



23rd Annual
Summer
Undergraduate
Research
Fest

Hosted virtually using the *VoiceThread* platform by the
College of Natural and Mathematical
Sciences

August 5 to 14, 2020

<https://surf.umbc.edu/virtual-surf-2020/>

A message from the Dean

Welcome to the 2020 Summer Undergraduate Research Fest (SURF) at UMBC. This year, due to the COVID-19 challenges and required changes on campus, CNMS is hosting a virtual and unique SURF event from August 5 – August 14.

This event defines the SUMMER STEM experience, where the focus is on high quality STEM classes, opportunities for research and applied learning experiences, and building a strong scholarly STEM community. By practicing and applying the skills of performing research this summer, our students follow in the footsteps of great scientists and researchers – making each a part of a grand scholarly community.



We are delighted to be able to offer this virtual SURF event so our students who have worked so diligently all summer will have the opportunity to participate in our distinctive annual SURF event. During this week, you will see student research presentations. As participants in SURF, you will be able to leave video, voice, or text feedback for the presenters thus affirming your personal “presence” with our students. Our presenters will be responding to your questions and interacting with you throughout the week.

We are proud of all that our students accomplished this summer. They are more knowledgeable, experienced, and skilled – better scientists. Their discoveries, their effort, their willingness to explore have added to the vault of scientific knowledge, which in the end - benefits society through an empowerment – an empowerment of understanding, prediction, and invention. Their success is also due to the tremendous effort, guidance and support provided by their mentors and across campus by our faculty and staff who support and engage our students every day. Please accept my heartfelt thank you to all of you who work with these outstanding students and help them reach their goals.

I thank you for visiting our virtual SURF event and encourage you to view the many outstanding works of our presenters and to interact with these remarkable students.

Welcome to the **Virtual SURF 2020** event,

William R. LaCourse, Ph.D.
Dean and Professor of Chemistry

ACKNOWLEDGEMENTS

The Virtual SURF 2020 represents a true collaborative effort. First, we want to thank Dr. April Householder who generously shared templates and her experiences from the 2020 URCAD when an online SURF 2020 was first being considered. Many thanks go to the very patient VoiceThread experts and instructional design team members from the Division of Information Technology who made the Virtual SURF 2020 possible. Another thanks goes to Melissa Penley Cormier for creating the banner from photos taken at the 2014 SURF. Another big thank you goes to Dr. Lola Brown, who volunteered to share her expertise and experiences through the presentation workshop, The Science of Poster & Oral Presentations, for prospective SURF presenters on July 15, 2020.

It is important to recognize Dr. William R. LaCourse, the CNMS Dean (and long-time SURF research mentor), for his continued support of SURF and undergraduate research at UMBC. We also want to thank the many program directors, program coordinators, department staff, and college personnel who continue to support SURF and undergraduate research opportunities - near and far. We thank the many faculty, lab, staff, and peer mentors of this year's SURF presenters who were willing to support these undergraduate researchers during the COVID-19 outbreak. Their dedication to students and their undergraduate research training is both admirable and amazing!

We also send our thanks to all the Virtual SURF 2020 visitors - especially those taking time to make this a truly interactive event by leaving written and recorded messages for the presenters.

Dr. Kathy Lee Sutphin, Assistant Dean of Academic Affairs, CNMS
Ms. Justine Johnson, Associate Director, Meyerhoff Graduate Program

MENTORS

Kudos to all of the mentors who supported this year's SURF student presenters. There are many types of mentors who support the research training of novice scientists that include student peers, program staff, graduate students, laboratory personnel, and research scientists. While space prohibits mentioning the names of the many mentors who made the Virtual SURF 2020 possible, we would like to acknowledge the following primary research mentors.

Dr.	Diane	Alonso	UMBC	Department of Psychology
Dr.	Michael	Betenbaugh	Johns Hopkins University	Department of Chemical and Biomolecular Engineering
Dr.	Charles	Bieberich	UMBC	Department of Biological Sciences
Dr.	Dawn	Biehler	UMBC	Department of Geography & Environmental Systems
Dr.	Rachel	Brewster	UMBC	Department of Biological Sciences
Dr.	Sheldon	Broedel	Past UMBC Adjunct Professor	Athena ES, Gardner Industries, LLC
Dr.	Maria	Cambraia Guimaro	UMBC	College of Natural & Mathematical Sciences
Dr.	Joseph	Carmicheal	University of Nebraska Medical Center	Department of Biochemistry and Molecular Biology
Dr.	Steven	Caruso	UMBC	Department of Biological Sciences
Dr.	Jonathan	Cohen	Princeton University	Princeton Neuroscience Institute, Department of Psychology
Dr.	Belay	Demoz	UMBC	Department of Physics
Dr.	Mary	Devadas	Towson University	Department of Chemistry
Dr.	Charles	Eggleton	UMBC	Department of Mechanical Engineering
Dr.	James	Foulds	UMBC	Department of Information Systems
Dr.	Jeffery	Gardner	UMBC	& Gardner Industries, LLC
Dr.	Christopher	Hennigan	UMBC	Department of Chemical, Biochemical, and Environmental Engineering
Dr.	Scott	Jones	NIST	Materials and Structural Systems Division
Dr.	Anupam	Joshi	UMBC	Department of Computer Science and Electrical Engineering

Dr.	Minjoung	Kyoung	UMBC	Department of Chemistry
Dr.	William	LaCourse	UMBC	Department of Chemistry and Biochemistry
Dr.	Jeff	Leips	UMBC	Department of Biological Sciences
Dr.	Weihong	Lin	UMBC	Department of Biological Sciences
Dr.	Helena	Mentis	UMBC	Department of Information Systems
Dr.	Curtis	Menyuk	UMBC	Department of Computer Science and Electrical Engineering
Dr.	Stephen M.	Miller	UMBC	Department of Biological Sciences
Dr.	Alan R.	Morrison	Brown University	Department of Internal Medicine (Cardiovascular Medicine)
Dr.	Achuth	Padmanabhan	UMBC	Department of Biological Sciences
Dr.	Sanjay	Purushotham	UMBC	Department of Information Systems
Dr.	Phyllis	Robinson	UMBC	Department of Biological Sciences
Dr.	Carlos	Romero-Talamas	UMBC	Department of Mechanical Engineering
Dr.	Katherine	Seley-Radtke	UMBC	Department of Chemistry and Biochemistry
Dr.	Jinglai	Shen	UMBC	Department of Mathematics and Statistics
Dr.	Viknesh	Sivanathan	Howard Hughes Medical Institute	Science Education
Dr.	Michelle	Starz-Gaiano	UMBC	Department of Biological Sciences
Dr.	Michael F.	Summers	UMBC	Department of Chemistry and Biochemistry
Dr.	Jianwu	Wang	UMBC	Department of Information Systems

PROGRAMS

Research experience programs and internships, both grant-funded and university-supported, provide career-focused training that supports undergraduate researchers during traditional summer semesters and/or academic years.

The SURF team would like to recognize the support given by these research programs and internships and their staff. This support and the related benefits to novice researchers provide early, life-changing professional research and presentation opportunities. These programs are listed as follows.

<i>Program</i>	<i>Support</i>	<i>Website</i>
COEIT Summer Research Experience Program	UMBC College of Engineering and Information Technology	https://coeit.umbc.edu/coeit-srep/
HHMI Scholars Program	Howard Hughes Medical Institute	https://www.hhmi.umbc.edu/hhmischolars/
Louis Stokes Alliance for Minority Participation Research Programs	UMBC - University System of Maryland	https://lsamp.umbc.edu/
U-RISE (MARC) Program	National Institute of General Medical Sciences at the NIH	https://urise.umbc.edu/
McNair Scholars	U.S. Department of Education Trio Program	https://mcnair.umbc.edu/
Meyehoff Scholars at UMBC	Supported by a network of institutional partners, friends, and donors	https://meyerhoff.umbc.edu/
NSF Research Experiences for Undergraduates	National Science Foundation	https://www.nsf.gov/crssprgm/reu/
STEM BUILD 2.0 at UMBC	Funded by the NIH Common Fund and managed by NIGMS	https://stembuild.umbc.edu/

Virtual SURF 2020

Presenters and Complete Abstracts

Listed in alphabetical order of the first presenter's last name

Consistent with its commitment to academic freedom, UMBC does not restrict the topics of inquiry that can be accepted for SURF, the conclusions that are reached in student work, or the representations chosen by the student and mentor for that work. A mentor-approved abstract describing the work and its intellectual context is required. Approval to present work at SURF is given by the faculty mentors of the students. All presenters have some connection to UMBC, its faculty, and/or its programs.

UMBC is committed to creating an accessible and inclusive environment for all students, staff, and visitors. This event will be auto-captioned. For information about *VoiceThread* accessibility support, please visit:
<https://wiki.umbc.edu/pages/viewpage.action?pageId=96537371>

CHARACTERIZING THE EFFECTS OF FERRITIN ON OVARIAN CELL MIGRATION IN *DROSOPHILA MELANOGASTER*

Susan Afolabi¹, Mallika Bhattacharya¹, Michelle Starz-Gaiano²

^{1,2}Department of Biological Sciences, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

Drosophila melanogaster, commonly known as the fruit fly, has well characterized genetics and is easy to manipulate genetically. Besides the availability of experimental tools, homology between *Drosophila* and mammalian proteins and genes makes *Drosophila* an excellent system to model developmental processes. Migratory cells in the female fruit fly ovaries migrate in clusters at a certain time in development and are known as border cell clusters. Border cell clusters are useful in understanding how collective cell migration works, which is important for disease progression, wound healing and animal development.

Our lab and others have discovered that steroid hormone signaling is important for regulation of border cell migration. We hypothesize that the ferritin complex plays an important role in this pathway. Ferritin is an iron storage molecular complex made of heavy and light chains which are encoded by 3 different genes in *Drosophila*: *fer 1hch*, *fer 2lch*, and *fer 3hch*. Our preliminary results indicate that varying the expression of ferritin genes affects border cell migration. In this project we are working to characterize the normal spatiotemporal expression of ferritin genes and predict how the ferritin gene cluster in border cells is genetically regulated. To do this, we are mining genomic data for transcriptional factor binding site information and regulatory sequence information. We identified the transcription factor Twist as a likely regulator of ferritin gene expression in addition to steroid hormone signaling.

Moving forward, we would like to characterize the role of ferritin subunits and describe how the protein complex works in different contexts as well as to investigate candidate regulators. We will also search genome-wide for transcriptional targets of the key transcriptional factors that regulate border cell migration. This work may suggest an important role for ferritin in other cell types that migrate even in other species.

This work was supported in part by the National Science Foundation grant IOS-1656550 to M.S.G. It is also supported by UMBC LSAMP and UMBC McNair programs.

CORRELATION BETWEEN MINOR TAIL PROTEIN OF BACTERIOPHAGES AND THE HOST

Achalefac Akem¹, Angela Kim¹, Emma Lorentz¹, Gloria Ogordi¹, Lee Harkless², Maria Cambraia^{1,3}, Steven Caruso²

¹STEM BUILD, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

²Department of Biological Sciences, University of Maryland, Baltimore Country, 1000 Hilltop Circle, Baltimore, MD 21250

³College of Mathematical and Natural Sciences, University of Maryland, Baltimore Country, 1000 Hilltop Circle, Baltimore, MD 21250

Bacteriophages are viruses that infect bacteria. They use tail fibers to attach to the receptors of bacteria prior to injecting their DNA into the cell, which allows them to reproduce using the host's cell machinery. Our research question focuses on determining the correlation between the minor tail proteins and the targeted hosts of the bacteriophages. It was then hypothesized that bacteriophages with similar minor tail proteins will infect the host bacteria in the same genus.

Two different methods were used to find the relationship between the minor tail proteins and the targeted hosts. For the first approach, phylogenetic trees were created to examine differences in phage clustering between the whole genome and the minor tail proteins. Bacteriophages containing the minor tail proteins of pham 14719 and pham 8861 were selected, and a phylogenetic tree using whole genome of those phages was created with VICTOR. To create the second tree, the minor tail proteins sequences of the selected phages were gathered from Phamerator, and concatenated, and then used to produce a maximum parsimony phylogenetic tree using MEGA.

Overall, the two phylogenetic trees both display a similar cluster pattern with each set of phages grouped into sub-clusters sharing the same host. However, two phages, ClubPenguin and Sporto, diverged from the genomic pattern. This suggests that the minor tail proteins of these two phages are more like those of the phages isolated on different host and belonging in different clusters. Further investigation is now necessary to investigate the relationship between minor tail proteins and their suspected host.

This research was supported by the Science Education Alliance, Howard Hughes Medical Institute, Chevy Chase, MD, and the National Institute of General Medical Sciences of the National Institutes of Health Under Award Numbers TL4GM118989, UL1GM118988, and RL5GM118987. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

MODELING THE MECHANICAL PROPERTIES OF CEMENT PASTE FOR OPTIMIZING 3D PRINTING APPLICATIONS USING COMPUTATIONAL MODELS DEVELOPED IN COMSOL MULTIPHYSICS

Ashley Amundsen¹, Dr. Charles Dionisio Eggleton¹, Dr. Scott Jones²

¹Department of Mechanical Engineering, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

²Materials and Structural Systems Division, National Institute of Standards and Technology, 100 Bureau Drive Gaithersburg, MD 20899

Concrete is a well-known material widely used throughout history, from the creation of hydraulic cement-based concrete in Ancient Rome to the invention of portland cement by Joseph Aspdin in 19th century England, it continues to play a critical role in many engineering applications. There are many different types of concrete, although the most basic definition defines it as a material made from mixing cement with water and other aggregates that, under the right conditions, will harden into a structure with significant strength. Due to its versatility, it is no surprise that builders are already using concrete for 3D printing applications. As we begin to use 3D printed concrete domestically, it is crucial to relate 3D printing processes to the mechanical properties of printed concrete. A first step in understanding the 3D printing process is to model the flow of cement paste in a simple 3D printer geometry. We model the viscosity of cement paste by fitting a power law model to rheological measurements made at NIST. By changing the parameters of the power law model for viscosity we can model the flow of cement pastes with different compositions. We use the rheological models of cement paste to simulate flow through a tube with a nozzle at the end using COMSOL Multiphysics. The simulations will provide us with predictions of the pressure needed to drive the flow, how the velocity of the cement paste depends on position in a channel/tube, and how shear stress/forces on the cement paste depend on position. Cement samples will be printed at NIST and their material properties will be measured. The simulation data will be used to correlate the material properties to the 3D printing processes. Further testing aimed at defining yield stress and plastic viscosity on various forms of cement paste will also take place.

THE CLASSIFICATION AND GENE EXPRESSION OF HOLIN IN *STREPTOMYCES* PHAGE THIQQUMS

Tyler Autrey¹, Toni Martin¹, Grace Tugado¹, Sharath Velliyamattam¹, Lee Harkless^{1,3},
Maria Cambraia^{1,2}, Steven Caruso^{1,3}

¹STEM BUILD, University of Maryland, Baltimore County, 1000 Hilltop Circle, Catonsville,
MD 21250

²College of Natural and Mathematical Sciences, University of Maryland, Baltimore County,
1000 Hilltop Circle, Catonsville, MD 21250

³Department of Biological Sciences, UMBC 1000 Hilltop Circle, Baltimore, MD 21250

With increases in antibiotic resistance, the potential usage of bacteriophages has been perceived as an alternative solution for treatment of bacterial infections. The specificity of phages, identified by host range, proves beneficial to the implementation of phage therapy. Therefore, additional information about the proteins used during the lytic cycle is essential. Holins are small proteins that control cell membrane breakage toward the end of the lytic cycle and allow endolysin to degrade the peptidoglycan layer. Holin is categorized into two common classes (class I and II); class I typically contains three transmembrane domains (TMDs) and class II contains two TMDs. The purpose of this research is to classify the holin in the *Streptomyces* phage Thiqqums' genome.

A literature review of holin and the lytic cycle enabled further exploration into the potential of phage therapy. To determine the characteristics of the Thiqqums' holin, software was utilized to compare the alignment of residues to known proteins. Phamerator displayed strong evidence for a holin gene, as three genomes within the same cluster (BI4) shared an E-value = 0.0e0 and 100% alignment.

In order to identify this specific protein class, the amino acid sequence of holin was analyzed through TOPCONS and SOSUI. SOSUI predicted that our holin has two TMDs, which indicated that Thiqqums may contain a class II holin. To gain a better understanding of holin's relationship to lysis, we conducted a literature review, compiling articles about lysis, holin's importance during lysis, and holin's influence on certain bacteria. The holin coded in *Streptomyces* phage Thiqqums is predicted to be a class II holin that affects gram-positive bacteria. For future experiments, we will investigate a range of phages to test their potency of eliminating two specific bacterial strains based on the type of holin they possess.

This research was supported by the Science Education Alliance, Howard Hughes Medical Institute, Chevy Chase, MD, and the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers TL4GM118989, UL1GM118988, and RL5GM118987. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

CHARACTERIZATION OF GENES INFLUENCING THE AGE-SPECIFIC CHANGES IN PHAGOCYTOSIS OF *DROSOPHILA MELANOGASTER*, USING AN *IN VIVO* PHAGOCYTOSIS ASSAY

Briah Barksdale¹, Shonda Campbell¹, Jeff Leips¹

¹Department of Biological Sciences, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

The innate immune response is an evolutionarily conserved process that is essential for host survival in almost all multicellular organisms. As we age, immune functions begin to decline, or immunosenesce, posing a serious risk to human health due to the reduced ability to fight infections. The way that age affects the immune response can vary greatly among individuals and populations, and this variation has a significant heritable component. These age-related changes also influence aspects of phagocytosis that are important for maintaining an adequate immune response; however, little is known about the genetic basis of cellular based immunosenescence. The goal of this project is to characterize the role of previously identified candidate genes in regulating age-specific changes in phagocytosis, to better understand the mechanisms that give rise to immunosenescence. This will be done using the model organism *Drosophila melanogaster*, and a newly developed *in vivo* phagocytosis assay to test if previously identified candidate genes regulate changes in phagocytosis with age. This information could lead to targets for therapeutic treatments and improve or restore immune function in elderly people.

Thank you Dr. Leips, my research mentor Shonda Campbell, the Leips Lab, the Meyerhoff Scholars Program, Louis Stokes Alliances for Minority Participation, and the Undergraduate Research Training Initiative for Student Enhancement. This investigation was supported by in part by a grant to University of Maryland, Baltimore County from NIH R03 AG061484-02 and Becton Dickinson Faculty Research Fund.

OPTIMIZING THE SEPARATION OF AN ANTIPARASITIC MEDICATION USING HIGH-PRESSURE LIQUID CHROMATOGRAPHY (HPLC)

Karis R. Barnett¹ and William R. LaCourse¹

¹Department of Chemistry & Biochemistry, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

Excess pharmaceutical waste in water is an emerging concern that can increase parasitic drug resistance, interrupt animal food chains, and threaten drinking water sources. A high-pressure liquid chromatography (HPLC) method with ultraviolet (UV) detection (210 nm) is under development for sensitively quantifying and separating antiparasitic medication praziquantel (PZQ) and related compound metronidazole (MET). This method has the potential to commercially monitor antiparasitic treatments administered to aquatic species, which can ultimately limit pharmaceutical waste in water. The latest HPLC method was altered over seven experiment trials to improve resolution and Gaussian shape of chromatogram peaks. The most efficient separation of PZQ and MET was achieved on a Phenomenex™ Luna C₁₈ analytical column (150 x 4.60mm, 5µm, 100Å) using acetonitrile:water at alternating ratios of 20:80 v/v and 80:20 v/v as a mobile phase. This separation resulted in the shortest acquisition time with satisfactory peak shape. Aquarium facilities may ultimately use this method to understand how to safely treat parasitic fish diseases while avoiding environmental damage.

The primary author would like to thank the LaCourse Lab Group and the MCAC for their support and guidance. This investigation was sponsored by the U-RISE Program supported by the National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 136497.

CONSEQUENCES OF TELOMERE SHORTENING IN THE MOUSE PROSTATE GLAND

Maria Bieberich¹, Michael Rubenstein¹, Alan Meeker², Charles Bieberich¹

¹Department of Biological Sciences, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

²Department of Pathology, Johns Hopkins University School of Medicine, 733 N Broadway, Baltimore, MD 21205

Telomeres are highly repetitive, non-coding DNA segments located at chromosome ends. Telomeres, together with the telomeric-binding protein complex Shelterin, protect chromosomes by providing DNA that can be lost without losing any genes during DNA replication. DNA replication does not completely synthesize the ends of both strands of linear DNA due to the mechanism of synthesis of the lagging strand, shortening chromosomes by 50-200 base pairs after each round of replication. Without telomeres, continuing chromosomal erosion can affect DNA that encodes for genes, leading to deletion mutations. Telomeres also stabilize chromosome ends, thus critically shortened telomeres also pose a threat to chromosomal stability by enhancing the risk of chromosomal end-to-end fusion and subsequent breakage during mitosis, leading to translocations and large-scale deletions, abnormalities commonly seen in cancer. In keeping with this, shortened telomeres in prostate epithelial cells have been linked to prostate cancer. We hypothesized that short, dysfunctional telomeres play a causal role in the disease. To test this hypothesis, we expressed a telomere-specific endonuclease in mouse prostate glands and examined its effect on telomere length using fluorescent *in situ* hybridization. We demonstrated that expression of telomeric endonuclease activity in prostate epithelial cells results in critically short telomeres. These mice will be monitored for the emergence of abnormalities in prostate histomorphology in an otherwise wild type background and in a mouse strain with forced overexpression of the human MYC oncogene. We predict that if our hypothesis is correct, we will see the appearance of early prostate cancer lesions in the wild type setting and accelerated tumorigenesis in the setting of MYC overexpression.

CHARACTERIZING BACTERIOPHAGE GENES CAPABLE OF INHIBITING BACTERIAL GROWTH

Duyen Bui¹, Jamie Mushrush¹, Danielle Heller², Viknesh Sivanathan²

¹U-RISE, University of Maryland Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

²Science Education Department, Howard Hughes Medical Institute, 4000 Jones Bridge Road, Chevy Chase, MD 20815

Antibiotic resistance is an increasingly important issue in the world today; we are engaged in an arms race with bacteria, and we are struggling to keep up. Bacteriophage may offer a novel approach to this problem, as they have been invading and killing bacteria for many thousands of years. By encoding genes that overtake the cellular mechanisms of the bacteria to reproduce, then rupturing the host bacteria in order to release new phage particles, bacteriophage manage to sustain their existence while eliminating their host. Thus, we are investigating genes from phages that infect *Mycobacterium smegmatis*, both because of its close relatedness to the pathogen *Mycobacterium tuberculosis*, and because of the abundance of characterized bacteriophages able to infect it. Because of this close relatedness, bacteriophage genes that are toxic to *M. smegmatis* could also be toxic in *M. tuberculosis*, creating an avenue for novel gene therapies.

Former lab members discovered that homologous gene products (gp) 47 and 54 from the mycobacteriophages Larva and Hammy respectively, inhibit the growth of *M. smegmatis*. As homologous genes products, the genes themselves share some commonalities; aligning these sequences reveal a highly conserved C-terminal domain and a poorly conserved N-terminal domain. Initial truncation analyses indicated that the conserved C-terminal domain of both proteins was not necessary for growth inhibition, and the less-conserved N-terminal domain of both proteins was toxic by itself. Therefore, the focus of this research is to 1) reproduce this truncation analysis in an optimized expression system to verify these observations, 2) identify features and residues of the amino acid sequence or subdomains that have a significant role in growth inhibition, and 3) identify the target bacterial protein of these phage proteins.

The U-RISE Program at the University of Maryland, Baltimore County (UMBC) is supported by the National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 136497.

APICAL CONSTRICTION MOLECULAR MACHINERY WITHIN THE ZEBRAFISH MEDIAL HINGE POINT

Allyson Caldwell¹, Dominique Brooks¹, Jonathan Werner¹, Maraki Negesse¹, and Rachel Brewster, PhD¹

¹Department of Biological Sciences, University of Maryland, Baltimore County, 1000 Hilltop Circle, Catonsville, 21250

Bending and folding of the neural plate to form the neural tube, otherwise known as neurulation, is an early and necessary morphogenetic event for the formation of the central nervous system. Failure of the neural tube to form properly leads to neural tube defects (NTDs). Despite the frequency of NTDs, the cellular and molecular mechanisms of neurulation remain poorly understood. We aim to establish the zebrafish as a model system to study neurulation and risk factors of NTDs. However, neurulation in zebrafish is thought to differ from that of more commonly used models to study NTDs, as hallmarks of neurulation, such as hinge points and neural folds, have not been observed in this organism. Through the use of immunolabeling and confocal microscopy we show apical localization of actin and myosin in medial cells of the zebrafish anterior neural plate, similar to the medial hinge points of other vertebrates. Furthermore, we confirmed, using blebbistatin, that disruption of this actomyosin network prevents apical constriction, hinge point formation and neural fold elevation and convergence. Our findings indicate that there is a high level of conservation of mechanisms of neurulation across vertebrates, paving the way for studies investigating genetic risk factors for NTDs using zebrafish.

The U-RISE Program at the University of Maryland, Baltimore County (UMBC) is supported by the National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 136497.

Synthesis of Flex-Guanosine Analogues as Potential Antiviral Therapeutics

¹Evan Carlyle, ¹Charlie Waters, ¹Katherine Seley-Radtke

Department of Chemistry and Biochemistry, University of Maryland, Baltimore County, MD
21250

Many nucleoside analogues are currently used today as therapeutics against cancers and viruses such as Human Immunodeficiency Virus (HIV), hepatitis B virus (HBV), and herpes simplex virus (HSV) among many others. However, growing resistance to these drugs poses a serious issue as viral enzymes can reduce drug binding affinities through point mutations and binding site conformational changes, rendering the drugs less potent against life threatening diseases.

To overcome this, the Seley-Radtke lab has done extensive work in producing nucleoside analogues with flexible purine base moieties, known as Fleximers. The added flexibility in the purine base moiety allows the nucleosides to adapt into conformations not normally accessible by the fused purine base moiety, while still maintaining activity. This activity is apparent when looking at the flex-analogues of acyclovir, an FDA approved drug for HSV. In contrast to acyclovir, the corresponding flex-analogues exhibited low micromolar activity against Ebola, Severe Acute Respiratory syndrome (SARS), Middle East Respiratory Syndrome (MERS), Dengue and Yellow Fever viruses. The ability to change conformations within a binding pocket allows for the fleximers to adapt their conformations to allow for better binding affinity, as well as to overcome point mutations in a binding pocket to retain their activity by engaging secondary amino acid residues not previously involved in the mechanism of action has been seen in previous studies utilizing Fleximers as molecular probes. The current aim of this project is to synthesize a series of Flex-2'-deoxy-G and Flex-G prodrugs and other 5' modifications to further explore their antiviral potential.

This work would not have been possible if it weren't for the funding provided by the NIH grants NIH/NIGMS T32 GM066706 and NIH/NIAID R21AI135252, and funding provided by the Meyerhoff Scholars Program and U-Rise Scholars program

IDENTIFICATION OF THE INITIAL NUCLEOCAPSID RECOGNITION ELEMENT IN THE HIV-1 RNA PACKAGING SIGNAL

Pengfei Ding¹, Siarhei Kharytonchyk², Alexis Waller¹, Ugonna Mbaekwe¹, Sapna Basappa¹, Nansen Kuo¹, Heather M. Frank¹, Christina Quasney¹, Aaron Kidane¹, Canessa Swanson¹, Verna Van¹, Mitali Sarkar¹, Emily Cannistraci¹, Ridhi Chaudhary¹, Hana Flores¹, Alice Telesnitsky², and Michael F. Summers¹

¹Department of Chemistry and Biochemistry, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD, 21250

²Department of Microbiology and Immunology, University of Michigan Medical School, 1301 Catherine St, Ann Arbor, MI, 48109

Selective packaging of the HIV-1 genome during virus assembly is mediated by interactions between the dimeric 5'-leader of the unspliced viral RNA and the nucleocapsid (NC) domains of a small number of assembling viral Gag polyproteins. We found that the dimeric 5'-leader contains more than two dozen NC binding sites with affinities that reside within a ~150-nt region of the leader sufficient to promote RNA packaging (core encapsidation signal, Ψ CES). The four initial binding sites with highest affinity reside near two symmetrically equivalent three-way junction structures. Unlike the other high-affinity sites, which bind NC with exothermic energetics, binding to these sites occurs endothermically due to concomitant unwinding of a weakly base-paired [UUUU]:[GGAG] helical element. Mutations that stabilize base pairing within this element eliminate NC binding to this site and severely impair RNA packaging into virus-like particles. NMR studies reveal that a recently discovered small-molecule inhibitor of HIV-1 RNA packaging that appears to function by stabilizing the structure of the leader binds directly to the [UUUU]:[GGAG] helix. Our findings suggest a sequential NC binding mechanism for Gag-genome assembly and identify a potential RNA Achilles' heel to which HIV therapeutics may be targeted.

This research was sponsored by the NIH/ NIGMS Grant #1P50GM103297 and was also supported in part by a grant to UMBC from the Howard Hughes Medical Institute through the HHMI Adaptation Project. All research was conducted at the Howard Hughes Medical Institute at UMBC.

***STREPTOMYCES* PHAGE CLUSTERING BASED ON TAIL LENGTH AND TAPE MEASURE PROTEIN**

Amanda Chen¹, Senali Dansou¹, Austin Fowler¹, Zachary Willis¹, Lee Harkless³,
Maria Cambraia^{1,2}, Steven Caruso³

¹STEM BUILD, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

²College of Natural and Mathematical Sciences, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

³Department of Biological Sciences, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

Bacteriophages, also called phages, are the most numerous microbial organisms on Earth and are known for infecting bacterial hosts. When discussing phages, biologists usually use the term cluster, which refers to a group of phages that share similar characteristics. Fascinated by the variety and number of clusters that exist, we decided to scrutinize various methods of clustering the phages.

In this project, we focused on the gene for the tape measure protein, which dictates tail length and transitions DNA from the phage to its bacterial host. Our goal was to investigate if clustering phages based on the tape measure protein would give us similar results as clustering based on tail length. We hypothesized that both clustering methods would give us the same results, thus confirming the correlation between tape measure protein and tail length.

To test our hypothesis, eight known clusters were picked and three phages were selected per cluster. The tail length of each phage was measured using Fiji and the amino acid sequence of each tape measure protein was recorded. Victor was used to make a phylogenetic tree based on the tape measure proteins to visualize how the phages are sorted. Finally, we clustered the tail lengths by sorting them from shortest to longest.

Our results show that the majority of the initial clusters are recovered with both clustering methods, and there is a correlation between the tape measure protein and tail length. Our results were influenced by the lack of adequate photos on PhagesDB for some of the selected phages, which possibly lead to inaccurate measurements.

Although our hypothesis is supported by the data, we believe that increasing the specificity of criteria for selection, such as the determination of the number of photos per phage would allow us to obtain more meaningful results in the future.

This research was supported by the Science Education Alliance, Howard Hughes Medical Institute, Chevy Chase, MD, and the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers TL4GM118989, UL1GM118988, and RL5GM118987. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

PLOTTING THE STABILITY BOUNDARY OF CNOIDAL WAVES IN MICRORESONATORS

Logan Courtright¹, Zhen Qi¹, Curtis Menyuk¹

¹Department of Computer Science and Electrical Engineering, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

In recent years, experimental efforts have been focused on creating broadband frequency combs using single solitons, where a laser is coupled into a microresonator to produce a stable waveform with a spectrum containing equally-spaced, frequency lines. Different approaches have been proposed to deterministically create a broadband frequency comb, but none have proved successful so far. The generation of cnoidal waves, which are periodic solutions to the Lugiato-Lefever Equation inside a microresonator, is one potential approach, but studying their use requires exploring a large parameter space. Since cnoidal waves must stay stable as the system parameters vary, it is necessary to identify the region in the parameter space where stable solutions exist.

Dynamical methods have been developed to find the boundaries of the stable regions, but these methods are only semi-automatic due to sharp corners that appear on the boundary. As a result, finding a complete boundary has been a time-consuming process. The solution can become unstable due to different types of bifurcations: saddle-node, transcritical, or Hopf. Sharp corners appear when the instability mechanism changes along the boundary. In this work, we developed methods that can continuously track the boundary through a corner in which two different Hopf bifurcations occur. The boundary is calculated through quadratic interpolation, using two stable points and one unstable point surrounding the boundary, with adjacent boundary points allowing the calculation of the stability boundary slope and thus prediction of adjacent points for interpolation. Through this method, the boundary is accurately and rapidly calculated. At corners, the interpolation method is changed to use the corner point as a fulcrum and sweep radially through the nearby stable region until another stability boundary is reached, re-establishing the stable and unstable points surrounding the boundary. Future work will expand this method to include different bifurcation mechanisms on the stability boundary.

This work is supported by NSF-REU grant no. ECCS-1807272.

ICESAT-2 AND LUFFT CHM 15K CLOUD BASE HEIGHT COMPARISON

Sergio Diaz¹, Ricardo Sakai², Belay Demoz¹

¹Department of Physics, University of Maryland, Baltimore County, 1000 Hilltop Circle,
Baltimore, Maryland 21250

²Department of Physics & Astronomy, Howard University, 2400 6th St NW, Washington, DC
20059

The sole instrument on board the Ice, Cloud, and land Elevation Satellite-2 observatory (ICESat-2) is the Advanced Topographic Altimeter System (ATLAS), a space-based lidar, records cloud base height and the Lufft CHM 15k, a ground-based lidar, also records cloud base height, but we do not know if the cloud base heights recorded by both lidar instruments are equivalent, as they should, therefore, my research focused on comparing the cloud base heights recorded by the ICESat-2 and Lufft CHM 15k ceilometers located at the University of Maryland, Baltimore County (UMBC) and Howard University Beltsville Campus (HUBC).

In total, six days' worth of cloud base height and backscatter data were used. ICESat-2 cloud base height and backscatter data was filtered by determining the time intervals in which the ICESat-2 was within 100km of UMBC and again when the ICESat-2 was within 100km of HUBC. This filtration was done using R and the haversine formula. These time intervals were then used to filter through the cloud base height and backscatter data recorded by the Lufft ceilometers at UMBC and at HUBC. Finally, the cloud base height recorded when the ICESat-2 was within 100km of UMBC was compared with the cloud base height recorded by the Lufft ceilometer at UMBC using several statistical analyses. This was also done with the cloud base heights recorded for HUBC.

Our studies show that the UMBC and HUBC cloud base height comparisons (ICESat-2 vs. Lufft ceilometer) resulted in rejecting the null hypothesis. Additionally, although there was an evident correlation between the cloud base height between ICESat-2 and Lufft ceilometer (for UMBC and HUBC), further research with more data are necessary to make a more accurate conclusion.

This research is based upon work supported by the U.S. Department of Commerce, National Oceanic and Atmospheric Administration, Educational Partnership Program, under Agreement No: NA16SEC4810006-NCAS-M. Additionally, we would like to thank NCAS-M ETSP program for their constant support.

SUPPORT STRUCTURES FOR THE CENTRIFUGAL MIRROR FUSION EXPERIMENT

Justin Drummond¹, Carlos A. Romero-Talamas²

¹Department of Civil Engineering, Howard University, 2400 6th St NW, Washington, DC 20059

²Department of Mechanical Engineering, University of Baltimore County, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

The objective of this project is to design a support structure for the plasma vacuum chamber and magnetic coils for the Centrifugal Mirror Fusion Experiment (CFMX) at UMBC and UMCP. The goal of CMFX is to investigate a novel form of high temperature magnetized plasma confinement, with the ultimate goal of producing fusion energy for commercial electricity generation. The structures for this experiment must be made of non-magnetic and non-conducting materials to avoid a magnetic response from the structure, since such response could interfere with the experiments. Structures should also be able to withstand high temperatures and still be mechanically strong enough to support several metric tons of weight. Computer aided design (CAD) and finite element (FEM) commercial software are being used to model the design of the support structures under various load scenarios and magnetic configurations. The design is in progress and the latest results will be presented.

The authors thank Ms. Justine Johnson, Dr. Erin Lavik, and UMBC for supporting this research opportunity.

THE ROLE OF N-LINKED GLYCOSYLATION ON MELANOPsin EXPRESSION AND SIGNALING FUNCTION

Adanna Ekekwe¹, Lee Harkless¹, Phyllis Robinson¹

¹Biological Sciences, University of Maryland, Baltimore County, 1000 Hilltop Circle
Baltimore, MD 21250

Melanopsin is a visual pigment that is expressed in intrinsically photosensitive retinal ganglion cells (ipRGCs), essential for nonvisual responses to light such as circadian photoentrainment. It is unknown whether N-linked glycosylation directly impacts melanopsin signaling or expression, however, evidence suggests that glycosylated melanopsin more strongly induces FOS expression in a tissue culture system. To determine whether N-linked glycans influence melanopsin, we will examine the calcium imaging and cellular expression (western blot and immunohistochemistry) of wild-type mouse melanopsin and mutant melanopsin which will lack both N-linked glycosylated sites. Previous literature showed that N-linked glycosylation has a little effect based on light-induced FOS expression, which is a less direct measurement of melanopsin activation, then testing melanopsin signaling by measuring calcium imaging assays, which is what we will perform in my proposed experiments. Using these methods, I will determine whether the function of the N-linked glycosylation impacts melanopsin signaling or expression, and compare this to previously published data.

I would like to acknowledge the UMBC Louis Stokes Alliance for Minority Participation (LSAMP) Summer Research Program and the Phyllis Robinson Lab.

USING AN ANIMAL MODEL OF HUMAN PROSTATE CANCER TO TEST NEW NANO-THERAPIES

Star Fernandez¹, Apurv Rege¹, and Charles J. Bieberich¹

¹Department of Biological Sciences, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

Prostate cancer is one of the leading cancers among males, with 1 in 9 men being diagnosed in their lifetime. In 2018, there were 358,989 prostate cancer deaths, a 28% global mortality rate. Although organ-confined disease is curable, metastatic prostate cancer is almost always lethal. New therapies to treat lethal forms of prostate cancer are desperately needed. Our laboratory has developed a mouse model that recapitulates key features of lethal human prostate cancer. The model, termed BMPC, is genetically engineered to harbor genomic changes that are common in human prostate cancer: overexpression of the oncogene MYC, and loss of the PTEN tumor suppressor. We hypothesized that BMPC mice could be used to test new prostate cancer treatments, including those based on nanoparticles. Nanoparticles are 10 to 100 nanometer particles that can be designed to carry drug cargoes directed to a specified target. Here, we report progress toward the development of a cohort of BMPC mice that will be treated with an experimental nanoparticle formulated to deliver mRNA encoding PTEN. Restoration of PTEN is anticipated to slow cancer progression by eliciting an anti-tumor immune response. To date, we have screened mice for the presence of the MYC and PTEN transgenes, and have identified several BMPC males. A pilot study using fluorescent nanoparticles is currently in progress.

Acknowledgement Statement: I would like to thank my research mentor, Dr. Charles Bieberich, and Apurv Rege for helping throughout my internship. We gratefully acknowledge LSAMP program for supporting this project.

REVIEW OF STRESS AND IMMUNITY IN DROSOPHILA

Alanah Follis¹, Jeff Leips²

^{1,2}Department of Biological Sciences, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

The purpose of this review and future research is to identify potential connections between stress and the immune responses. A number of recent studies with *Drosophila* and other insects have reported that a variety of physical stressors trigger immune responses, specifically increased expression of immune response genes in response to stress. This review seeks to summarize the current literature and explore the connection between physical stressors and immune responses, specifically the genetic basis of this connection in insect model systems. Given the genetic similarity of fruit flies to humans, this review will provide insight into stress and immunity in other organisms including humans. The review will highlight directions of future research to understand the mechanisms underlying this connection and understand the contributions individual environmental stressors have on the immune system.

This project is funded by the Scholar Research Institute (SRI) of The UMBC McNair Scholars Program.

WHOLE GENOME COMPARISON OF BACTERIOPHAGES INFECTING PATHOGENIC AND NON-PATHOGENIC MYCOBACTERIUM SPECIES

Kevin Gibbons¹, Josh Ogbenna¹, Mia Penn¹, Maria Cambraia^{1,2}, Lee Harkless³, and Steven Caruso³

¹STEM BUILD, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

²College of Natural and Mathematical Sciences, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

³Department of Biological Sciences, UMBC 1000 Hilltop Circle, Baltimore, MD 21250

Antibiotic-resistant bacterial infections are a major public health crisis infecting 2-3 million people and killing 35,000 people per year in the US. These infections are harder to treat and result in higher mortality rates. The use of Bacteriophages, viruses that infect bacteria, in phage therapy are an emerging therapeutic for treating antibiotic-resistant infections. We examined ten phage genomes obtained from Phagesdb.org that infect pathogenic and non-pathogenic mycobacterial species. Mycobacterial hosts were selected because there was a wide range of species present on Phagesdb. *M.smegmatis* was selected because it was the most represented non-pathogenic *Mycobacterium* host species, and *M.avium* was chosen because it was the sole pathogenic *Mycobacterium* host species. 10 phages were selected in total, 5 infecting *M.smegmatis* and 5 infecting *M.avium*. Gene content similarity was carried out using the web-based tool on Phagesdb, which provides a measurement of how similar their gene content is. Our results show that the gene content of phages infecting pathogenic hosts vs the gene content of phages infecting non-pathogenic was 66.9% similar. This indicates that there are some genomic differences. Phamerator was then used to identify differences in the genomes of the phages, from which a list was compiled. We did not find any genes that were exclusively present in either group of phages. Further functional characterization of these gene products was attempted by identification of structural homology using HHPred. From which we did not find any protein structure matches that exclusively appeared in phages infecting pathogenic vs. non-pathogenic bacterial hosts. Overall, we did not find any major differences between our phages infecting pathogenic vs. non-pathogenic bacterial species. Looking at these phage genomes further advances our basic understanding of phages, which could be used to create phage therapies for treating pathogenic bacterial species such as *M. avium*.

This research was supported by the Science Education Alliance, Howard Hughes Medical Institute, Chevy Chase, MD, and the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers TL4GM118989, UL1GM118988, and RL5GM118987. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

APPLICATION OF DROOP MODELS IN ALGAL CULTURE

Isaiah Hayes¹, Richard Eng², Amanda Li², Dr. Michael Betenbaugh²

¹Baltimore Polytechnic Institute, 1400 W Cold Spring Ln., Baltimore, MD 21209

²Department of Chemical and Biomolecular Engineering, Johns Hopkins University, 3400 N. Charles St., Baltimore, MD 21213

Mathematical models in biotechnological applications serve as powerful contributions and tools in research for the purpose of prediction and data analysis. This current study applies the Droop model to describe algal growth dynamics. In this work, the Droop model was used to interpret experimental data collected from *Chlorella vulgaris* (iCZ946). This process enables specific conclusions to be drawn about growth behavior and deepens the understanding of the organism as a whole. With respect to the experiment itself, the data collected describes chlorophyll and biomass production based on varying nitrogen feed, given the effect of high light and low light conditions. The algae were distinguished as 'batch' and 'fed-batch'. The other observed component of the experiment was the impact on the amount of chlorophyll produced by the algae as a function of internal nitrogen concentration. The results of using this method to analyze this data demonstrate the capability of the Droop model to interpret how algal growth and physiology can fluctuate in different environments. It presents a way of interpreting what those fluctuations could mean for the experiment, or similar experiments. This type of modeling can extend past *Chlorella vulgaris* and presents an opportunity to simulate the dynamics of other microbial species.

Acknowledgements: Special thanks to the National Science Foundation (1332344), for the funding in this research. Another thanks to Chien-Ting Li, Jeffrey Reeser, Nelson Ndahiro, and Kent Rapp for the mentoring in research.

ASSESSING THE IMPACT OF PHOSPHOMIMETIC MUTATIONS ON MOUSE MELANOPSIN SIGNALING

Andrew Hennigan¹, Alexis Rubin¹, Phyllis Robinson¹

¹Department of Biological Sciences, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

Melanopsin is a visual pigment expressed in intrinsically photosensitive retinal ganglion cells (ipRGCs). Melanopsin contributes to image and non-image forming visual processes, including circadian photoentrainment. It is hypothesized that Protein Kinase A (PKA) plays a role in attenuating the signaling of photo-activated melanopsin, a relationship that we are interested in studying. Our laboratory has previously shown that wild-type melanopsin signaling is attenuated when cyclic AMP-dependent PKA is activated *in vitro*. Consistent with this, the PKA-dependent reduction in melanopsin signaling was prevented when all three putative PKA phosphorylation sites (S182, T186, S287) on the intracellular loops were mutated to non-phosphorylatable residues. We hypothesize that the phosphorylation of PKA at sites S182, T186, and S287 is required for PKA to attenuate melanopsin signaling. We have successfully generated a phosphomimetic melanopsin construct in which the three described sites have been changed to negatively charged residues that mimic phosphorylation. We verify appropriate expression and localization of the construct via Western blot and immunohistochemistry. Calcium imaging demonstrates that phosphomimetic melanopsin signaling is greatly attenuated. This research will contribute more to our understanding of the role of melanopsin in circadian rhythms and photoentrainment, helping us to better understand the maintenance of these characteristics in an organism.

Funding provided by NIH Grant 5RO1EY027202-02 to PRR and the U-RISE Program at the University of Maryland, Baltimore County (UMBC) is supported by the National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 136497.

ONLINE LEARNING AND STUDENT SATISFACTION DURING COVID-19

Ting Huang¹, Diane Alonso¹

Department of Psychology, University of Maryland, Baltimore County, 1000 Hilltop Circle,
Baltimore, MD 21250

The COVID-19 outbreak in the spring of 2020 interrupted the life of every person on this globe. For students taking in-person courses, it meant that traditional learning came to a halt and was replaced with involuntary distance learning instead. This sudden shift may have impacted students' affective experience in learning. In this unprecedented learning environment, it is imperative for educators to test different methods of instruction to restore positive student satisfaction and help maintain academic progress. This research proposal provides a two-phase study that aims to identify students' perception of the new online learning environment. In Phase I, a survey will be used to receive feedback from university students regarding their online learning experience during the pandemic. Based on past research on the topic of online learning, the survey results are expected to uncover instructor course design, institutional resources, student self-efficacy, level of engagement, and learning outcomes as factors influencing student satisfaction. Additionally, stress regarding COVID-19 will be analyzed as another factor that may impact academic satisfaction. The data will then inform the experimental study in Phase II that varies the course design and opportunities for student engagement to examine what factors may enhance student satisfaction. The findings of this study are expected to provide a richer learning environment for students during COVID-19 and further the research on distance learning.

This project is funded by the Scholar Research Institute (SRI) of The UMBC McNair Scholars Program and the UMBC Undergraduate Research Award (URA).

STABILITY ANALYSIS OF CAR FOLLOWING CONTROL OF LINEAR VEHICLE DYNAMICS WITH A GENERAL MPC HORIZON

Ben Hyatt¹, Jinglai Shen¹

¹Department of Mathematics and Statistics, UMBC, 1000 Hilltop Circle, Baltimore, MD, 21250

The continued advancement of autonomous vehicle technology in recent years provides a unique opportunity to correct poor traffic dynamical performance resulting from irregular human driving behavior. To this end, car-following control schemes have been developed which regulate the actions of a platoon of autonomous vehicles as an interconnected system, thereby reducing undesired congestion and oscillations in traffic flow. In the development of such algorithms, it is especially important to verify dynamical stability so as to ensure optimal control is consistently maintained.

We study a linear discrete-time dynamical system modeling the kinematics of a platoon of connected and autonomous vehicles (CAVs) driving on a straight roadway behind an uncontrolled leading vehicle. Here, the acceleration of each CAV is treated as a control. That is, in response to the motions of the leading vehicle, the control scheme adjusts the accelerations of each of the following vehicles in order to achieve desired transient and asymptotic dynamics. At each discrete timestep, the optimal solution of a general p -horizon model predictive control (MPC) problem determines the next control input. Accordingly, through stability analysis and numerical techniques, we seek to demonstrate the stability of this car-following control scheme and choose suitable penalty weights for desired dynamical performance. Our current results prove closed-loop stability up to a horizon of $p = 3$, and we further speculate through numerical observations that the closed-loop system is Schur stable for a general p -horizon. Future work will aspire to prove this conjecture.

This material is based upon work supported by the National Science Foundation under Grant No. NSF CMMI-1902006.

BUILDING A GUI TO EVALUATE NUTRIENT VARIATION ON BACTERIA METABOLISM

Christian Johnson¹, Amanda Li², Richard Eng², Dr. Michael Betenbaugh²

¹Baltimore Polytechnic Institute, 1400 W Cold Spring Ln., Baltimore, MD 21209

²Department of Chemical and Biomolecular Engineering, Johns Hopkins University, 3400 N. Charles St., Baltimore, MD 21218

Making a graphical user interface (GUI) is a critical component for computers as it makes the computer more user-friendly and interactive by displaying visual elements users can click, point, and drag on. Without GUIs, users would have to memorize copious amounts of commands and know how to use them properly. This project utilizes the advantages of building a GUI by modeling and programming in MATLAB, which is the programming platform of choice. The goal of the project is to model *E. coli* metabolism through the COBRA Toolbox by allowing a user to change incoming nutrient feed and outputting glucose uptake and biomass values. This is important because it allows scientists to be able to visualize data on an *E. coli* model and to easily change and observe how different variables can affect the glucose uptake and biomass values. For the GUI, the variation buttons graph the type of variation selected versus the metabolite selected from the drop down button. If the user clicks the “change initial nutrient feed” button, it will allow the user to type the corresponding value and then click on the “GO” button on the side to alter the metabolite feed that is shown on the graph. The implications behind the final version of the GUI would be that it helps users be able to easily model different types of genome-scale models in a more efficient way instead of having to take the time to learn how to code to do the same task.

Special thanks to Amanda Li, Richard Eng, Jeffrey Reeser, and Dr. Michael Betenbaugh for mentoring. Another thanks to NSF (1332344) for supporting the research.

USING GENOME SCALE MODELS TO SIMULATE VIRAL INFECTION IN HEK-293 CELLS

Elayna Kemp¹, Nelson Ndahiro²,
Dr. Michael Betenbaugh²

¹Baltimore Polytechnic Institute, 1400 W Cold Spring Ln., Baltimore, MD 21209

²Department of Chemical and Biomolecular Engineering, Johns Hopkins University, 3400 N. Charles St., Baltimore MD 21213

This study involves the simulation of HEK-293 (human embryonic kidney) cells to determine HEK-293 nutrient uptake and biomass production with and without infection of AAV2 (adeno-associated virus). Understanding the nutrient uptake and viral proliferation of AAV2 is useful for the field of gene therapy. HEK-293 cells have stable growth and protein production capabilities, and AAV2 infections are safe and capable of infecting a broad range of cells, making these ideal for gene therapy applications. Computer programs MATLAB and COBRA Toolbox were used for the modelling of HEK-293 metabolism along with a download of Recon 2.2, a highly predictive genome scale model that shows the set of biochemical reactions within human metabolism. Using these programs, HEK-293 metabolite uptake data [Quek, L. et al.] was added to constrain Recon 2.2, and flux balance analysis was used to determine HEK-293 biomass production rate. Metabolic reactions for generating viral cell mass were added to the model such as the DNA sequence of AAV2 from NCBI GenBank and the protein sequences of the AAV2 capsid from UniProt database. The predicted biomass production rate of the HEK-293 cells was compared with and without the infection of AAV2, and compared to experimental data. It was found that the growth rate was altered by the viral genome, which can be used in the study of viral proliferation and applicable to gene therapy.

Special thanks to support from the Johns Hopkins research team: Jeffrey Reeser, Amanda Li, Richard Eng, and Kent Rapp. Also thank you National Science Foundation for the funding and making this research possible (Grant number 1332344).

ASSESSING POTENTIAL INDICATORS OF ONLINE RADICALIZATION

Mohammed Khalid¹, Anupam Joshi²

¹Department of Information Systems, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

²Department of Computer Science and Electrical Engineering, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

Online social networks are an essential communication tool and provide many uses while generating a wide swath of information. However, these networks are becoming a major platform for advocates of violent extremism to assemble, communicate, and propagate extremist ideology. With the increase in violent extremist plots motivated by adherents of Islamist ideology, detecting radicalization of violent extremists can be a key component in identification and prevention of future terrorist attacks. The long-term goal of this project is to see if social media postings can be used to identify radicalization as it happens. While our initial focus is on Islamists, the approach can be used to detect radicalization in other domains.

Our initial approach is to use the simplest technology possible, namely exploring if usage of certain words can be a leading indicator of radicalization. By utilizing term frequency-inverse document frequency (tf-idf) approach and stop-words filtering, this project aims to answer: is there a way to assess the words utilized by known violent extremists and determine if the prevalence of these words within a body of a given text provides signs of radicalization? Can a method be developed to elicit, from words in a given document, whether a person is utilizing terminology used by known and suspected supporters of terrorism?

The indicators of radicalization, ascertained through expert-vetted banks of words used by known extremists who then went on to partake in the commission of terrorist activity, can be used to assist law enforcement agencies, prosecutors, and organizations devoted to fighting extremism in detecting vulnerable targets prior to the commission of violent activity, thus contributing to counterterrorism and public safety initiatives. Another question our research will address is whether these expert-provided words can be augmented by words automatically inferred by the system as it comes across labeled examples of social media documents.

This research project is supported in part by an Undergraduate Research Award (URA) grant through the Office of Undergraduate Research, and in part by the UMBC McNair Scholar Research Institute (SRI).

FERROFLUIDS FOR HYPERTHERMIA APPLICATIONS

Lynn Krushinski^{1,2}, Kameron Langford¹, William Korzi¹, Bryan Augstein¹, Orianna Thomas¹, Dr. Vera Smolyaninova¹, Dr. Ellen Hondrogiannis¹, and Dr. Mary Sajini Devadas¹
¹Department of Chemistry, Towson University, 8000 York Rd, Towson, MD, 21286

Nanomedicine is a rapidly growing field with the potential to revolutionize healthcare. The focus is put mostly on the synthesis of biocompatible magnetic nanoparticles for their unique size dependent physical and chemical properties, which make them particularly suitable for novel treatments, most specifically chemotherapy applications. The synthesis and study of gold coated iron cobalt nanoparticles in a colloidal form allow for a better understanding of how biocompatible nanoparticles can be functionalized for several novel chemotherapy treatments, with the focus being magnetic hyperthermia. However, there are several challenges which are associated with the synthesis and characterization of these particles which must be overcome before these can be used in a clinical setting. Most importantly, the synthesis must produce particles in a consistent and desirable size range, which have achieved a complete gold coating for each individual particle in order to achieve complete biocompatibility with physical properties suitable for magnetic hyperthermia treatments.

This research was funded by DARPA AMEBA HR0011-17-C-0115, NSF MRI 1626326, FCSM Undergraduate Research Grant, Towson University Faculty startup, GSA and the School of Emerging Technology grant.

IDENTIFYING THE DIFFERENCES IN THE GENOMES OF BI2 AND BI4 PHAGE SUBCLUSTERS

Amir Ledbetter¹, Emily Marinko¹, Caroline Moore¹, Precious Oyinloye¹, Maria Cambraia^{1,2}, Lee Harkless³, Steven Caruso³

¹STEM BUILD, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

²College of Mathematical and Natural Sciences, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

³Department of Biological Sciences, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore MD 21250

Today, humans are facing the decreasing effectiveness of antibiotics. Antibiotics are often used as a treatment for bacterial infections, leading to increasing numbers of antibiotic-resistant bacteria. There is a rising need to develop alternative ways to treat bacterial infections that do not cause antimicrobial resistance. An alternative way of treating bacterial infections would be with bacteriophages since viruses cause bacterial cell death and are able to evolve over time with the bacteria. A better understanding of the bacteriophages' genetic makeup is integral to the implementation of bacteriophages as a substitute.

We looked at actinobacterial phages in the BI2 and BI4 subclusters and compared their genomes. The BI2 and BI4 subclusters include nine phages isolated on *Streptomyces scabiei*, the etiological agent of potato scab disease. The Gene Content Similarity (GCS) was analyzed, the positions of the genes were studied using Phamerator, and a dendrogram was created using hierarchical clustering based on capsid width, capsid aspect ratio, and body aspect ratio to look at cluster membership in order to identify any differences between the two subclusters. Differences in the genetic makeup of both subclusters were identified through this analysis.

Interestingly, the dendrogram's clustering indicated that Thiqqums, a BI4 subcluster bacteriophage, is more closely connected to the BI2 cluster than the BI4 cluster, and vice versa with Scap1, a BI2 phage. This may illustrate similar morphological coding genes between the subclusters. Furthermore, it was discovered that BI2 subcluster genomes are much smaller than that of BI4 subcluster genomes as BI4 bacteriophage genomes have more genes in them on average. Additionally, we have found that the gene content similarity between the two subclusters averages around 50%, suggesting that although the phages from these two subclusters infect the same bacteria, they may not be as closely related as originally thought.

This research was supported by the Science Education Alliance, Howard Hughes Medical Institute, Chevy Chase, MD, and the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers TL4GM118989, UL1GM118988, and RL5GM118987. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

INCREASING TRIACYLGLYCEROL (TAG) PRODUCTION WITH GENE MINING TECHNIQUES IN VARIOUS ALGAL SPECIES

Aditi Madabushi^{1,2,3}, Robin Bridgman¹, Stephen M. Miller¹

Department of Biological Sciences, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250¹, Department of Live Sciences, BCCC, 2901 Liberty Heights Ave, Baltimore, MD 21215², Mount Hebron Highschool, 9440 Old Frederick Rd, Ellicott City, MD 21042³

The need for biofuel production is continually increasing as nonrenewable fuel sources run out and energy demands surge. Algae are promising as biofuel producers because they grow rapidly, uptake CO₂, produce large amounts of oil, and can grow on marginal (non-crop) land. Algal biofuels are extracted from polar and nonpolar lipids. A class of nonpolar lipids known as triacylglycerols (TAGs) are the preferred neutral lipids for biofuel production due to their nearly 100% conversion of biomass to biofuel. TAGs are highly concentrated energy deposits compared to other alternatives, making them attractive for usage. The focus of this research is to find mechanisms to improve production of TAGs by identifying genes present in algal species that can influence TAG production. The species used for this research were chosen for their application as model systems (*Chlamydomonas reinhardtii*) or abilities to produce large amounts of oil (*Nannochloropsis oceanica*, *Chlorella vulgaris*). This study uses bioinformatic and gene mining techniques through Phytozome and MycoCosm databases to devise an *in silico* strategy for enhanced biofuel production. Analysis of these species through the gene mining techniques, protein alignment and keyword search methods, will help create an inventory of TAG related genes. Our preliminary findings showed different numbers of fatty acid and TAG biosynthetic genes present in *N. chloropsis* compared to *C. reinhardtii*. These results could provide a possible correlation between the number of genes and the amount of TAG produced in an organism. Understanding the respective fatty acid and TAG pathways for these algal species will provide an in-depth understanding of the genes important for these pathways. It may help devise strategies to make algal species superior in TAG production and determine species that are best biofuel producers. The project's outcome could be instrumental in translating laboratory studies towards the goal of enhanced biofuel production.

This work was funded by a grant (REM supplement to NSF-EFRI-1332344) from the National Foundation (NSF) Directorate for Engineering (ENG) Office of Emerging Frontiers in Research and Innovation (EFRI).

EXAMINATION OF BEHAVIORAL AND PHYSIOLOGICAL EFFECTS OF E-CIGARETTE FLAVORINGS AND VAPOR ON IMMUNE RESPONSE IN TONGUE OF MICE MODELS

Olufolake Majekodunmi¹, Avantika Krishna¹, Tatsuya Ogura¹ and Weihong Lin¹
¹Department of Biological Sciences, University of Maryland Baltimore County, 1000
Hilltop Circle, MD, 2150

Electronic nicotine delivery systems, also known as e-cigarettes were introduced in 2003, since then their use has exponentially increased. These flavors promote the use of e-cigarettes by evoking pleasant senses and masking aversive feelings associated with nicotine intake. To investigate the taste of e-cigarette flavors and their masking ability on nicotine-containing fluid, a two-bottle taste test was performed with the flavoring agent, vanillin. Two groups of mice were tested: wild-type and Transient Receptor Potential M5 Knockout (TRPM5-KO) mice. TRPM5-KO mice lacked TRPM5-expressing taste receptor cells resulting in insensitivity to sweet, umami, and bitter tastes. In order to explore the immune response of taste receptor cells, a method was performed. Mice were exposed to vanillin e-liquid with nicotine solution, or air for 4 weeks. Mice were then fixed and tissue sections of the circumvallate papillae, fungiform, and foliate papillae of the tongue were collected. Mast cells are tissue cells that are involved with inflammatory responses. These are responsive to tissue damage, were stained with toluidine blue dye, and degranulated mast cell percentage will be examined. Our results indicate a potential method in examining the effects of vanillin e-liquid exposure in relation to taste and oral health.

This work was supported by the UMBC Undergraduate Research Award, National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 136497, and NIH / NIDA DA046349

INVESTIGATING THE LINK BETWEEN CELL CYCLE GENES AND CELL DIVISION NUMBER IN THE VOLVOCINE GREEN ALGAE.

Marie-Rose Mayifuila¹, Sierra Wallace¹ and Stephen M. Miller¹.

¹Department of Biological science, UMBC, 1000 Hilltop Circle, Baltimore, MD, 21250

Most multicellular organisms evolved from their common unicellular ancestors >600 million years ago, making it challenging to learn how this important transition occurred. Multicellularity evolved in the volvocine green algae, including unicellular *Chlamydomonas reinhardtii* and multicellular *Volvox carteri*, only ~200 million years ago. A key feature of multicellularity is control of cell division number. The reproductive cells of *V. carteri* divide 11-12 times whereas *C. reinhardtii* undergoes at most five mitotic divisions. It is hypothesized that cell division number in these organisms is under genetic control. Here we set out to inventory cell cycle genes in *C. reinhardtii* and *V. carteri* to determine if differences in gene number for certain cell cycle gene classes could be correlated to cell division number. We used resources such as Harmonizome (database of human cell cycle proteins), BLAST (basic local alignment search tool), Phytozome (plant genome portal that permits keyword and BLAST searches) and the NCBI (national center for biotechnology information) to identify the cell cycle genes. We investigated cyclins, cyclin dependent kinases, and retinoblastoma pathway genes, and report our preliminary findings, which should set the stage for better understanding the evolution of cell division control in the volvocine algae.

This work was funded by a grant (REM supplement to NSF-EFRI-1332344) from the National Foundation (NSF) Directorate for Engineering (ENG) Office of Emerging Frontiers in Research and Innovation (EFRI).

CHLAMYDOMONAS REINHARDTII AND VOLVOX CARTERI RIBOSOMAL PROTEIN GENE INVENTORY AND DATA ANALYSIS: LOOKING FOR CLUES TO THE EVOLUTION OF CELLULAR DIFFERENTIATION

Catherine Mbuashu-Ndip, JD Seah, Stephen M. Miller
Department of Biological Sciences, UMBC, University of Maryland, Baltimore County, 1000
Hilltop Circle, Baltimore, MD 21250

The question of how multicellular organisms with differentiated cell types evolved from single-cell ancestors is central to biology. In most organism lineages, this transition happened more than 600 million years ago, making the research of multicellularity and cellular differentiation difficult. However, the volvocine green algae, including unicellular *Chlamydomonas reinhardtii* and multicellular *Volvox carteri* are promising models for studying multicellularity because they shared a common ancestor much more recently (~200 million years ago). In addition, *V. carteri* possesses just two cell types, reproductive and somatic, making *V. carteri* and *C. reinhardtii* exceptional models for studying cell differentiation. This study focuses on *rlsD*, a *V. carteri* gene we believe to be important for understanding the evolution of cellular differentiation. Previously we showed that overexpressing *rlsD* represses growth, and a preliminary analysis of RNAseq data suggested that ribosomal protein genes might be repressed by *rlsD*. Now, we are using Phytozome, an algal and plant genome database, to compare the numbers and types of ribosomal protein genes in *C. reinhardtii* and *V. carteri*, and we are analyzing RNAseq data to determine which ribosomal protein genes are repressed by *rlsD* and to what extent. So far our inventory includes 85 *C. reinhardtii* ribosomal protein genes and 81 *V. carteri* ribosomal protein genes. Also, RNAseq data analysis reveals that >80% of *V. carteri* ribosomal protein genes are repressed by *rlsD* overexpression. Our studies could lead to hypotheses that can be tested in the lab and become the basis for research into the possible link of ribosomal protein genes to the evolution of Volvox.

This work was funded by a grant (REM supplement to NSF-EFRI-1332344) from the National Foundation (NSF) Directorate for Engineering (ENG) Office of Emerging Frontiers in Research and Innovation (EFRI).

DECADES OF DRUGS AND TERROR: AN ANALYSIS OF THE RACIALIZED OPIOID EPIDEMIC IN BALTIMORE CITY

Malaysia McGinnis¹, Dawn Biehler¹

¹Department of GES, UMBC, 1101 Hilltop Cir, Baltimore, MD21250

Baltimore City is plagued by militarized police and harsh sentencing, both justified by the policies and discourse of the War on Drugs since the late 1970s. There is a great dependence on the disenfranchisement, over-policing, and oppression of Black people in neighborhoods reduced to high drug traffic areas. The 80s crack-cocaine epidemic in Baltimore City left the groundwork for the racialized opioid crisis that continues to develop throughout the early 2000s, with effects felt even today. Using Black Geographies as a theoretical lens, this research analyzes historic news reports and more recent narratives to understand how the War on Drugs constructed technologies for controlling Black communities while representing Black people as lacking spatiality.

I draw primarily upon the work of Wilson, Bledsoe and Wright, McKittrick, and Hawthorne regarding capitalism's anti-blackness and conceptions of Black people's a-spatiality. This study uses discourse analysis of news sources including primary and secondary accounts of the personal effects of the war on drugs in Baltimore in answering questions like: What happens when systemic racism is defined by the suffering of Black people? Why does Black suffering often coincide with confinement, whether physically, mentally, or economically? I contribute to this discussion that the war on drugs since the 1970s has justified the “need” for a militarized police force and produced a racialized opioid crisis in Baltimore City through the 2010s.

This work is supported by the McNair Summer 2020 SRI Program

ESTABLISHING A CELL-BASED HIGH-THROUGHPUT SCREEN TO IDENTIFY PATHWAYS TARGETING ZNF217 LEVELS IN OVARIAN CANCER CELLS

Nithya Navarathna¹, Achuth Padmanabhan¹

¹Department of Biological Sciences, University of Maryland Baltimore County,
1000 Hilltop Circle, Baltimore, MD 21250

Ovarian cancer continues to be the fifth leading cause of cancer-associated deaths among women in the United States. Due to the lack of early reliable diagnostic markers, the majority of patients have metastatic disease at diagnosis. The 5-year survival rate in women with metastatic ovarian cancer is extremely low (<30%), highlighting the urgent need to identify new therapeutic targets. Previous studies revealed that Zinc Finger Protein 217 (ZNF217) is overexpressed in metastatic breast, ovarian, and lung cancer cells. Ectopic ZNF217 expression in ovarian cancer cells enhanced the metastatic ability of these cells. Further, siRNA mediated ZNF217 depletion in metastatic ovarian cancer cells resulted in cancer cell death and tumor regression in mice. Despite ZNF217's role in metastatic progression, cancer cell survival, and its potential as an anti-cancer therapeutic target, targeting ZNF217 in a clinically translatable manner has not been achieved yet. To overcome this limitation and to determine the clinical potential of targeting ZNF217, I will establish a cell-based high-throughput screen to identify small molecules that causes ZNF217 depletion in ovarian cancer cells. Specifically, I will use lentivirus-mediated gene delivery to stably express Red Fluorescent Protein (RFP)-tagged ZNF217 in the ovarian cancer cell line SKOV3. The expression and cellular localization of RFP-tagged ZNF217 will be verified using Western blotting and fluorescent microscopy respectively. Since the RFP signal intensity will correspond to cellular ZNF217 levels, I will determine the utility of these cells in a high-throughput platform by validating the changes in RFP signals to measure changes in cellular ZNF217 levels. Once the utility of the SKOV3-ZNF217-RFP cells is established and the optimal conditions for the assay is identified, I will collaborate with the high-throughput screening facility at the University of Maryland Baltimore to screen compound libraries and identify novel small molecules capable of depleting ZNF217 in ovarian cancer cells.

This work was supported through an URA award to N.N and research funds from UMBC to A.P. N.N is also supported through the LSAMP Summer Research 2020 award.

APPLYING GENERALIZED ADDITIVE MODELS FOR CLIMATE ANALYSIS

Achuna B. Ofonedu¹, Pei Guo², Jianwu Wang²

¹School of Engineering, Catholic University of America, 620 Michigan Ave NE, Washington, DC 20064

²College of Engineering & Information Technology, University of Maryland Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

One of the most well-known regression models in data science is the standard linear regression model. Although linear models are simple to interpret, it is very limited in making assumptions about data and lacks the ability to capture non-linear patterns. These issues are what generalized linear models (GLMs) aim to solve by providing more flexibility. Generalized additive models (GAMs) are an extension of GLMs, consisting of a sum of smoothing functions which aims to better capture patterns in the data.

A fundamental research problem is discovering cause-effect relationships between variables. This research focuses on finding causal relationships between atmospheric variables using incremental learning with generalized additive models (GAMs). It will look further into the design and parallelization of GAMs, how these models can be used for incremental learning for Granger causality, and the model's several other applications in data analysis.

To begin, climate data stored in time series was gathered and lagged to discover Granger causality, given that lagged explanatory variables help improve prediction capabilities of the response variable. The incremental learning portion happens when new variables are added to the causality model and parameters are updated. The objective is to acquire a causality graph that represents the causal relationships between atmospheric variables which can be updated as new variables enter the model.

After running the data through a backfitting algorithm to fit GAMs and conducting F-tests to discover Granger causality, it was concluded, from the structure of the causality graph, that there exist several causal connections between variables at different locations with varying degrees of influence. What remains to be studied is comparing this causal discovery approach to other methods to rate their accuracy and efficiency between each other. The findings present causal relationships between atmospheric variables which domain experts can utilize for other applications of research.

The project is funded by the Leadership Alliance Summer Research - Early Identification Program (SR-EIP) and the authors gratefully acknowledge the University of Maryland Baltimore County College of Engineering and Information Technology for their support and Dr. Wang for his mentorship and guidance. This project is partially funded by the grant CAREER: Big Data Climate Causality Analytics from the National Science Foundation (grant no. OAC-1942714).

THE EFFECTS OF HYPERGLYCEMIA ON NEURULATION

Chelsea Okeh¹, Rianna Zacharias¹, Maki Negesse¹, Rachel Brewster¹ Ph.D.

¹Department of Biological Sciences, University of Maryland Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

Neurulation is the process via which the neural tube, the tissue that develops into the brain and spinal cord, is formed during early embryogenesis. A flat sheet of cells, called the neural plate, bends, folds and closes to form this tube. Impaired neurulation leads to the formation of neural tube defects (NTDs), such as spina bifida or anencephaly, found in about 3,000 pregnancies each year in the United States. NTDs are caused by both genetic and environmental factors. In recent years, a significant correlation between diabetic mothers and babies born with NTDs has led to the conclusion that hyperglycemia is an environmental risk factor that increases the incidence of these birth defects. Furthermore, a mouse model of diabetes has confirmed that high glucose prevents neural tube closure and revealed that elevated levels of reactive oxygen species and apoptosis are likely to underlie this defect.

This study aims to establish the zebrafish as a model to study environmental factors causative of NTDs and more specifically focuses on the effects of hyperglycemia. We hypothesize that if mechanisms underlying neurulation are conserved in zebrafish, neural folds would fail to fuse in hyperglycemia. To test this, zebrafish embryos were placed in solutions of varying glucose concentrations at dome stage and removed at 5 and 7 somites stages, the time period when the lateral edges of the neural plate, the neural folds, come together and fuse. The embryos were fixed at their respective stages and processed for *in situ* hybridization, using the neural fold marker *emx3* as a riboprobe. We will present our data measuring the distance between the neural folds across treatment groups and expect to observe an increased distance in the hyperglycemic groups if our hypothesis is correct.

This investigation was funded by the Howard Hughes Medical Institute's Precollege and Undergraduate Science Education Program, the Louis Stokes Alliance for Minority Participation program at UMBC and the U-RISE Program at UMBC. The U-RISE Program at the University of Maryland, Baltimore County (UMBC) is supported by the National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 136497.

IL-1 β – VEGF-A SIGNALING AXIS IN ATHEROSCLEROTIC CALCIFICATION

Crystal Parry, Joshua Berus¹, Cadence Lee², and Chris Mantsounga²
Alan R. Morrison^{1,2}

¹ Department of Internal Medicine (Cardiovascular Medicine), Brown University Providence, RI 02903

² Providence VA Medical Center, Providence, RI 02908

Today, atherosclerotic heart disease is the leading cause of morbidity and mortality today in the world. Coronary artery disease caused by atherosclerosis is characterized by lipid deposition, inflammation, and calcium deposition in the wall of blood vessels. Pro-inflammatory cytokine interleukin 1 beta (IL -1 β) contributes to much of the inflammation that is characteristic of atherosclerosis. Previous research on two signal transducers, RAC1 and RAC2, demonstrated that RAC2 modulates IL-1 β . RAC2 knockout mice demonstrated increased RAC1 activity, resulting in increased levels of IL-1 β and atherosclerotic calcification. The Morrison laboratory also focuses on studying vascular endothelial growth factor A (VEGF-A), a growth factor that promotes the formation of blood vessels, regarding calcification. Preliminary data suggests the promoter region of the gene encoding VEGF-A is activated by IL-1 β signaling. A major goal of this study is to assess the relationship between VEGF-A, IL-1 β , and atherosclerotic calcification. Our hypothesis is that increased levels of IL-1 β are associated with increased VEGF-A expression and consequent atherosclerotic calcification. We used enzyme-linked immunosorbent assays (ELISA) to determine the levels of IL-1 β and VEGF-A in blood serum samples from ApOE knockdown mice. ApOE mice were used as a model animal because they can simulate atherosclerotic conditions in mice. Macrophage knockdown of IL-1 β expression led to reduced VEGF-A expression and reduced atherosclerotic calcification, supporting a causal relationship. These results were validated by comparing levels of IL-1 β , VEGF-A, and calcification in human subjects. Future studies are underway to demonstrate that VEGF-A causes calcification, using macrophage-specific knockdown of VEGF-A expression in atherosclerotic ApOE knockdown mice. By understanding the mechanistic relationship between IL-1 β , VEGF-A, and atherosclerotic calcification, new therapeutic strategies can be developed to combat atherosclerosis such as inhibitors of IL-1 β and VEGF-A signaling.

This research is sponsored by the National Heart, Lung, and Blood Institute, National Institutes of Health, R25HL088992, RO1HL139795, CPVB COBRE NIGMS NIH P20GM103652, VA-ORD CDA-2 7IK2BX002527. This project has also been supported by the U-RISE Program. The U-RISE Program at the University of Maryland, Baltimore County (UMBC) is supported by the National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 136497.

DETERMINATION OF GLUCOSOME SPECIFICITY USING COLOCALIZATION ANALYSIS OF 4-D IMAGES OF METABOLIC PATHWAYS

Michelle Ramsahoye¹, Erin Kennedy¹, Minjoung Kyoung¹

¹Department of Chemistry, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

Membrane bound organelles like the mitochondria confine metabolic pathways such as glycolysis (energy production via the breakdown of glucose). Metabolic pathways in the cytoplasm have been considered to be uniformly distributed. However, we found that enzymes associated with glucose metabolisms are compartmentalized in living cells. We also found that the formation of multi-enzyme compartments associated with glucose metabolism, referred to as glucosomes, is facilitated by liquid-liquid phase separation.

In this project, we tested whether glucosomes have specificity to glycolysis and gluconeogenesis. We thus visualized glucosomes and purinosomes, another enzyme assembly associated with de novo purine biosynthesis pathway in living cells by using our home-built lattice light sheet microscopy (LLSM). The sub-diffraction limited 3D images of glucosomes and purinosomes in living cells were analyzed by Manders' Colocalization Coefficient method.

Our results support that glucosomes do not colocalize with purinosomes and they have no spatial relationship, indicating that glucosomes are specific to enzymes associated with glucose metabolism. The spatial relationship between glucose metabolism and de novo purine biosynthesis may vary based upon cellular demand.

Future research aims towards the development of user-friendly software for extracting spatial information between enzyme compartments upon various conditions from the 4-D image data.

Acknowledgements: Student research funding grants: MARC U*STAR T34 HHS 00026, The Meyerhoff Graduate Program NIGMS IMSD: 2R25 GM55036, Chemistry Biology Interface Training Program: T32 GM066706, Research funding: R01 GM134086, R01 GM125981, R03 CA219609.

UMBC is constructed on the historical lands of the Paskestikweya, now recognized as citizens of the Cedarville Band of Piscataway Conoy, the Piscataway Indian Nation, and the Piscataway Conoy Tribe. We respectfully acknowledge Indigenous right to identity, sovereignty, and self-determination.

RADIATION THERAPY POTENTIATION VIA FERROPTOSIS INDUCTION FOR THE TREATMENT OF PANCREATIC DUCTAL ADENOCARCINOMA

Alexandra Seas^{1,2}, Joseph Carmicheal Ph.D.², Nolan File², Chi Lin M.D.² Sicong Li D.Sc.², Sukhwinder Kaur Ph.D.², Surinder K. Batra Ph.D.²

¹Chemical, Biochemical and Environmental Engineering, University of Maryland Baltimore County (UMBC), Baltimore, MD 21250

²Department of Biochemistry and Molecular Biology, University of Nebraska Medical Center, Emile St, Omaha, NE 68198

Pancreatic ductal adenocarcinoma (PDAC) is the third leading cause of cancer death in the United States. Although surgical resection is the only curative option, the vast majority of PDAC cases are detected when resection is no longer possible. This has initiated the search for new sensitizing agents to increase the effectiveness of current treatments. This study focuses on improving efficacy of neoadjuvant radiation therapy, thereby increasing the number of PDAC cases that are eligible for resection.

Ferroptosis is a recently discovered iron-dependent form of cell death, which occurs due to a buildup of lipid peroxides. It is facilitated by the inhibition of system X_c (comprised of SLC3A2 and SLC7A11 proteins) and subsequent depletion of glutathione-peroxidase-4 (GPX4), a protein that converts lipid peroxides to nontoxic lipid alcohols. Erastin is a small-molecule that inhibits system X_c, thereby inducing ferroptosis. PDAC is under a considerable amount of oxidative stress and is heavily reliant upon antioxidative mechanisms, making it a prime target for ferroptosis induction.

Radiation treatments cause damage by generating reactive oxygen species, which can induce lipid peroxidation. Decreasing GPX4 levels allows lipid peroxides to build up and trigger ferroptosis, thus increasing the effectiveness of radiation treatments. **We hypothesized that pharmacological induction of ferroptosis can be used as a novel radiation sensitizer for the treatment of pancreatic ductal adenocarcinoma.**

Our studies confirmed that GPX4 and SLC7A11 expression is elevated in PDAC compared to healthy tissue. Additionally, GPX4 expression increased with radiation at the mRNA and protein level in cell lines and tissues. PDAC cells, when treated with erastin, exhibited decreased expression of GPX4, indicating inhibition of system X_c. Finally, pharmacologically induced ferroptosis was effective in sensitizing PDAC cells to radiation-mediated damage. Furthermore, ferroptosis induction via system X_c inhibition is an effective radiation sensitization modality that can increase the efficacy of radiation therapy.

The U-RISE Program at the University of Maryland, Baltimore County (UMBC) is supported by the National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 136497. This research was funded in part by the UNMC MD/PhD Summer Undergraduate Research Program, and the Department of Biochemistry and Molecular Biology

TOWARDS USING CONVOLUTIONAL NEURAL NETWORKS TO PREDICT HUMAN BEHAVIOR AND NEURAL REPRESENTATIONS

Joshua Slaughter¹, Joshua Peterson^{2,4}, Marius Cătălin Iordan^{3,4}, Jonathan Cohen^{3,4}

¹Department of Computer Science and Electrical Engineering, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

²Department of Computer Science, Princeton University, 201 Nassau Street, Princeton, NJ 08544

³Princeton Neuroscience Institute, Princeton University, 201 Nassau Street, Princeton, NJ 08544

⁴Department of Psychology, Princeton University, 201 Nassau Street, Princeton, NJ 08544

As humans, we categorize objects at different levels of specificity (e.g. ‘animal’, ‘dog’, ‘pug’, ‘Mr. Woof’), but the middle level of generality (‘dog’) is privileged both in human perception (Rosch et al. 1976) and in the patterns of activity it elicits in the human brain (Iordan et al. 2015). Conversely, recent advances in machine learning have put forth convolutional neural networks (CNNs). CNNs can identify object categories present in natural images with a high degree of accuracy (Krushevsky et al. 2013). However, the pattern of errors that humans and networks make remain quite different, and current neural networks lack the flexibility of human perceptual categorization across multiple levels of generality. To address this issue, we re-trained the final layers of a state-of-the-art CNN (Peterson et al. 2018) to incorporate a similar perceptual bias as present in human behavior: basic-level categorization preference using two normed stimulus sets of 2,104 naturalistic images from 4 and 9 basic level object categories, respectively (Iordan et al. 2015). Our manipulation generated a new neural network organization that was highly correlated with human behavioral judgments of similarity, as well as with patterns of activity elicited by the images in object-selective regions of the human brain (LOC), but not in early visual cortex (V1). This suggests that it may be possible to increase the correspondence between the internal organization of CNNs and the human brain’s visual processing stream, without sacrificing categorization performance, while simultaneously improving the alignment between the network’s predictions and human behavior.

The U-RISE Program at the University of Maryland, Baltimore County (UMBC) is supported by the National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 13649

LONG-TERM EFFECTS OF THE CLEAN AIR ACT: THERMODYNAMIC MODELING OF AEROSOLS AND AEROSOL PH IN BALTIMORE, MARYLAND

Diane Stonestreet¹, Christopher Hennigan²

¹Department of Mechanical Engineering, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, Maryland 21250

²Department of Chemical, Biochemical, and Environmental Engineering, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, Maryland 21250

The Clean Air Act has had a significant impact on air quality since its formation in 1970; restrictions and regulations have led to an overall decrease in air pollution, such as SO₂ and NO_x. Aerosol pH as well as its effects on the environment are less well understood, therefore it may be helpful to understand the impact of decreasing air pollution on aerosol pH. The goal of this research is to correlate trends in SO₂ and NO_x with trends in aerosol pH in Baltimore, Maryland to determine how heavily the Clean Air Act has influenced aerosol pH over the last several decades. This will be done by compiling publicly available aerosol concentration data for Baltimore County from the Environmental Protection Agency Air Quality System and employing the use of the Extended Aerosol Inorganics Model (E-AIM) thermodynamic equilibrium model to estimate pH. Aerosol pH, as well as ambient particle concentrations will be measured on a biweekly basis over a period of 15-20 years so that pH data can be analyzed in relation to average biweekly SO₂ and NO_x concentrations.

This project is funded by the Scholar Research Institute (SRI) of The UMBC McNair Scholars Program

GENERATION OF A *DP2* MUTANT IN *VOLVOX CARTERI* THROUGH THE CRISPR/CAS9 GENE EDITING SYSTEM

Sierra Wallace¹, James Williams¹, Michael LaScola¹, Stephen M. Miller Ph.D¹,
¹Department of Biological Sciences, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

Volvox carteri, a multicellular green alga, is an ideal model organism for investigating the origins of multicellularity because it has two cell types and is closely related to unicellular *Chlamydomonas reinhardtii*. One key multicellularity trait that is poorly understood is regulation of cell division number. *Volvox* typically does 11-12 mitotic divisions while *Chlamydomonas* does one to five. This study focuses on the retinoblastoma-regulated cell division activator, dimerization partner (DP). *Chlamydomonas* has only one *dp* gene, while *Volvox* has two *dp* genes, *dp1* and *dp2*. *Volvox dp1* mutants do fewer rounds of cell division than the wild type. The goal of this project is to understand the role of *dp2* in cell division number. The CRISPR/Cas9 editing system was used to knock out *dp2*. We co-transformed single-guide RNA (sgRNA) genes with a Cas9-gene plasmid into *Volvox*. We obtained transformants for each sgRNA, grew populations of them in culture, and sequenced the targeted regions. One transformant population included both wild type and mutant sequences at the target site and from that population we obtained a pure *dp2* mutant with a frameshift mutation leading to an early stop codon. At gross inspection, this mutant appears not to be obviously affected for cell division, but we are in the process of more carefully characterizing the phenotype. This work should lead to a better understanding of the role of Dp proteins in regulating cell division number in *Volvox*.

The U-RISE Program at the University of Maryland, Baltimore County (UMBC) is supported by the National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 136497. This work was also supported by grant NSF-EFRI-1332344 from the National Foundation (NSF) Directorate for Engineering (ENG) Office of Emerging Frontiers in Research and Innovation (EFRI).

COVID-19: EXPLORING THE OPPORTUNITIES AND BARRIERS OF TELEHEALTH & TELEREHABILITATION SERVICES FOR STROKE SURVIVORS

Frances Watson¹, Adegboyega Akinsiku², Dr. Helena Mentis²

¹Department of Computer Science and Electrical Engineering, University of Maryland Baltimore County, 1000 Hilltop Circle, Catonsville, Maryland 21250

²Department of Information Systems, University of Maryland Baltimore County, 1000 Hilltop Circle, Catonsville, Maryland 21250

Stroke is the leading cause of long term disability in the United States and rehabilitation is an important aspect of the recovery plan of care for stroke survivors. However, due to the disruptive nature of COVID-19 pandemic, health services and rehabilitation for stroke survivors have needed to be achieved remotely. Thus, telehealth and telerehabilitation has become a critical element in providing effective healthcare services. The following study was motivated to further understand the opportunities and challenges that providers and patients experienced using telerehabilitation. Specific research questions included: How were providers able to meet the clinical care needs of the patient? How has telerehabilitation made treatment more accessible? How are providers able/unable to adapt to the wide-ranging needs of the patients? What contextual/social barriers limit the efficacy of telerehabilitation for different populations?

We conducted a series of 60-minute interviews approximately three months after the state of Maryland was put into quarantine. The interviews were with medical rehabilitation specialists (Physiatrists, Occupational Therapists, Physical Therapists, Rehabilitation Psychologists and Neuropsychologists). At the time of submission, we have interviewed nine providers. Our analysis will take the approach of how to make telerehabilitation more accessible for patients with lower socio-economic status as well as taking into consideration the design of such platform. Interview transcripts are being open-coded, and we have discovered several themes from this analysis. Some of our early findings include caregiver's role in effective telerehabilitation, loss of collegiality amongst colleagues, specific health disparities becoming more evident, and healthcare is more accessible to a specific population. In the future we plan on interviewing stroke survivors and caregivers and then use the design requirements developed from our findings to create an ideal telehealth and telerehabilitation platform.

I would like to acknowledge the Undergraduate Research Award program for supporting my research as well as NSF grant #1552837.

CUSTOMIZABLE TOOLS FOR MEASURING POLYMER DEGRADATION

Jameka Wiggins¹, Sheldon Broedel Sr.², Jeffery Gardner²

¹Department of Chemical, Biochemical, and Environmental Engineering, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, Maryland 21250

²Gardner Industries, LLC, 1450 South Rolling Road, Baltimore, Maryland 21227

Man-made plastics and natural biomass are a rich source of carbon-based chemicals. There is growing interest in developing more efficient methods for converting these polymeric materials into value-added chemicals. A challenge in working with polymers is they are insoluble in aqueous solutions. Consequently, they interfere with direct photo- and fluorometric measurements. To eliminate this problem, we have devised 3D printed biomass containment devices that simplify the measurement of polymer degradation in real-time. A related device is a centrifuge filter. We have designed a reusable filter device that fits into standard sized centrifuge tubes and can be used with a filter of any pore size. The utility of the device was demonstrated using a dye release assay.

The assay used Azocoll, an insoluble protease substrate to which a dye is covalently attached. Proteolytic degradation results in the release of soluble dye. The Azocoll in buffered saline was placed into the top portion of the centrifuge devices fitted with 0.2 μm filters. A protease solution was dispensed into the filter devices at staggered time intervals and incubated. The devices were centrifuged to separate the released dye from the substrate. The absorbance at 520 nm of the filtrate solution was measured. The results showed a time-dependent increase in absorbance in the filtrate, which was indicative of the Azocoll substrate being degraded by the protease. It is predicted that by changing the pore size of the filter, polymer fragments of different sizes can be obtained thereby permitting more precise analyses of polymer degradation.

I would like to thank the NSF Louis Stokes Alliance for Minority Participation (LSAMP) for funding my research this summer. In addition, I would like to thank my mentors Dr. Sheldon Broedel and Dr. Jeffery Gardner for their guidance this summer. Finally, I would like to thank the McNair and LSAMP staff and scholars for their overwhelming support throughout my summer research process.

Mining Medical Images and Text for Clinical Decision Making

Lorrayya Williams¹ and Dr. Sanjay Purushotham²

¹Department of Computer Science, Calvin University, 3201 Burton St. SE Grand Rapids, Michigan, 49546

²Department of Information Systems. University of Maryland Baltimore County, 1000 Hilltop Circle, Baltimore, Maryland 21250

Medical images and clinical notes provide rich information about the underlying diseases. Even though clinicians regularly use them for diagnosis; images and notes are unstructured, and current EHR systems do not use them for clinical decision making. In this project, we study the problem of medical images and text mining so that end-to-end deep learning models can be built to understand the medical images. The first part of our project involves extracting medical images and associated clinical data from the open source Medpix database run by the NIH. In the second part, processing the images and text is done using Optical Character recognition and related techniques to remove patient identifiable information. Finally, novel deep learning models will be developed to leverage multimodal medical images and text in the context of clinical decision making.

I would like to thank Dr. Purushotham for mentoring me throughout my project. The COEIT for funding and support of my research.

EXAMINING THE ROLE OF CANONICAL HISTONES, VARIANTS AND HISTONE-MODIFYING ENZYMES IN THE EVOLUTION OF MULTICELLULARITY IN THE VOLVOCINE LINEAGE

Sheila N. Yeboah¹, Mitra Harrison², Stephen M. Miller²

¹Department of Chemistry and Biochemistry, UMBC, 1000 Hilltop Cir, Baltimore, MD 21250

²Department of Biological Sciences, UMBC, 1000 Hilltop Cir, Baltimore, MD 21250

The evolution of multicellularity in the volvocine green algae began with the divergence of lineages from a common unicellular ancestor ~200 million years ago, which led to the emergence of multicellular *Volvox carteri* and the unicellular *Chlamydomonas reinhardtii*. By comparison, animals diverged from their most recent unicellular ancestor over 600 million years ago. Their close relatedness, along with developmental simplicity make these algal species an excellent model system for investigating the evolution of multicellularity. Histones are small proteins that condense DNA into the chromatin of eukaryotic nuclei. Histones may have played a role in the unicellular-multicellular transition, but this hypothesis has not been extensively studied. Enzymatic modifications to histone tails and the replacement of canonical histones with histone variants are two major types of epigenetic modifications that induce chromatin states affecting DNA replication, transcription and repair. This study explores the possible role of histone variants and histone modification enzymes in the evolution of multicellularity in the volvocine lineage. We first inventoried annotated histones, their variants and some histone modification enzymes in both *C.reinhardtii* and *V.carteri* from Phytozome, an algal genome database, then performed a BLAST search for unannotated proteins. We also are analyzing RNAseq data to identify interesting differences in expression patterns for these genes. We found that *C.reinhardtii* has twice as many histone genes than *V.carteri*, and that the two organisms have a similar number of histone modification enzyme genes. This study may uncover a specialized role for histone variants and histone modifying enzymes in these species and help elucidate their role in the evolution of multicellularity.

This work was funded by a grant (REM supplement to NSF-EFRI-1332344) from the National Foundation (NSF) Directorate for Engineering (ENG) Office of Emerging Frontiers in Research and Innovation (EFRI).

Congratulations to all Virtual SURF 2020 Presenters and their Mentors



Note to SURF Presenters:

As you build your resume or curriculum vitae (CV), remember to include your conference presentations as part of your academic experience. Your mentor or program director can assist you with the most correct format to use to list your SURF presentation. Also, there are many helpful resources available on the Internet.