

Faculty Mentors, Project Titles, and Descriptions

Fall Research Semester

Students, please note:

- 1 Review the list of projects below.
- 2 Identify at least 3 projects that you would be interested in participating in.
- 3 Use these projects when you fill out the Research Semester application form.

Summary list of projects

(More detailed information for most projects is available stating on page 6)

Faculty Mentor	Title of Project(s)	Contact Information
Ahn, Changwoo Professor Department of Environmental Science and Policy	The Dirt Project	Changwoo Ahn cahn@gmu.edu
Alishetty, Suman Assistant Professor Department of Bioengineering	Ionizable lipid designs and synthesis	Suman Alishetty salishet@gmu.edu
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
Blackwell, Kim L. (Avrama) Professor	Signaling Pathways Involved in Striatal Synaptic Plasticity Modeling neurons of the basal ganglia	Avrama Blackwell kblackw1@gmu.edu

Molecular Neuroscience, Volgenau School of Engineering	<i>(Dr. Blackwell is not accepting students this fall)</i>	
Chiari, Ylenia Assistant Professor Department of Biology	Project description will be available in March	Ylenia Chiari ychairi@gmu.edu
Couch, Robin Associate Professor Department of Chemistry and Biochemistry	Development of New Antibiotics Small molecule metabolomics Biosensor/Electronic Nose	Robin Couch rcouch@gmu.edu
Epstein, Elisabeth Assistant Professor Department of Biology	Interspecies Cross-Talk in Natural Microbial Communities	Elisabeth Epstein eepstei@gmu.edu
Fowler, Amy Assistant Professor Environmental Science and Policy	Impacts of Salinity on invertebrate and vertebrate community composition in the Potomac River, VA The discovery of a new castrating isopod parasite in estuarine crabs of the Chesapeake Bay Salinity tolerances of invasive Japanese mystery snails Reproductive output of native and invasive populations of the mud crab <i>Rhithropanopeus harrisi</i>	Amy Fowler Afowler6@gmu.edu
Freeman, Elizabeth Associate Professor School of Integrative studies	Nocturnal behavior of rhinoceros See also: https://integrative.gmu.edu/people/freeman	Elizabeth Freeman efreeman@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 pgillevet@gmu.edu

<p>Girgis, Michael Assistant Professor Department of Bioengineering</p>	<p>Identification and quantification of post translational modification of RNA using mass spectrometry.</p> <p>Development of N-terminal derivatizing agents to enhance ionization of poorly ionizable peptides.</p> <p>A mass spectrometry-based assay to assess enzymatic activity of Sulf-1 enzyme.</p>	<p>Michael Girgis myassagi@gmu.edu</p>
<p>Glaberman, Scott Associate Professor Environmental Science & Policy</p>	<p>Host-Parasite Interactions in Galapagos Marine Iguanas</p>	<p>Scott Glaberman sglaberm@gmu.edu</p>
<p>Grant, Geraldine M. Associate Professor and Chair, Department of Biology</p>	<p>Mechanisms of Idiopathic Pulmonary Fibrosis</p>	<p>Geraldine M Grant ggrant1@gmu.edu</p>
<p>Hakami, Ramin Associate Professor School of Systems Biology</p>	<p>Exosome-mediated intercellular communication during bacterial infections.</p> <p>Host signaling during infection with biodefense bacterial agents.</p> <p>Host response to SARS-CoV-2 infection</p>	<p>Ramin Hakami rhakami@gmu.edu</p>
<p>Hanley, Daniel Assistant Professor Department of Biology</p>	<p>Perceptual and cognitive processes governing egg recognition in wild birds</p> <p>A holistic examination of visual signals</p>	<p>Daniel Hanley dhanley2@gmu.edu</p>
<p>Hoemann, Caroline Professor Bioengineering</p>	<p>See:</p> <p>https://bioengineering.gmu.edu/profile/view/443811</p>	<p>Caroline Hoemann choemann@gmu.edu</p>
<p>Lee, Kyung Hyeon Assistant professor Department of Chemistry and Biochemistry</p>	<p>Leukotriene A4 hydrolase as a target for Alzheimer's Disease.</p> <p>Idiopathic pulmonary fibrosis (IPF) treatment by blocking sulfatase-1 (Sulf-1).</p> <p>Chronic obstructive pulmonary disease (COPD) targeting leukotriene A4 hydrolase CRISPR research.</p>	<p>Kyung Hyeon Lee kleep@gmu.edu</p>

<p>Lim, HC Assistant Professor Department of Biology</p>	<p>Machine-learning based identification of bird songs from tropical Asia collected with autonomous audio recorders</p>	<p>Haw Chuan Lim hlim22@gmu.edu</p>
<p>Luther, David Assistant Professor Department of Biology</p>	<p>Long-term trends in forest communities and functional diversity Assessing the effectiveness of conservation actions for endangered species</p>	<p>David Luther dluther@gmu.edu</p>
<p>Dr Claudius Mueller Research Assistant Professor School of Systems Biology</p>	<p>Deciphering the communication between tumor cells and sub- populations</p>	<p>Claudius Mueller cmuelle1@gmu.edu</p>
<p>Narayanan, Aarthi Associate Professor Department of Biology</p>	<p>Broad spectrum antiviral targets Host response modulation by antiviral peptides</p>	<p>Aarthi Narayanan anaraya1@gmu.edu</p>
<p>Oleo, Valerie Associate Professor Department of Biology</p>	<p>Environmental factors and vertebrate development</p>	<p>Valerie Olmo volmo@gmu.edu</p>
<p>Paige, Mikell Associate Professor Department of Chemistry & Biochemistry</p>	<p>Total synthesis of natural products Strategies in medicinal chemistry</p>	<p>Mikell Paige mpaige3@gmu.edu</p>
<p>Peters, Esther Associate Professor Department of Environmental Science and Policy</p>	<p>Using Histology to Understand Interactions between Organisms and the Environment</p>	<p>Esther Peters epeters2@gmu.edu</p>

<p>Pollack, Anna Assistant Professor Global & Community Health</p>	<p>Environmental Chemical Exposure and Women's Health</p>	<p>Anna Pollack apollac2@gmu.edu</p>
<p>van Hoek, Monique Professor School of Systems Biology</p>	<p>Antimicrobial Peptides Novel Antibiotics</p>	<p>Monique Van Hoek mvanhoek@gmu.edu</p>
<p>Von Fricken, Michael Assistant Professor Department of Global and Community Health</p>	<p>Collect and analyze <i>Ixodes scapularis</i> ticks for Lyme disease in low elevation settings along the Appalachian Trail in Virginia</p>	<p>Michael Von Fricken mvonfric@gmu.edu</p>
<p>Wu, Yuntao Professor School of Systems Biology</p>	<p>Screening for anti-HIV activity using an HIV-Rev dependent reporter cell Screening anti-HIV activity from small-molecule inhibitors targeting cellular signaling pathways.</p>	<p>Yuntao Wu ywu8@gmu.edu</p>
<p>Weeks, Andrea Associate Professor Department of Biology Director Ted R. Bradley Herbarium (GMUF)</p>	<p>Evolution of Madagascar myrrh trees: species discovery</p>	<p>Andrea Weeks aweeks3@gmu.edu</p>
<p>Projects at Johns Hopkins University Bloomberg School of Public Health For information about the projects at Johns Hopkins please contact Dr. Valerie Olmo</p>	<p>Sumoylation, DNA repair and chromosome segregation Dissecting clonal diversity in melanoma to overcome therapy resistance and metastasis Mechanisms and Influences of the Microenvironment on Metastasis</p>	<p><i>Contact:</i> Dr. Valerie Olmo volmo@gmu.edu</p>

Detailed descriptions of Projects

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.

Ionizable lipid design and synthesis

Ionizable lipids for fabricating lipid nanoparticles found important utility in the delivery of mRNA as a new vaccination modality during the COVID19 pandemic. The lipids finding the most success contain an ionizable amine functionality that is protonated under acidic conditions to give a positively charged head group with a lipophilic tail. These charged head groups are formulated with mRNA to form lipid nanoparticles presumably through interactions of the positively charged nitrogen atom and the negatively charged backbone of the mRNA sequence. In our project we will design and synthesize new lipids that have potential in improving the properties of the lipid nanoparticles.

Dr Ancha Baranova

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

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 it is believed that HDL promotes the removal of excess cholesterol from peripheral tissues and delivers it to the liver for excretion. By monitoring the NMR 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."

Modeling neurons of the basal ganglia

The goal of the project is to create simplified neuron models that have electrical activity similar to real neurons. The project involves using the Brian simulator to perform parameter optimization. Python programming experience required. The student will learn how to simulate neurons using Brian, gain additional python skills, learn about characteristics of neuron firing patterns, and learn about striatal physiology.

** Dr. Blackwell is not accepting students this fall.*

Dr Ylenia Chiari
Assistant Professor
Department of Biology

Conservation Genetics of the gopher tortoise (*Gopherus polyphemus*) in Northern Florida

In the eastern portion of its range (east of the Mobile and Tombigbee Rivers in Alabama, Georgia, Florida, and South Carolina), the gopher tortoise (*Gopherus polyphemus*) is a candidate species for federal listing as a Threatened species by the US Fish and Wildlife. The gopher tortoise receives particular attention from conservation and management agencies in the southeastern United States because of its role as a keystone species. Tortoise burrows provide refuge and resources for more than 300 species (Hubbard 1893, Diemer 1986, Lips 1991, Witz et al. 1991, Kinlaw and Grasmueck 2012). There is a gap in knowledge of tortoise population structure and habitat use in coastal areas particularly along barrier islands, which may impact the listing decision. This proposed project would help fill that gap by determining population connectivity through genetic analyses. This project focuses on extracting DNA and amplifying mitochondrial DNA and microsatellite loci from samples collected at St. Vincent National Wildlife Refuge (SVNWR) and on the mainland (about 30 Km west of the Refuge) to study tortoise colonization of the island and estimate the population size of gopher tortoises at SVNWR. SVNWR is located in Franklin and Gulf Counties, Florida along the northern Gulf of Mexico coast. Because of its size (~12,000 acre), available habitat, lack of anthropogenic development, and persistent but poorly understood gopher tortoise population, this Refuge would serve as an ideal template for describing characteristics of coastal tortoise populations. Management decisions on the Refuge, and at other coastal land holdings of interest to USFWS are dependent on available data for this species yet little is known about these populations including population structure and population size.

This project is for one student. The student will be in charge of extracting DNA, amplifying mitochondrial DNA and microsatellite loci, and running the analyses on these data.

Dr. Robin Couch
Associate professor
Chemistry and Biochemistry Department

The development of new antibiotics

Small molecule metabolomics

Biosensor/Electronic Nose

For more information, please see:

<http://mason.gmu.edu/~rcouch/>

Dr. Elisabeth Epstein

Assistant professor

Department of Biology

Many diverse groups of bacteria use quorum sensing (QS) to regulate their behaviors in response to changes in population density. Characterized QS systems have been shown to regulate the expression of genes required for pathogenesis, host-symbiont interactions, and bioluminescence, among many others. QS allows for communication and coordination of multicellular behaviors between bacteria of the same species (intraspecies communication) as well as between very distantly-related organisms (interspecies communication). Additionally, it is now well known that diverse taxa from all domains of life produce inhibitors of QS to influence the behavior of microbial communities. The best characterized microbes using or inhibiting QS are those that can grow in lab conditions. Therefore, there is a massive under-reporting of microbes that use QS, as far fewer than 1% of bacterial/archaeal taxa can grow in lab conditions.

This project aims to identify the composition of unculturable microbial soil communities that can either 1) inhibit QS (i.e., by producing quorum quenching compounds, QQ) or 2) are able to produce inter-species QS inducer molecules. We will do this by using strains of the well-characterized QS system in *Vibrio campbellii* which regulates bioluminescence. A mutant “recipient” strain of *V. campbellii* can respond to, but not produce, QS signals. The presence of exogenous QS signal results in production of bioluminescence by this recipient strain. The exogenous QS signal may be supplied by a mutant “donor” strain of the same species or by QS signal present in the environment.

Undergraduate students who have had basic courses in microbiology will be ready to succeed in this project. Besides using standard culturing methods in the lab and learning how to employ our bioluminescence assay, students will collect soil samples from different environments. Students will extract eDNA from the soil samples as well using the samples in our established bioluminescence reporter assay to detect the presence of QS or QQ activity. eDNA from soil samples showing either QS or QQ activity will be sent for 16S rRNA gene sequencing. Undergraduates will examine the 16S rRNA gene data set using BLAST and other databases to determine the composition of the bacterial communities with QS or QQ activity.

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

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 harrisi* 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. harrisi* 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. harrisi*. 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. harrisi* 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. harrisi*. 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.

The discovery of a new castrating isopod parasite in estuarine crabs of the Chesapeake Bay

Chesapeake Bay populations of the Harris mud crab (*Rhithropanopeus harrisi*) host a suite of parasitic organisms, but the two most common are an invasive rhizocephalan (*Loxothylacus panopaei*) and a putatively native entoniscid isopod (*Cancrion* sp.) (pers. obs.). *L. panopaei* was first introduced into Chesapeake Bay in the 1960s, where its lifecycle, impacts, and abiotic tolerances have been extensively studied. Recently, we have documented an isopod endoparasite infecting *R. harrisi*. Working with collaborators, this parasite was identified as an entoniscid, mostly likely from the genus *Cancrion*, and experts are describing it as a new species. Despite the extensive knowledge on *L. panopaei*, there is extremely limited knowledge on the life history or host relationships of entoniscid parasites in general, except that some species negatively impact host reproduction. Of all the literature on entoniscid parasites, none discuss or mention *Cancrion* sp. infecting *R. harrisi*. There are several aspects of this host-parasite that can be explored – seasonality of infection, number of broods expelled

related to salinity or temperature, the survival of the isopod larvae across salinities/temperatures, the effect of parasitism on being preyed upon by other organisms, identifying alternative hosts, etc. Dr. Fowler will work with the student to determine questions which interest them.

Salinity tolerances of invasive Japanese mystery snails

Invasive Japanese mystery snails are found in the Potomac River and various other tributaries of the Potomac River. These snails are 5-10x larger than any of the native snails and bear live young that mature inside female snails. Here, we are interested in determining the salinity tolerances of the juvenile snails, as they can be extracted directly from the female after dissection and placed in different salinity treatments.

Reproductive output of native and invasive populations of the mud crab *Rhithropanopeus harrisi*

Invasive populations of organisms are hypothesized to leave behind predators and pathogens, thus allowing for increased energy resources to be available for reproduction. We will test this hypothesis by counting the eggs attached to female mud crabs (*Rhithropanopeus harrisi*) collected from Finland versus populations collected by the student from the Chesapeake Bay and North Carolina. Additional sampling may be possible, depending on funding.

Dr Elizabeth Freeman

Associate Professor

School of Integrative Studies

Nocturnal behavior of rhinoceros

Investigating animal behavior within captive/zoological settings provides valuable information that can be applied to welfare and management strategies. We are using game cameras to understand the nighttime behavioral patterns of white and black rhinoceros in US zoos. To date, we have video footage from ~80 rhinos (2/3 white and 1/3 black rhinos) distributed among 24 different zoological institutions. Little is known about their sleep patterns and we are hoping to unlock that mystery. This game camera study is part of a larger initiative to monitor the well-being, physical health and reproduction of rhinos in human care. Just like for humans, we believe that sleep duration/quality is critical to advancing individual health and well-being. For this project, a student will be organizing and analyzing game camera videos to understand the duration of and times that white and black rhinos sleep in zoos.

See also:

<https://integrative.gmu.edu/people/freeman>

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 communities 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.

Identification and quantification of post translational modification of RNA using mass spectrometry.

RNA post-transcriptional modification refers to the changes that occur to an RNA molecule after its synthesis from DNA, but before its final functional form. These modifications can include chemical alterations to the RNA molecule, such as methylation or adenosine-to-inosine editing, as well as the addition of different types of RNA-binding proteins. These modifications play a crucial role in regulating the stability, localization, and translational efficiency of RNA molecules. Additionally, they can also alter the coding information of the RNA, leading to variations in the final protein product. Some common examples of post-transcriptional modifications in RNA include alternative splicing, polyadenylation, and editing of messenger RNA (mRNA). In this study we are utilizing mass spectrometry as a diagnostic tool to measure the type and extent of RNA modification.

Development of N-terminal derivatizing agents to enhance ionization of poorly ionizable peptides.

In bottom up proteomics, proteins are digested to smaller peptides and measured by mass spectrometry. Many peptides may exhibit poor ionization behavior because of the nature of the amino acid sequence. The purpose of this study is to synthesize a tag to derivatize the N-terminal of small peptides to enhance their ionization and boost the instrument sensitivity.

A mass spectrometry-based assay to assess enzymatic activity of Sulf-1 enzyme.

Sulfatase 1 (SULF1) is an enzyme that belongs to the sulfatase family of enzymes. It is involved in the degradation of heparan sulfate proteoglycans, which are complex carbohydrates that play important roles in cell signaling, cell adhesion, and the regulation of growth factors. SULF1 has been implicated in various physiological processes, including angiogenesis, tumorigenesis, and the regulation of immune responses. Abnormal regulation of SULF1 activity has been linked to several diseases, including cancer and atherosclerosis. The purpose of this study is to develop a reliable and sensitive MS based assay to evaluate the activity of SULF1 enzyme in presence and in absence of an enzyme inhibitor.

Dr. Scott Glaberman

Assistant Professor

Department of Environmental Science and Policy

Host-Parasite Interactions in Galapagos Marine Iguanas

Marine iguanas are only found in the Galapagos Islands. They have a unique life history among reptiles, feeding on algae in the ocean and forming large groups on land that can number in the hundreds. These iguanas are also host to both ectoparasites, such as ticks, and endoparasites, which include a blood parasite related to malaria. The goal of this project is to genetically type blood parasites from iguanas through the archipelago and determine whether there is a single species or multiple species infecting their hosts. In addition, the evolutionary relationship of parasites from iguanas from different islands will be determined. This project will primarily involve skills in genetic sequencing, evolutionary biology, and population genetics. Courses in genetics, evolution, or microbiology, or experience in laboratory molecular biology are helpful but not required.

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.

- 1.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 – TGFβ1 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 TGFβ and any other IPF related cytokine is unknown. This project involves the exposure of these cells to TGFβ1, IL1β, PDGF and TNFα.
- 1.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

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.

Host response to SARS-CoV-2 infection

This project involves two aspects of COVID-19 infection: 1) preparation of cell cultures and their treatment with candidate therapeutics to test their efficacy against SARS-CoV-2; 2) analysis of host cell immune response to SARS-CoV-2 infection. The infections will be performed by a member of the laboratory who is certified to work in the BSL-3 containment and the inactivated samples will be brought out into the BSL-2 level for performance of the assays for this project by the Research Semester student. The student will learn in depth a variety of molecular biology and microbiology techniques in the course of this project, including cell culturing techniques, inhibition assays, cell viability assays, and Western blot analysis.

Perceptual and cognitive processes governing egg recognition in wild birds

Avian brood parasitism occurs when one bird (a parasite) lays its eggs in another birds' nest (a host). This alternative reproductive tactic allows parasites to offload parental care on their hosts, which must either pay these costs or adapt tactics to avoid parasitism. Many hosts have adapted mechanisms to avoid the costs of parasitism through recognizing and removing the young of brood parasites (either as eggs or young). Theoretical models of co-evolution have long assumed that hosts detect and remove a parasite's egg based on how different it appears to their own egg. Such choices depend on the visual perception of the host and down-stream cognitive decision rules it applies during egg recognition. However, recent research has demonstrated that these long-assumed perceptual and cognitive mechanisms underlying these host defense systems do not predict host egg recognition. Instead, hosts have strong biases against eggs of specific colors (rather than how those eggs' colors differ from their own egg's color). Such patterns alter the patterns and process of co-evolution. During this semester you will explore how perceptual-cognitive processes may explain host choices in the field and how those may have shaped the co-evolution between parasites and their hosts. You will gain experience with visual modelling and processing field and museum data.

A holistic examination of visual signals

Visual signals are vital for plants and animals. These signals transmit information from a sender to a specific receiver, such that the receiver may act on that information appropriately. It is therefore vital to understand the signal (the information sent), the information content (the transmitted message), and how that information is received (the visual abilities of the receiver). Many organisms see quite differently than us, because they have fewer visual photoreceptors, have additional visual photoreceptors (e.g., ultraviolet), or the sensitivity of the photoreceptors they have differ than our own. Sensory ecologists use this information to learn about how organism navigate the world around them and make choices about food and mates that impact their fitness. However, while sensory ecologists have made substantial progress to understand signals from the perspective of a receiver, a large amount of contextual information is typically ignored. This information involves how the signal appears in comparison to other visual information and how/when it is displayed. In this project you will use novel technology that can capture full visual fields as animals would perceive them. In this case, we will examine how nectar guides (ultraviolet dark bullseyes on some flowers) help orient honey bees to nectar rewards. We will integrate visual modeling in natural light conditions across space and time to demonstrate the utility of considering a richer array of contextual information.

Kathleen E. Hunt

Assistant Professor,

Department of Biology and Smithsonian-Mason School of Conservation

Baleen, horn and tusk: Reconstructing patterns in stress and reproduction from hormone patterns in whale baleen, antelope horns and narwhal tusks

Slow-growing tissues such as whale baleen, antelope horn, and narwhal tusk have recently been found to contain reproductive hormones and stress hormones and can serve as detailed, years-long record of reproductive cycles and stress over time. Such specimens can be used to calculate pregnancy rate in females, evaluate testosterone cycles in males, assess patterns in stress across years, and even can allow us to "look back in time" to compare past populations to present populations (for example, to assess the impact of current climate change). A new project focusing on Smithsonian museum specimens of blue and fin whale baleen from World War II will focus on identifying pregnancy rate of adult female whales at a time when the oceans were still relatively pristine. Baleen from several other species of whale, including the critically endangered North Atlantic right whale and the bowheads of the Arctic, are also available for student projects on individual whales. In another project, hormones in antelope horns (from Kruger National Park, South Africa, and the SMSC) will be inspected to determine whether human disturbance from tourism and poaching causes long-term elevations in stress hormones. New sample types under investigation include narwhal tusk and elephant tail hairs. Students will have the opportunity to visit Smithsonian "backstage" areas, will help drill powder from specimens and extract hormones from the powder, will learn how to do hormone assays, will produce real data on reproduction and stress, and (if interested) can contribute to papers. This project is primarily lab-based, with some visits to the Smithsonian National Museum of Natural History.

Leukotriene A4 hydrolase as a target for Alzheimer's Disease.

Alzheimer's disease (AD) is an irreversible, progressive neurodegenerative disease, which is the most common type of dementia among humans. Historically, strategies for treating AD focused on the inhibition of amyloid- β ($A\beta$) plaques and neurofibrillary tangles but failed to show any meaningful benefit in treating AD. Therefore, a new therapeutic target for AD is very much needed. Our study will explore the leukotriene A4 hydrolase (LTA4H) pathway as a potential new target for treating AD. LTA4H is an M1 metalloenzyme with two functions: (1) epoxy hydrolase (EH), LTA4H hydrolyzes LTA4 to LTB4, which is a pro-inflammatory process, and (2) aminopeptidase (AP), LTA4H degrades the tripeptide Pro-Gly-Pro (PGP), which is an anti-inflammatory process. Recent studies have shown that LTB4 may participate in the etiology of AD, indicated by an increase in steady-state levels of γ -secretase proteins. In addition, inefficient cleavage of PGP can lead to acetylation at the N-terminus by reactive aldehydes to afford N-acetyl Pro-Gly-Pro (AcPGP), which has been reported to mediate neurodegeneration in inflammatory disorders of the central nervous system (CNS). Therefore, our study will characterize the effect of modulating LTA4H enzyme activity for AD in vitro.

Idiopathic pulmonary fibrosis (IPF) treatment by blocking sulfatase-1 (Sulf-1).

Idiopathic pulmonary fibrosis (IPF) is a progressive interstitial lung disease of unknown etiology, characterized by scarring in the lung and impaired pulmonary function. The pathogenetic mechanisms leading to IPF are poorly understood, and there are currently no effective therapies. There are several studies on heparan sulfate 6-O-endosulfatase, Sulf1, which is up-regulated in the IPF lungs and involved in the pathogenesis of IPF. Therefore, our study will focus on the isolation of recombinant human Sulf1 in E.coli to characterize the enzymatic activity of Sulf1 using 4-MUS as a substrate.

Chronic obstructive pulmonary disease (COPD) targeting leukotriene A4 hydrolase CRISPR research.

The leukotriene A4 hydrolase (LTA4H) enzyme is a protein with two dichotomous functions in the lung. As an epoxide hydrolase (EH), LTA4H catalyzes the hydrolysis of leukotriene A4 (LTA4) to leukotriene B4 (LTB4), which results in neutrophilic inflammation. In contrast, several studies suggest that LTA4H aminopeptidase (AP) activity promotes the resolution of neutrophilic infiltration by catalyzing the hydrolysis of the tripeptide proline-glycine-proline, (PGP). A previously published X-ray crystal structure showed that D375 is involved in EH activity. Our previous studies showed that Q136 could have a role in tripeptide substrate recognition and catalytic turnover by rotational freedom in AP activity. Therefore, our study will focus on the expression of D375N (no EH, but significant AP activity) and Q136N (no effect on EH but abolish AP) LTA4H mutants to characterize the enzymatic activity of the two.

Dr HC Lim

Assistant Professor

Department of Biology

Machine-learning based identification of bird songs from tropical Asia collected with autonomous audio recorders

Many rainforest bird species are at risk of population decline and local extirpation due to habitat degradation and fragmentation. To study species specific sensitivity and response to habitat fragmentation, autonomous recorders will be deployed in Borneo study sites. The correct identification of bird species enables downstream occupancy modeling and identification of factors that drive species decline.

Dr David Luther
Assistant Professor
Biology Department

Long-term trends in forest communities and functional diversity

In the project “long-term trends in forest communities and functional diversity” we are looking at how biodiversity and its relationship to ecological processes are changing over time in forested ecosystems. We merge species presence data and data about morphological traits, and behaviors to assess how the presence and absence of specific species contribute to overall ecosystem health. Some aspects of this project are based locally in Virginia, others assess forests of North America, while some are based in the Amazon rainforest.

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 their association with population increases in the threatened species.

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 Aarthi Narayanan

Associate Professor,

Department of Biology

Broad spectrum antiviral targets

This project will focus on our small molecules portfolio and will assess how specific host targets, including the signal transduction enzymatic machinery, influence viral infections. This project will explore how common targets intersect with and influence the establishment of a productive viral infection in the context of multiple acutely infectious viruses that cause human disease.

Host response modulation by antiviral peptides

This project will explore how evolutionarily conserved antiviral peptides or newly designed synthetic versions impact the ability of a virus to infect a target cell. The project will also address different strategies to help peptides find their intracellular host targets and modulate the innate immune responses.

Both projects will also look at how virus-infection induced inflammatory events cause tissue damage and how intervention strategies can help mitigate the deleterious consequences of acute viral infection.

Dr Valerie Olmo
Associate 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.

Total synthesis of natural products

Natural products from terrestrial or marine sources have been used to discover new drugs to treat diseases. The molecular structures derived from nature can afford new motifs that have not previously been exploited in drug discovery. Additionally, the challenges of assembling these new structural motifs require the development of new synthetic methodology.

Strategies in medicinal chemistry

Medicinal chemistry involves the design and synthesis of small molecules as potential new drugs. The discipline is highly interdisciplinary and involves working with biochemists, biologists, pharmacologists, etc. A common theme in medicinal chemistry is to identify a biological target that can be modulated with a small molecule, and then optimize the structure of the small molecule for increased potency against the target. In this project, we will follow established synthetic routes to synthesize new small molecules to assay against an enzyme target. We will work with a biochemist to interpret the effect of chemical structure on modulating the enzyme.

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, protozoans) 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.

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).

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

Assistant Professor

Department of Global and Community Health

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, *Ixodes 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 Andrea Weeks
Associate Professor

Dept. Biology

Director of the Ted R. Bradley Herbarium (GMU)

Evolution of Madagascar myrrh trees: species discovery

Description: Madagascar is often referred to as the eighth continent in recognition of its spectacularly diverse and unique biota. It is also among the most environmentally degraded regions on the planet, which adds urgency to research regarding the discovery and analysis of its biodiversity. This RS project will take place in a molecular systematics lab on the Fairfax campus and will focus on collecting and analyzing genetic data necessary for describing newly-discovered species that are endemic to island, the Madagascar myrrh trees. Students will learn to apply lab techniques of DNA extraction, PCR, agarose gel electrophoresis, DNA sequence preparation, and phylogenetic analysis of comparative DNA sequence data for these as-yet-undescribed species. Students will also become familiar with the multi-faceted process of scientific species description

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.

Please email Dr. Wu for more information at:

ywu8@gmu.edu

Projects at the Johns Hopkins University Bloomberg School of Public Health

If you are interested in an opportunity to participate in the Fall Research in the Biochemistry and Molecular Biology Department at the Johns Hopkins University Bloomberg School of Public Health, please contact Dr. Olmo (volmo@gmu.edu)

Matunis, Michael: *Sumoylation, DNA repair and chromosome segregation.* Research in the Matunis lab focuses on understanding how sumoylation promotes genome integrity through effects on repair of DNA doublestrand breaks and control of accurate chromosome segregation. Because of its essential roles in these and other processes, defects in sumoylation are associated with multiple human cancers. Studies have included understanding how sumoylation affects the DNA repair activities of the cancer susceptibility factors BLM and BRCA1.

Rebecca, Vito: *Dissecting clonal diversity in melanoma to overcome therapy resistance and metastasis.* The Rebecca laboratory focuses on understanding non-genetic mechanisms of resistance leveraged by stem cell-like tumor cell subpopulations critical in the escape of melanoma cells from targeted- and immune-therapy. Their particular focus is on how melanoma cells “hijack” developmental signaling cassettes to drive transient metastatic and drug resistant cell states. Their studies encompass quantitative tools, genetic editing, molecular biology, *in vivo* patient-derived xenograft therapy trials and bioinformatic analyses to arrive at a comprehensive understanding of actionable vulnerabilities for stem cell-like subpopulations of cancer cells.

Weeraratna, Ashani: *Mechanisms and Influences of the Microenvironment on Metastasis.* The Weeraratna laboratory focuses on the effects of the tumor microenvironment on metastasis and therapy resistance. Their particular focus is on how the aging microenvironment guides metastasis and therapy resistance in melanoma. Their studies encompass biophysical changes that affect the ability of both tumor and immune cells to migrate, that affect vasculature integrity thus dictating routes of metastasis, and also secreted changes that drive metastatic signaling and response to therapy. The Weeraratna laboratory has also undertaken a global analysis of how the aged microenvironment promotes metastasis.

Please contact Dr. Olmo for more information (volmo@gmu.edu).