters, Esther Associate Professor, Department of Environmental Science and Policy	**Using Histology to Understand Interactions between Organisms and the Environment**	Esther Peters epeters2@gmu.edu
Pollack, Anna Assistant Professor, Global & Community Health	**Environmental Chemical Exposure and Women's Health**	Anna Pollack apollac2@gmu.edu

Van der Ham, Joris Assistant Professor, Environmental Science and Policy	**Ecology of Carrion Insects**	Joris Van der Ham jvanderh@gmu.edu
van Hoek, Monique Professor, School of Systems Biology	**Antimicrobial Peptides** **Novel Antibiotics**	Monique Van Hoek mvanhoek@gmu.edu
Von Fricken, Michael Assistant Professor Department of Global and Community Health	**Systematic Review on Risk of Zoonotic Disease Transmission from Rodents on Zoo Grounds** **Collect and analyze Ixodes scapularis ticks for Lyme disease in low elevation settings along the Appalachian Trail in Virginia**	Michael Von Fricken mvonfric@gmu.edu
Wu, Yuntao Professor, School of Systems Biology	**Screening for anti-HIV activity using an HIV-Rev dependent reporter cell** **Screening anti-HIV activity from small-molecule inhibitors targeting cellular signaling pathways.**	Yuntao Wu ywu8@gmu.edu
Quest Diagnostics Chantilly	**https://biology.gmu.edu/research/fall-research-semester/**	**Contact Dr. Grant at ggrant1@gmu.edu**
Smithsonian Conservation Institute – Front Royal VA.	**https://smconservation.gmu.edu/** GEORGE MASON UNIVERSITY WHERE INNOVATION IS TRADITION — Smithsonian — Smithsonian-Mason School of Conservation	**Contact Dr. Grant at ggrant1@gmu.edu**
ATCC American Type Tissue Culture Collection	**https://www.atcc.org/**	**Contact Dr. Grant at ggrant1@gmu.edu**
IUCN International Union for conservation of nature	**https://www.iucn.org/regions/washington-dc-office/our-work/biodiversity-assessment-unit** **DC Office https://www.iucn.org/regions/washington-dc-office/our-work** **Projects** **An update to the knowledge of Mexican reptile diversity.** **An update to the knowledge of Mediterranean reptile diversity.** **Beginnings of a consolidated global checklist of reptile species.** **Collation of information on the reptile species of Central Africa.** **A modern checklist of Central American freshwater fishes.** **A modern checklist of Central American freshwater mollusks and dragonflies.** **A provisional checklist of the freshwater mollusks of South America.**	**Contact Dr. Grant at ggrant1@gmu.edu**

Description of Potential Projects
Department of Biology
Fall Research Semester

Dr Changwoo Ahn
Professor
Department of Environmental Science and Policy

The Dirt Project

The goal of the project is to collect, research, and thus create a suite of bibliography of literature and media resources for an interdisciplinary education on "**soil (dirt)**", focusing on urban soil ecology, combined with scientific investigation of soil color changes that would visually signify and trace the impacts of hydrologic, ecological, and cultural processes as affected by urbanization and climate change.

Dr Giorgio Ascoli
Professor
Molecular Neuroscience, Volgenau School of Engineering

The Hippocampome Project

In the same vein as a genome, the Hippocampome is envisioned as the ultimate knowledge base describing the structure, activity, and function of the hippocampus, the brain region responsible for processing conscious autobiographic memories and plans. The foundation of this project is a catalogue of the many classes of neurons found in the hippocampus and the wiring diagram that interconnects all of them. The descriptions of these classes are distilled from data published in peer-reviewed journals. Compiling and collating all of this knowledge into a single computerized resource will uncover new correlations and interrelations that will help discover the cellular mechanisms of hippocampal function and dysfunction. The student will learn to identify dendritic and axonal morphologies, microscopy techniques for their visualization, how they relate to the surrounding nervous tissue, and their effect on neuronal activity and network function. See also http://hippocampome.org and http://krasnow1.gmu.edu/cn3

NeuroMorpho.Org

NeuroMorpho.Org is a central, one-of-a-kind online neuroscience resource that provides free worldwide access to 3D digital reconstructions of neurons. Neurons are traced from microscopy imaging in many types of research laboratories, from the study of pharmacology to that of development. These same data can be reanalyzed for additional discoveries, including computational models of brain function. Data are deposited in NeuroMorpho.Org from various species ranging from flies, to rats, to humans, to elephants. Millions of neurons have been downloaded in more than 100 countries. NeuroMorpho.Org is a leading project in the emerging trend of data sharing in the neuroscience community that aims to maximize the research potential of collected data. The student will learn to identify dendritic and axonal morphologies, microscopy techniques for their visualization, how they relate to the surrounding nervous tissue, and their effect on neuronal activity and network function. See also http://NeuroMorpho.Org

Dr Ancha Baranova
Associate Professor
School of Systems Biology
Director, Study of Chronic Metabolic Diseases

Molecular Pathways Involved in the Pathogenesis of Non-Alcoholic Fatty Liver Disease and Other Obesity Related Pathologies

Obesity is the abnormal or excessive increase in adiposity. Lately, obesity has got attention as the state of low grade chronic inflammation characterized by both macrophage infiltration of AT and increased production of pro-inflammatory cytokines that play a role in insulin resistance (IR). Non-alcoholic fatty liver disease (NAFLD) is a common disease that comprises a morphological spectrum of liver pathologies ranging from simple triglyceride accumulation in hepatocytes (fatty liver or hepatic steatosis) to inflammatory conditions (non-alcoholic steatohepatitis; NASH), eventually leading to fibrosis and cirrhosis.

The major goals of the proposed studies are designed to provide novel insight into the molecular mechanisms by which adipose tissue of obese individuals promotes the development of secondary complication of obesity.

Techniques: ELISA assays, Bio-Plex assays, qRT-PCR, Cell culture

1. Clinical Data Analysis in Metabolic Disease

This is a joint project with Dr. Alan T. Remaley at the National Institutes of Health (NIH) and PhD Bioinformatics student Tiange Cui.

Cholesterol is transported in blood by different classes of lipoproteins, which differ in their association with cardiovascular disease (CVD). Cholesterol on low density lipoproteins (LDL) is positively associated with CVD because when in excess it is deposited in the vessel wall where it causes atherosclerosis. In contrast, cholesterol on high density lipoproteins HDL is inversely related to CVD because is believed that HDL promotes the removal of excess cholesterol from peripheral tissues and delivers it to the liver for excretion. By monitoring theNMR signal from the terminal methyl group one can determine both the quantity and size of the different major and minor classes of lipoproteins and provides the most detailed analysis of lipoproteins. We are looking for students who are interested in using the latest tools in cluster analysis and other related techniques to develop a classification system of lipoprotein phenotypes to determine whether it can be used for assessing cardiovascular risk. Data from 5000 participants in the Multi Ethnic Study of Atherosclerosis will be used for the analysis. Students in this project will gain experience in complex data analysis from large data sets and will the basics of lipoprotein metabolism

and the pathogenesis of atherosclerosis and the use of cardiovascular biomarkers. A general understanding of basic statistics will be required.

Metabolomics of chronic diseases

Dr. Baranova and Dr. Chandhoke (School of Systems Biology)

Non-alcoholic fatty liver disease (NAFLD) is a consequence of sedentary life style and high fat diets with an estimated prevalence of about 30% in western countries. It is associated with insulin resistance, obesity, glucose intolerance and drug toxicity. Several studies have already investigated later stages of the disease, including NASH. The cumulative alterations in bile acids, BCAA metabolite and amino acid metabolism gene profiles represent either contributing factors to the development of NASH adaptive physiological response to disease-induced hepatic stress in NASH patients. In addition, a number of other metabolite studies were performed but not yet reviewed systematically. In course of this project, the students will collate the literature and write a comprehensive review of the findings in metabolome studies performed in patients with NAFLD and NASH as well as collecting the compendium of the techniques used for metabolome profiling. The review that is to be written will include both studies of NAFLD/NASH associated changes in human metabolome along with relevant metabolic observations made in animal models of NAFLD/NASH.

Student will also learn use of coulometric array detection coupled with HPLC (CoulArray® HPLC) instrumentation and perform analysis of metabolites in a set of serum samples collected from patients with various metabolic conditions, including NAFLD and cancer (this work is to be performed both at Inova and at PW campus)

Dr. Avrama Blackwell
Professor
Molecular Neuroscience, Volgenau School of Engineering

Signaling Pathways Involved in Striatal Synaptic Plasticity

The striatum is a brain structure that governs habit and skill learning. In addition, Parkinson's Disease and Huntington's Disease are neurodegenerative diseases that involve the striatum. Habit learning involves plasticity of excitatory synaptic inputs from the cerebral cortex, which occurs when cortical inputs are followed by dopamine inputs. In contrast, Parkinson's disease is caused by degeneration of the dopamine neurons. We are studying the cellular and subcellular mechanisms that produce dopamine-dependent plasticity and learning.

"The project involves the creation and simulation of single neuron and network models. The student will learn python programming, how experimental design applies to computer simulations. Knowledge of calculus and computer programming is recommended."

Dr Ylenia Chiari
Assistant Professor
Department of Biology

Conservation genetics of Kemp's ridley sea turtle

Sea turtles have experienced population declines due to the effects of various human influences. *Lepidochelys kempii* (Kemp's ridley sea turtle) is considered one of the most endangered sea turtle species due to 95% of nesting occurring at only one beach in Mexico and a dramatic population decline due to heavy poaching of nests. Although population size has bounced back from this decline and numerous conservation efforts have been made to protect nests in Mexico and head start hatchlings at beaches in Texas, this species is still considered critically endangered. Major conservation questions that remain include the long term impacts of the population bottleneck, the contribution of each nesting beach to the adult stock of individuals, and the unknown migratory routes of juveniles born outside the main nesting beach in Mexico. This project focuses on using genetic method to address some of these questions. The student working on this project will learn how to extract DNA from different tissue samples, amplify genetic markers, and analyze the obtained genetic and population data. Project for one student.

Sensorial ecology and evolution of coloration in geckos

The diversity of color patterns and their ease of observation have made this trait a popular subject for evolutionary biology studies. Across-species associations between color patterning and ecological and behavioral traits have allowed inferences and predictions to be made about the functions of coloration in different organisms. These include antipredator functions, interspecific signaling functions, mate attraction, to support discrimination between potential mates and rivals, assist in thermoregulation, protect from ultraviolet radiation, and support immune function. To study the function of coloration in different body parts across different species of geckos, we integrate the computational analysis of large datasets (phylogenetic and ecological comparative analyses) with behavioral data collected on geckos kept in captivity. Students involved in this general project may be involved in an exclusively computer based projects for which they will learn how to search the literature, build database and run comparative analyses or may be involved in behavioral projects to study how geckos respond to different visual and olfactory stimuli. Project for at least two students.

Shell shape variation within and among species of Galapagos tortoises

Adult Galapagos tortoises possess two main shell morphologies – saddleback and domed. Domed shells are cupula-like structures while saddleback have a higher anterior opening and are relatively smaller in size and more compressed on the side than domed shells. Although within the same species shell shape varies largely – including large variation between males and females – each species of Galapagos tortoise is either domed or saddleback. The different shell shapes have been proposed to be adaptive, although it

is currently not clear for which specific function or habitats these shells are adapted. Historically, variation in shell shape has been used to define the taxonomy of Galapagos tortoises, but genetic data have revealed a more complex evolutionary history in these organisms, with similar shell shapes having evolved independently many times.

We have developed and applied a method to reconstruct the shell shape of Galapagos tortoises in 3D from digital images. We have a very large dataset of digital images belonging to numerous individuals of both existing and extinct species of Galapagos tortoises. For this project, students will learn how to reconstruct shells of Galapagos tortoises in 3D from already available digital images. Morphological data (3D coordinates) obtained from these reconstructions will be used to address questions aiming at resolving the taxonomy of tortoises living on one of the Galapagos islands (San Cristobal) and to address questions related to the adaptive evolution in shell shape variation among species of Galapagos tortoises. Students will learn how to use 3D reconstruction software and to run statistical analyses in R. Project for one student.

Dr Lorelei Crerar
Assistant Professor
Department of Biology

Ancient DNA Analysis and Sirenian Phylogeny

The student will work with a graduate student in the testing and development of protocols used to extract and sequence ancient DNA. The student will carryout research, compile results of BLAST phylogeny and help to produce a scientific paper that will be published in the literature. The student will become familiar with the use of laboratory equipment needed for DNA extraction (micropipettes, centrifuge, rocking water bath) as well as the use of the PCR machine. The student will also work to locate grant monies suitable for this project.

Student Learning Objectives:

The student intends to learn how to extract DNA from bone samples both ancient and modern. The student will work with PCR techniques to amplify DNA and finally with a capillary sequencer in order to obtain sequence for ancient DNA. The student will also participate in a project to determine the relatedness of extant manatees, dugongs and Steller's sea cows. Using DNA sequences that have been submitted to the NIH, the student will work with his mentor in order to develop phylogenetic trees relating manatees and dugongs. The aim of this project is publication in a scientific journal.

Dr Kim De Mutsert
Assistant Professor
Department of Environmental Science & Policy

Using eDNA to help determine river herring spawning population size

The use of environmental DNA is an exciting new area of research, where a water sample can be used to detect the presence of fish species in the water. Methods have recently been developed to detect two overfished anadromous fishes: Alewife and Blueback Herring. In collaboration with the Smithsonian Environmental Research Center and Horn Point Laboratory, this project will aid in developing a method to estimate abundance (rather than just presence) of Blueback Herring and Alewife with eDNA, by analyzing the eDNA of water samples from creeks where the abundance of the species is determined using net collections.

Dr Theodore Dumas
Associate Professor
Molecular Neuroscience, Psychology

Pharmacological Ignition of Hippocampal Function in Juvenile Rats

Episodic memories are memories of one's personal experience. The hippocampus is the primary brain structure involved in forming episodic memories. How hippocampal neurons operate to encode episodic memories is presently unclear, but appears to involve activity-dependent functional alterations at synapses, the communication points between neurons. Interestingly, episodic memories are not formed until late in the postnatal period across mammalian species, suggesting delayed development of the hippocampus. As such, the developmental emergence of episodic memory presents a valuable model for understanding the neuronal properties that are critical for memory formation. We have found that excitatory synapses in the rat hippocampus are weak in their ability to activate postsynaptic neurons until the end of the third postntatal week. This is the same age at which hippocampal-dependent learning and memory abilities are first observed in this species, suggesting that insufficient synaptic excitation limits memory formation or retrieval. Drugs that cause excitatory synaptic responses to last longer also increase postsynaptic activation in juvenile rats. We have delivered the same drugs to behaving animals and examined their ability to learn hippocampal-dependent maze tasks. We have preliminary evidence that suggests that prolonging excitatory synaptic responses improves memory in juveniles. Current experiments test the impact of prolonged synaptic excitation on synaptic plasticity and network activity patterns during maze exploration.

Synaptic and Cognitive Development in NMDA Receptor Chimeric Mice

Neural network development and information processing in the brain both require synaptic plasticity. As circuits in the mammalian forebrain mature, synaptic plasticity is adjusted to better suit information processing. Disruption of this process has been implicated in various neurodevelopmental disorders, including autism spectrum disorders. In the rodent hippocampus, this transition happens late in postnatal development, culminating in the emergence of hippocampal-dependent learning and memory abilities at the end of the third postnatal week. This research aims to explore the molecular determinants of the developmental alterations in synaptic plasticity and emergence of cognitive abilities. Forebrain glutamatergic N-methyl-D-aspartate receptors (NMDARs) exist primarily as quatramers with two NR1 and two NR2 subunits. Auxiliary NR2 subunits regulate numerous facets of receptor function. Conductance regulating domains exist in the extracellular amino and transmembrane regions while synaptic targeting and intracellular signaling domains exist in the intracellular carboxy terminus. At hippocampal Schaffer collateral (SC-CA1) synapses, NMDARs contain predominantly NR2B subunits during early postnatal development and NR2A subunits after the end of the third postnatal week. As such, the developmental NR2 subunit switch produces numerous changes in NMDAR function. Interestingly,

the shift in NMDAR composition parallels developmental changes in the ability to induce activity-dependent synaptic plasticity and completion of the shift marks the onset of adult-like spatial navigation. We have generated transgenic mice that express NMDARs with chimeric NR2 subunits at SC-CA1 synapses, which allows for separation of the NR2-dependent conductance and intracellular signaling properties. We are currently conducting research the molecular, physiological, and behavioral level to better understand which NMDAR properties are most closely related to the age-related changes in synaptic plasticity and in learning and memory abilities

Dr Rebecca E Forkner
Associate Professor
Department of Biology

Bumblebee epidemiology – Pathogens and flower use in declining pollinator species

North American bumble bees are declining or found in significantly reduced portions of their former ranges across the United States. The fungal, gut parasite *Nosema* is thought to be the cause of this pollinator crisis. This project seeks to answer several open questions regarding the epidemiology of this dysenteric disease to establish how it is maintained and transmitted among bumble bees (*Bombus*) in the wild. This project will identify sources of infection – both of new and sustained infections – of *Nosema*, in bumble bees. Specifically, we wish to 1) verify if queens are primarily responsible for maintenance and transmission of the disease to new colonies across seasons, 2) establish if there are consistent species differences in infection rates, 3) identify environmental sources of *Nosema*, such as floral resources (nectar and pollen), soil (nest locations), or other plant material (nesting material, including plant leaves and stems), 4) investigate species-specific factors that may be related to differences in infection rates (e.g. gut microbiome, flower handling time, host plant preferences), 5) determine if floral resources that are shared among bumble bee species or between bumble bees and honey bees may facilitate transmission of *Nosema,* 6) identify the degree to which specific flowers may act as reservoirs or sources of infection due to differences in floral morphology (e.g., presence of corollas), and 7) ascertain if specific geographic locations persistently have infected *Bombus* colonies, and if so, what biotic factors characterize those locations (e.g. presence of specific floral resources, plant communities, or other pollinators).

This project involves laboratory DNA and genomic analyses. The student researcher would be responsible for processing queen, worker, and male bumble bees in the lab (identification, sterilization, dissection), extracting bee, bacterial, and parasite DNA, and conducting PCR and phase contrast microscopic analysis of parasite infection. In addition, the student will learn to create pollen reference collections and determine host plant use by different bumble bee castes. The student would also have the opportunity to assist graduate students in the field in collecting bumble bee workers and queens, or to learn genomic techniques for the analysis of bacterial communities.

Insect Driven Changes in Autumn Phenology

Changes in climate in the Northern Hemisphere have impacted the timing of both spring and autumn. This project investigates the role that leaf-feeding insects play in the colors we see in deciduous tree leaves in autumn. In particular, the research will test the idea that insect damage can either advance or delay the timing of leaf loss under certain conditions and can alter expression of anthocyanins, the compounds responsible for orange, red, and purple leaf colors. The research challenges two traditional beliefs about autumn foliage color: that the timing and degree of autumn coloration can be predicted exclusively from the temperature, moisture, and day length conditions experienced by trees and that the

visible colors we enjoy are simply byproducts of senescence. By examining a suite of deciduous trees common to eastern North America, this study will contrast how trees that express anthocyanins compare to yellow-colored autumn trees, which contain carotenoids as their primary pigment, when leaves are damaged.

This project involves significant outdoor field work, including planting and monitoring saplings. Students would be responsible for measuring chlorophyll and anthocyanin concentrations, insect damage, leaf loss, and color production for four species of tree saplings. Students would assist the professor at the State Arboretum in Boyce, VA one full day each week, and would also accompany the professor to the Shenandoah National Park during leaf fall in October. Students would also have the opportunity to learn chemical assay techniques for the assessment of anthocyanin concentrations.

Effect of climate change on wing coloration in butterflies

Temperature variation can alter wing morphology in butterflies through a variety of mechanisms, including the induction of cold-shock (CSH) or summer-morph-producing (SMPH) hormones. Such temperature-induced changes underlie the seasonal wing shape variation seen in some tropical Nymphalid butterflies, such as *Junonia almana* (Figure 1). Although these changes have been well studied in tropical butterflies, they have been overlooked in temperate species with the exception of recent genomic studies of painted ladies, *Vanessa cardui.*

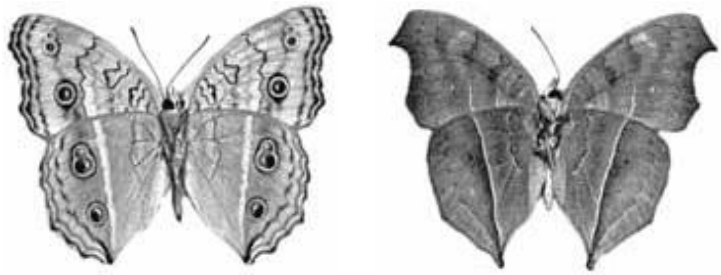

Figure 1. Ventral wing color and margin shape of *Junonia almana* in wet (left) and dry (right) season.

Predictions of future climate models suggest that temperatures will show more extreme fluctuations at higher latitudes, such as areas in Northern Virginia, potentially exposing butterflies in those areas to cold shock during overwintering periods or extreme heat during summer development. To determine if predicted temperature variation is great enough to generate changes in wing morphology, this project simulates different levels of variation in overwintering and pupal development temperatures in order to compare effects of climate change for temperate species that display phenotypic variation in wing color.

This project involves a large amount of laboratory and computer work. The student will be responsible for rearing caterpillars and pupae under different climate regimes that simulate future variation in

winter and spring/summer temperatures at different latitudes and estimating corresponding changes in butterfly wing size and coloration using imaging software. Species investigated will include *Vanessa cardui* (Painted Lady) and *Pieris rapae* (Cabbage White). Experiments may also involve exposing butterfly larvae and pupae to environmental contaminants

Dr Amy Fowler
Assistant Professor
Department of Environmental Science and Policy

Impacts of salinity on invertebrate and vertebrate community composition in the Potomac River, VA

Abstract: The composition of aquatic invertebrate and vertebrate communities is inexplicitly tied to salinity, especially in tidal regions. Salinity stress can impact community dynamics directly or indirectly through competition, predation, and parasitism. One particularly interesting community interaction that we will be investigating in the Potomac River, VA is that of an introduced barnacle parasite (*Loxothylacus panopaei*) and its mud crab hosts (*Rhithropanopeus harrisii* and *Eurypanopeus depressus*). *L. panopaei* was introduced via the oyster aquaculture trade from the Gulf of Mexico to the Chesapeake Bay in the 1960s, where it continues to infect up to 90% of local mud crab populations. While *R. harrisii* can exploit low salinities (down to 1ppt), the parasitic barnacles cannot survive well at sustained salinities below 10ppt. Therefore, it is possible that a low salinity refuge exists for *R. harrisii*. For our study, we will determine the community composition of invertebrates and vertebrates along a salinity gradient (0 – 20ppt) in the Potomac River, paying particular attention to the *L. panopaei* and *R. harrisii* interaction. Using these field data, we will examine how salinity mediates the physiological (i.e., heart rate, respiratory rate, morphological changes) and behavioral impacts (e.g., cleaning the parasite, interactions with predators) of *L. panopaei* on *R. harrisii*. These data will provide useful insight into how aquatic invertebrate communities change along a salinity gradient and how salinity can impact an interesting host – parasite interaction.

Dr Cara Frankenfeld
Assistant Professor
Global & Community Health, College of Health & Human Services

Nutrition and Environmental Risk Factors for Human Health Conditions

Epidemiology is the study of the distribution and determinants of disease frequency in human populations and the application of this study to control health problems. Student/s will analyze existing human data to evaluate nutritional and environmental risk factors, including phytoestrogens, environmental toxins, or geographic location. Work may involve analyzing nutrient intake from dietary records, evaluating dietary and environmental biomarkers from existing data, or comparing different methodologies. Specific diseases and health conditions that student/s may evaluate include obesity, metabolic syndrome, or other chronic health conditions. Student/s will integrate biology knowledge with the application of epidemiological and biostatistical concepts.

Dr Sina Gallo
Assistant Professor
Department of Nutrition and Food Studies
College of Health and Human Services

Website:

http://chhs.gmu.edu/faculty-and-staff/gallo.cfm?_ga=1.7964530.1543996254.1477596264

Dr Patrick Gillevet
Professor
Department of Biology
Director, MicroBiome Analysis Center

Metabiome of Human Disease

We have been applying a systems biology approach to characterize the Metabiome of these host and microbial communities (microbiome) to determine which features are associated with the disease state. We define the Metabiome as all the interactions between the host and the microbiome. The initial thrust is based on Knowledge Discovery to define the correlations between features and disease classes but the ultimate goal is to develop new hypothesis that can then be tested using traditional hypothesis driven experimental procedures. We are looking at a number of human diseases that are associated with dysbiosis of the bacteria community in the human gut. These include Alcoholic Liver disease, Inflammatory Bowel Disease, Autism, and Colon cancer. Students will have the opportunity to work in the wet lab using NexGen sequencing, metabolomics, and transcriptomics technology and state-of-the-art bioinformatics pipelines.

Microbial Ecology of Environmental Disease

We have been applying a systems biology approach to characterize microbial communities in the natural environment. These studies involve characterization of complex microbial commnities and natural environments and looking at metabolic and expression functionality of these system. We are looking at a number of diseases or conditions that are driven by environmental factors such as Coral Diseases and Lobster Shell disease. We are also look at bioremediation processes in oil spills, the biogeochemistry of natural cold seeps, and plant-rhizosphere-microbiome interactions. Students will have the opportunity to work in the wet lab using NexGen sequencing technology and state-of-the-art bioinformatics pipelines.

Phylogenomics and Population Genetics

We have been applying Nextgen sequencing to various projects in molecular systematics and population genetics of Swans, Rhinos, Falcons, and Corals. Students will have the opportunity to work in the wet lab using NexGen sequencing technology and state-of-the-art bioinformatics pipelines.

Dr Geraldine Grant
Associate Professor
Department of Biology

Mechanisms of Idiopathic Pulmonary Fibrosis (IPF)

Idiopathic Pulmonary Fibrosis is a fatal interstitial lung disease that kills over 40,000 individuals each year – more than die from breast cancer. Currently there are not therapies and no cure for this disease and patient survival time post diagnosis is less than 5 years. There are a number of projects currently available in my lab to investigate the potential role of particular proteins in IPF.

A. *Effect of cytokine exposure on the activation status of a novel human lung fibroblast population***.** Cytokine exposure plays a major role in the differentiation of human fibroblasts in the wound response – the pathway which is believed to be out of control in IPF. Transforming growth factor beta – TGFB1 is the most prevalent cytokine expressed in IPF and is capable of transforming normal fibroblasts into their activated wound repairing myofibroblast phenotype. We have isolated a novel population of Normal and IPF fibroblasts. The response of these cells to TGFbeta and any other IPF related cytokine is unknown. This project involves the exposure of these cells to TGFb1, IL1beta, PDGF and TNFalpha.

B. *Investigation for novel surface marker for human fibroblasts and myofibroblasts***.** Fibroblast biology and investigations are marred by the lack of a suitable marker for their isolation. At present fibroblasts are isolated by outgrowth from tissue pieces…a procedure that results in loss of phenotype and dedifferentiation of cells to a "fibroblast-like" phenotype. The only currently accepted marker for fibroblasts is expression of alpha smooth muscle actin (alpha-SMA) – an internal marker and of no use in isolation of fibroblasts in mixed cell culture. We have isolated a novel population of fibroblasts by differential binding from both IPF and normal tissue. In addition, we have carried out extensive genomic analysis. This project will involve analysis of large genomic data sets to derive a candidate list for common surface markers between both populations AND exclusive surface markers that may serve as a biomarkers and tools for isolation

Dr Ramin Hakami
Assistant Professor
School of Systems Biology

Exosome-mediated intercellular communication during bacterial infections

Exosomes are small membrane bound extracellular vesicles that carry biological macromolecules from the site of production to target sites either in the microenvironment or at distant sites away from the origin. Recent studies have demonstrated that exosomes play a significant role in cell-cell signaling, cancer progression, host immune responses, infectious diseases, and even as carriers of prions, and The role of exosomes during the progression of infection is a subject that has garnered enormous interest in recent years. The focus of our research is to understand the fundamental mechanisms of how exosomes are involved during infection with pathogenic bacteria or viruses, including infection with the biodefense agents Yersinia pestis (Yp) and B. pseudomallei (Bp). We have examined various purification strategies for isolation of CD63+ exosomes released from a human monocytic cell line infected with Yp, and have performed a comparative analysis of exosomal miRNA profiles between infected and uninfected cells. Our results have shown that distinct exosomal populations are released from cells and have also demonstrated the enrichment of specific miRNAs within exosomes obtained from infected cells. Students on this project will perform functional studies of specific miRNAs that show strong enrichment in exosomes derived from infected cells. During the course of this project students will learn several main and important microbiology-related techniques, including culturing bacteria, measuring bacterial growth, setting up infection experiments, tissue culture techniques, protein analysis techniques such as Western blot analysis, cell staining, and microscopy techniques. In addition, students will learn the techniques for isolation and characterization of exosomes.

Host signaling during infection with biodefense bacterial agents

New drugs with greater potency against bacterial infections are urgently needed in order to combat bacterial infections more efficiently and to counter naturally occurring and man-made antibiotic resistant strains. One main focus of our research is discovery of new measures to combat the biodefense agents Y. pestis (Yp) and B. pseudomallei (Bp), two agents for which effective therapeutic measures are needed. Yp is a model organism for pathogenic gram-negative bacteria and is the etiological agent of the plague. Yp can cause high mortality rates, especially in pneumonic form. Plague is now categorized as a reemerging disease given the rise in the number of reported human cases during the past two decades and the reappearance of outbreaks in various countries after decades of quiescence. Yp is also of great concern given the documented history of its use in biowarfare and the potential for its use for bioterrorism considering its high lethality and relative ease of production. Similar to Yp, Bp is a gram-negative biodefense agent. Bp can cause disease in both humans and animals and can infect a wide range of animal species, including mammals, bird, and shellfish. In humans, Bp causes melioidosis, often characterized by

fever, cough, and chest pain in patients that present with the active form of the disease. Discovering host signaling pathways of importance that are engaged by dangerous pathogens such as Yp and Bp could lead to discovery of novel and potentially multiagent therapeutic measures that are immune to development of antibiotic resistance mechanisms. To address this critical need, students will perform functional studies of host signaling proteins that are involved during Y. pestis and B. pseudomallei infection, in order to understand the roles that these proteins play during infection. Only highly attenuated strains of Yp and Bp (approved for BSL-2) will be used. The important host proteins that have been identified and selected using a novel protein microarray platform called RPMA will be studied for their roles during infection. Students will learn several main and important microbiology-related techniques, including culturing bacteria, measuring bacterial growth, setting up infection experiments, tissue culture techniques, protein analysis techniques such as Western blot analysis and immunoprecipitation, cell staining, and microscopy techniques.

Dr R.C. Jones
Professor
Department of Environmental Science and Policy

Water Quality and Aquatic Ecology in the Tidal Potomac River and its Local Tributaries

Specific topics available include: water quality monitoring, E. coli monitoring, stream macroinvertebrates and periphyton, river plankton dynamics, and harmful algal blooms.

Dr Nadine Kabbani
Associate Professor
Molecular Neuroscience, School of Systems Biology

Axon Growth and Regeneration in the Brain

Our laboratory studies the molecular mechanisms by which nicotinic acetylcholine receptors (nAChRs) signal and operate in the developing and adult brain. We are investigating how nAChRs direct neuronal development by examining the role of nAChRs in growing axons and growth cones. Growth cones are important developmental structures that play a role in neuronal survival and target selection within the developing brain. We have developed a neuronal culture system to examine the contributions of nAChRs in growth cones of neurons from the hippocampus and cortex. We are currently investigating the mechanisms driving growth and movement of axons.

Dr HC Lim
Assistant Professor
Department of Biology

Analysis of gut metagenomic sequences of a primarily herbivorous waterfowl

Studies of gut microbiomes of all types of animals show that healthy resident bacterial communities enhance fitness of their hosts through a variety of means. These bacteria could help to digest recalcitrant food materials (eg, wood for termites), protect against enteric pathogens by forming biofilms in the gut and by priming the hosts' immune system, and break down phytotoxins such as alkaloids and phenolics. Using massively high-throughput DNA sequencing, scientists are able to sequence genes of most species of bacteria residing within a gut environment. This allows them to characterize these bacterial communities taxonomically, as well as to create a comprehensive gene catalog in order to profile the functional and enzymatic capacities of these communities.

This study focuses on bacterial communities residing within the ceca of Canada geese. Resident populations of the Canada goose in North America had exploded in recent years. This has raised concerns about them being reservoirs of potential pathogens for humans and domestic animals. Canada geese consume mainly plant materials, and have enlarged ceca (located just before the large intestine) which store food material. The ceca have a high density of bacteria, which play an important role in terms of breaking down cellulose. The student will use bioinformatic tools to map sequencing reads to databases. He/she will also conduct de novo assembly of reads and make gene predictions. Identified genes will be placed within the context of known metabolic pathways in order to functionally profile the bacterial communities. The student is required to have a strong interest/background in evolution or genomics, and is comfortable with working in the unix environment (or not afraid to learn).

Genomic study of tropical birds

Advances in DNA sequencing technologies allow genome-scale data to be generated more cheaply than before. For the field of evolutionary biology, this allows questions related to genome evolution, speciation, population structure, selection and phenotype-genotype linkage to be tackled with a higher level of resolution. Multiple genome-scale datasets on tropical birds from Panama and Borneo are available for the student to conduct genome assembly, genome annotation and population genomic analyses (eg variant calling, study of gene introgression across a hybrid zone). The student is required to have a strong interest/background in evolution or genomics, and is comfortable with working in the unix environment (or not afraid to learn).

Dr David Luther
Associate Professor
Biology Department

The Evolution of Acoustic Competition in Songbirds

Just as the ecological theory of niche competition applies to food resources it can apply to other resources. In this project we use niche competition to assess acoustic signals, bird songs and frog calls, to investigate if they avoid having similar signals at the same time and location which would reduce competition and improve signal detection. Results of the project will focus on the ecology and evolution of animal communication and how species interactions can influence animal communication strategies. This project will also be in conjunction with research from the National Park Service Soundscape division as recordings from Teton National Park will be used for the project. The student participating in this project will learn to identify a variety of bird songs and frog calls based on acoustic and visual cues. The student will also become proficient at using Raven a sound analysis program as well as participate in collaborative statistical techniques and meetings with scientists from the National Park Service. Finally the student will be asked to participate in writing a scientific paper based on the results of the project.

Assessing the effectiveness of conservation actions for endangered species

Conservation actions, such as habitat protection, attempt to halt the loss of threatened species and help their populations to recover. Various research has examined the efficiency and the effectiveness of actions individually. However, conservation actions generally occur simultaneously so the full suite of implemented conservation actions should be assessed. We will use national (Endangered Species Act and global datasets (IUCN RedList) to assess the effectiveness of all categories of conservation actions for a wide variety of taxa in terms of there association with population increases in the threatened species.

Dr Kylene Kehn-Hall
Associate Professor
National Center for Biodefense & Infectious Diseases,
School of Systems Biology

Novel Therapeutics for Viral Infections

Currently there are no therapeutics for Zika virus (ZIKV), Rift Valley fever virus (RVFV), or Venezuelan equine encephalitis virus (VEEV). These viruses are transmitted by mosquito and cause emerging infectious diseases. Students will be assigned compound(s) and will explore their toxicity and efficacy against ZIKV, VEEV, and/or RVFV. Work will only involve BSL-2 viruses (e.g. vaccine strains will be utilized for VEEV and RVFV). Students will learn techniques such as cell culture, viral infections, plaque assays, q-RT-PCR assays, luciferase assays, and cell viability assays.

Altered Signaling Pathways in Virally Infected Cells

A combinatorial proteomics and transcriptomics analysis pipeline is being used to identify cellular factors important for the infectivity and replication of Zika virus (ZIKV), Rift Valley fever virus (RVFV), or Venezuelan equine encephalitis virus (VEEV). Students will be assigned to analyze altered proteins and/or transcripts in ZIKV, VEEV, or RVFV infected cells. Work will only involve BSL-2 viruses (e.g. vaccine strains will be utilized for VEEV and RVFV). Students will learn techniques such as cell culture, viral infections, plaque assays, q-RT-PCR assays, and western blot assays.

Dr Claudius Mueller
Research Assistant Professor
Center for Applied Proteomics and Molecular Medicine- School of Systems Biology.

Deciphering the communication between tumor cell sub-populations

Tumor heterogeneity, the presence of genetically and phenotypically diverse cell populations within a tumor, is a major obstacle in the development of effective treatment. Resistant clones, which may only make up a small fraction of the total tumor cell mass, persist and expand to lethal tumors following treatment. But how is this heterogeneous mix of tumor cell sub-populations maintained? Is it simply the result of high genomic instability and spatial heterogeneity within the tumor tissue? Or is the tumor cell society actively maintaining its diversity?

Cancer cells are known to cooperate with and manipulate host cells of the tumor microenvironment to ensure tumor survival and regulate angiogenesis and metastasis. But the communicative network between individual tumor cells remains elusive and largely unstudied. We developed a cell culture model, using a brain cancer cell line, that allows us to eavesdrop on tumor cell-cell communication and cooperation. Using this model, we have observed that slow growing, perceived "weaker" cancer cells, are supported in the presence of a more "aggressive" population. At the same time, the "weaker" cell sub-population regulates the migration of the "aggressive" sub-clone. But how do these cells communicate with each other? And which principles govern this tumor sub-clone alliance?

Students will learn various 2D and 3D cell culture techniques, fluorescence and bright-field microscopy, as well as proteomics technologies (Western Blotting, Reverse Phase Protein Microarrays), with the ultimate goal to decipher and block the communication between these tumor cell sub-populations.

Dr Valerie Olmo
Assistant Professor
Department of Biology

Environmental factors and vertebrate development

Since the 1950s, it has been understood that environmental factors can have significant, and at times detrimental, impacts on embryonic development. Advances in technology have made it possible to study the teratogenic effects of environmental factors at the morphological, cellular, and molecular levels. The Developmental Biology laboratory uses the zebrafish model organisms to further our understanding of the interplay between the environment and embryonic development. In particular, the research semester student would choose a teratogen (alcohol, nicotine, bisphenol-A, or temperature) and design a project to further our understanding of how these teratogens impact embryonic development.

Dr Mikell Paige
Associate Professor
Department of Chemistry & Biochemistry

Targeting the Leukotriene A4 Hydrolase Enzyme for the Treatment of Emphysema

The leukotriene A4 hydrolase (LTA4H) enzyme is a bifunctional enzyme that promotes inflammation as well as the resolution of inflammation. Emphysema is characterized by persistent pulmonary inflammation. Inhibiting the pro-inflammatory effects of the LTA4H enzyme was shown to not be efficacious in the clinic. We hypothesize that a secondary function of the enzyme that promotes resolution of inflammation is critical for halting emphysema-associated pulmonary inflammation. In this project, we will explore the enzymology of the LTA4H enzyme in a reductionist approach to mimic the environment of the lung in vitro.

Targeting IL-1B:IL-1RAcP:IL-1R1 Complex for Treating Osteoarthritis and other Inflammatory Diseases

Osteoarthritis is the most common form of arthritis and is the leading cause of chronic disability in the US. The IL-1 signaling cascade is found to be an important therapeutic target for treating the inflammatory response in osteoarthritis. We intend to design peptide inhibitors of IL-1 that inhibits IL-1B:IL-1RAcP:IL-1R1 complex formation by disrupting key hotspots of the protein-protein interactions. The project will involve production of recombinant protein and the development of a high throughput assay for characterizing the effect of peptide inhibitors on complex formation in vitro.

Design, Synthesis, and Characterization of Inhibitors of Metabolic Targets for the Treatment of Lung Cancer

Generally, cancer involves proliferating cells that require much energy. Non-selective chemotherapies can be a successful strategy, because the cytotoxic drugs are rapidly taken up by cancer cells, which result in cell death. However, the non-specificity of these drugs leads to multiple side effects. Herein, we intend to target specific metabolic pathways in order to target cancer cells over normal cells. This project will involve production of the recombinant citrate transport enzyme and the development of a citrate transport in vitro assay for characterization of potential inhibitors.

Dr Esther Peters
Associate Professor
Department of Environmental Science and Policy

Using Histology to Understand Interactions between Organisms and the Environment

The study of cells, tissues, organs, and organ systems is critical not only to learn about the physiology and metabolism of an organism, but to gain knowledge of that organism's relationships with other organisms (e.g., viruses, bacteria, protozans) and the impacts of environmental changes that the organism experiences. Alterations in the cells and tissues from exposure to biotic and abiotic stressors can lead to disease, impairment in the organism's vital functions, organs, or systems. The GMU Histology Laboratory supports research on non-human diseases, systematics and taxonomy, physiology, microbiology, molecular biology, or other areas, using light microscopy to learn how changes in structure affect function. Projects undertaken in the laboratory include microbial diseases of corals, effects of ingested metals in drinking water on rats and mice, reproduction in local fish species, distinguishing species of invasive gastropods, and digestion in fireworms. The student will learn histological techniques to mount tissue sections of samples from field or laboratory experiments (either a current lab project or one of their choice) and basic slide reading skills to gain an appreciation of the power of this field in organismal and environmental research. The student will also conduct literature research and prepare a short report on their observations.

Dr Anna Pollack
Assistant Professor
Global & Community Health College of Health & Human Services

Environmental chemical exposure and women's health

Environmental epidemiologists are interested in the study of disease in populations of people and how modifiable exposures may influence population health. Exposure to environmental chemicals within personal care products are widespread and may lead to adverse health effects. Exposure to chemicals in personal care products, diet and lifestyle factors and are not entirely understood. In particular, the chemicals of interest include phenols such as: bisphenol A and triclosan, and parabens. These chemicals have chemical structures that enable them to impact hormonal binding in experimental settings. These chemicals are therefore classified as endocrine disruptors, which have health implications on reproductive health, cancers, and possible links to obesity and diabetes. Their possible health effects in humans are an ongoing area of research. As people are exposed to multiple chemicals and there are multiple factors that combine to cause disease processes, it is necessary to implement statistical modeling to appropriately understand the exposure-disease relationship of interest. The student will learn statistical modeling necessary for epidemiologic research and the project will focus on phenol and paraben chemical exposures, predictors of exposure (including diet and lifestyle factors).

Dr Joris Van der Ham
Assistant Professor
Department of Environmental Science and Policy

Ecology of Carrion Insects

Carrion ecology studies biological processes that occur during decomposition of organic material, typically animal cadavers. One of these processes is the ecological succession of insect communities associated with carrion. These communities, mostly beetle and fly species, change in a predictable manner as a cadaver decomposes over time. There is, however, still much to learn about what drives the changes in community composition during the decomposition process. This community approach in carrion ecology also has potential implications for forensic entomology.

Students who are interested in carrion ecology will have the opportunity to learn to design and conduct their own field experiment, identify numerous insect species, analyze data, and will contribute to our understanding of carrion community ecology.

Dr Monique van Hoek
Professor
School of Systems Biology

Antimicrobial Peptides

Antimicrobial peptides are small peptides that act against bacteria. Students will be assigned a peptide and will explore its activity against various pathogens, including multidrug resistant bacteria. Students may also design rational variants of their peptide in order to improve its performance characteristics or perform synergy experiments. Skills taught will include (1) bacterial culturing, McFarland standards, CLSI standards. (2) antimicrobial peptide assays (3) biofilm assays (4) hemolytic assays (5) cytotoxicity assays (6) advanced data analysis (IC50 plots, etc), (7) bioinformatic analysis of peptide sequence and prediction of structure. This project can accommodate more than one student; each student will study a different peptide or a different bacteria.

Novel Antibiotics

Novel antibiotics are critically needed. Students will be assigned candidate compounds that have potential to be antibiotics in order to explore their activity against various pathogens, potentially including multidrug resistant bacteria. These may be natural products or chemically synthesized molecules. Students may also design checkerboard assays to determine synergistic or antagonistic activity. Skills taught will include (1) bacterial culturing, McFarland standards, CLSI standards. (2) MIC assays (3) biofilm assays (4) cytotoxicity assays (5) advanced data analysis (IC50 plots, etc), (6) bioinformatic analysis of bacterial genomes to identify possible drug targets (7) advanced literature searches to develop the background of the antibiotic and its potential mode of action. This project can accommodate more than one student; each student will study a different antibiotic or a different bacteria.

Dr Michael von Fricken
Department of Global and Community Health
George Mason University MS 5B7
4400 University Drive
Fairfax, VA 22030-4444

Systematic Review on Risk of Zoonotic Disease Transmission from Rodents on Zoo Grounds

This project will have a student(s) compiling a detailed review of previous reports of zoonotic disease transmission originating from rodents in zoos. Rodents are common vertebrate pests on zoo grounds, competing and often interacting with non-native exotic animals for food. This interface increases the risk of transmission of agents capable of causing severe illness in humans and animals. Disease issues in zoo animals are also of concern as they may serve as reservoirs of zoonotic pathogens. Zoo veterinarians should be familiar with rodent-borne pathogens, both within their region and regions where zoo life originate. Additionally, they should have an understanding of the risk of transmission, methods to control wild rodents reservoirs, and preventive measures that minimize exposure of pathogens to zoo staff and visitors. The student(s) will work alongside the instructor and staff members from the Smithsonian Institute at the National Zoological Park, during this period of research, to compile information about the nature and risk of rodent borne pathogens that pose a high risk to animal caretakers and veterinarians working in zoo settings.

Collect and analyze *Ixodes scapularis* ticks for Lyme disease in low elevation settings along the Appalachian Trail in Virginia.

Student(s) will be expected to hike portions of the Appalachian Trail (AT) in the late Summer and early Fall months with the instructor to drag and flag for *ixodes* ticks. Study will incorporate field epidemiology, medical entomology, and if possible, lab methods focusing on molecular characterization of *Borrelia sensu lato* and *Borrelia burgdorferi* in collected ticks. As temperatures continue to rise, I*xodes scapularis* ticks are expanding farther south, potentially introducing Lyme disease to new regions of rural Virginia. This study will incorporate extensive background research on the geographic distribution of tick vectors in Virginia, a targeted sampling approach based on National parks in VA, and prolonged hours in the field flagging for ticks.

Dr James Willett
Professor
School of Systems Biology

Exploring Metabolic Changes in Very Old Nematodes

What happens as late stage robust adults transition into that terminal state preceding death? Do metabolic markers correlate with the phenotypic changes so characteristic of senescence? Altered locomotion, increased cellular fragility and accumulation of cellular pigmentation are characteristic of senescence in most animals, including ourselves.

Dr Yuntao Wu
Professor
School of Systems Biology

Screening for anti-HIV activity using an HIV-Rev dependent reporter cell

Screening anti-HIV activity from small-molecule inhibitors targeting cellular signaling pathways

Dr Neil Cox
International Union for conservation of nature

An update to the knowledge of Mexican reptile diversity

One of the initial regions reviewed during the progress of the GRA was Mexico, home to over 800 reptile species. Unfortunately, owing to slow progress in the GRA some of the data for Mexico (collected largely in 2005) is now outdated and requires a review and planning on how these data can be updated to ensure they are relevant for conservation priority setting from 2018 onwards. The student undertaking this project will compare the information already existing for endemic and/or globally threatened species as part of the GRA with information in The Reptile Database (Uetz), and will clearly record where changes are needed. There will also be an opportunity to work (through correspondence) with leading Mexican herpetologists to ensure data (including spatial data) are appropriately updated in a standardized IUCN format. Training will be given.

Special Skills Needed

Spanish language (advanced); GIS capabilities (beginner); attention to detail; taxonomy (beginner).

Key non-GMU Partners

IUCN-CI Biodiversity Assessment Unit; Conservation International; national experts

IUCN Global Reptile Assessment (GRA)

IUCN-CI Biodiversity Assessment Unit; Conservation International; national experts

1. An update to the knowledge of Mediterranean reptile diversity.

There is regular interest in the conservation of reptile species from the Mediterranean, and as such it clearly important that knowledge on species that are priorities for conservation funding and direct action is well maintained. For many species from the North African and Eastern portions of the Mediterranean, it is suspected that taxonomic concepts (critical for decision-making) are out of date within the IUCN system. The student will review the species data currently held by IUCN for North Africa and the Eastern Mediterranean (in collaboration with regional experts and GRA team) and will make recommendations on updates following their research on the fauna of these regions. Training will be given where needed.

Special Skills Needed

GIS capabilities (beginner); attention to detail; taxonomy (beginner); Spanish and/or French advantageous

Key non-GMU Partners

IUCN-CI Biodiversity Assessment Unit; Conservation International; national experts

2. Beginnings of a consolidated global checklist of reptile species.

Currently there is no agreed standardized checklist of the approximately 10,500 reptile species of the world. Dr Peter Uetz and the GRA have developed similar, but different lists of the names of reptile species in the world. There is now an increasing need to consolidate these lists into a single global checklist for conservation practitioners. The student will work with the GRA team to identify discrepancies between Peter Uetz's Reptile Database, and the emerging GRA list of reptile species. This will require both automated and manual checking of sizable species lists, reporting on differences and potentially provision of recommendations on how the lists can be consolidated.

Special Skills Needed

Database/spreadsheet manipulation and analysis (esp. Access and Excel); Taxonomy (good)

Key non-GMU Partners

IUCN-CI Biodiversity Assessment Unit; Conservation International; IUCN Red List Unit (Cambridge); The Reptile Database.

3. Collation of information on the reptile species of Central Africa

Little work to date has been undertaken by IUCN on the conservation status of a broad range of reptile species native to Central Africa - including many very poorly known taxa. As part of completing the GRA within the 2018 deadline, it is important for IUCN staff to have all of the latest information available in one place (SIS database) on this region and its reptile fauna. The research undertaken by the student will form the baseline for future investigations. This work requires an eye for detail, and thoroughness - especially when tracking down older reference material for poorly-known species. Training will be given in SIS and the appropriate GIS software.

Special Skills Needed

French language skills (good); database/spreadsheet manipulation; ability to standardize work e.g. references; taxonomy (basic); GIS capabilities (basic).

IUCN Global Freshwater Biodiversity Assessment (GFBA)

1. A modern checklist of Central American freshwater fishes.

As part of a wider, ongoing, project the IUCN-CI BAU is responsible for the collation of data on the status of freshwater biodiversity in the Americas. The highly diverse fish fauna of Central America remains a considerable gap in our knowledge of prospective conservation priorities for the Americas. As part of this project, the student will work on developing a fully up to date list of Central American freshwater fishes within the IUCN SIS database. The student will also gather together spatial data that will be used at a later stage for standardized mapping the distributional ranges of these fishes. There will be an opportunity to work through correspondence with regional experts and the IUCN regional office (ORMACC) as part of the research.

Special Skills Needed

Spanish language skills (good); Database/spreadsheet manipulation and analysis (esp. Access and Excel); Taxonomy (good); GIS (basic/beginner).

Key non-GMU Partners

IUCN-CI Biodiversity Assessment Unit; Conservation International; IUCN-ORMACC Regional Office; IUCN-SSC Freshwater Fish Specialist Group.

2. A modern checklist of Central American freshwater mollusks and dragonflies.

Within the review of freshwater species that IUCN-CI BAU is responsible for in the Americas, two important invertebrate groups are the dragonflies (odonata) and mollusks. There currently do not appear to be consolidated regional checklists for either of these groups for Central American countries, and this lack of a species list is an impediment to focused conservation prioritization for freshwater species for the region. The proposed project would require a student to undertake research in developing two updated and taxonomic ally agreed species lists (odonata and mollusks) for Central America. Collaboration, through correspondence, will be expected between the student and regional experts/partners in the development of these lists. Training will be given in the appropriate software needed to record the work.

Special Skills Needed

Spanish language skills (good); Database/spreadsheet manipulation and analysis (esp. Access and Excel); Taxonomy (good); GIS (basic/beginner).

Key non-GMU Partners

IUCN-CI Biodiversity Assessment Unit; Conservation International; IUCN-ORMACC Regional Office; IUCN-SSC Mollusc and Odonata Specialist Groups

3. A provisional checklist of the freshwater mollusks of South America.

Currently, there is no consolidated checklist of freshwater mollusc species from continental South America. While IUCN-CI BAU has considerable knowledge of the mollusks of the Tropical Andes, this leaves substantial gaps in knowledge for other areas of presumed high molluscan diversity (e.g. Orinoco drainage). With a global standard checklist, work can advance on better understanding conservation priorities in South America for this often highly threatened groups of species. The student will work with regional collaborators (through correspondence) to compile a standard checklist of freshwater mollusks for South America. Training will be provided in the most appropriate means of recording this research including GIS spatial data where it is available.

Key non-GMU Partners

IUCN-CI Biodiversity Assessment Unit; Conservation International; IUCN-Sud Regional Office; IUCN-SSC Mollusc and Odonata Specialist Groups

Key non-GMU Partners

Spanish/Portuguese language skills (good); Database/spreadsheet manipulation and analysis (esp. Access and Excel); Taxonomy (good); GIS (basic/beginner).