Summer Undergraduate Research Fest

SURF'S UP!

August 9, 2023

University Center Ballroom and UC 312
University of Maryland, Baltimore County

Hosted by the College of Natural & Mathematical Sciences

UMBC

Hosted by the

COLLEGE OF NATURAL AND MATHEMATICAL SCIENCES

surf.umbc.edu

SURF'S UP!

Schedule

8:15 a.m.
Presenter Check-in

8:15 – 8:45 p.m.
Poster Set-up & Continental Breakfast

9 – 9:15 a.m.
SURF Opening (UC 312)

9:15 – 9:45 a.m.
Lightning Round Talks

10 – 10:45 a.m
Poster Session #1

10:45 – 11:30 a.m.
Poster Session #2

11:45 a.m.
Closing, Special Recognition of Mentors and Presenters (UC 312)

PRESENTERS:
surf.umbc.edu/2023-presenters

ABSTRACTS:
surf.umbc.edu/2023-abstracts

NEW!

The UMBC Beckman Scholars Program will lead the effort this year in hosting Lightning Round Talks at SURF 2023. Lightning talks are short-form talks, which are unlike traditional conference presentations, panels, or lectures. Each presenter gets five minutes and may use up to 5 slides. The main goal of Lightning talks is to spark new conversations and collaborations across disciplines with fast-paced presentations.

Six SURF presenters have been selected for a 5-minute Lightning Round talk. There will not be an opportunity for Q&A following the Lightning Round talks, however attendees may ask questions at the presenters poster during their designated poster session.

Participating Programs

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

The SURF team would like to recognize the support given by these research programs to promising researchers for early professional research and presentation opportunities. These programs are listed as follows.

COEIT Summer Research Experience Program
UMBC College of Engineering and Information Technology
coeit.umbc.edu/nsf-reu

HHMI Scholars Program
Howard Hughes Medical Institute
meyerhoff.umbc.edu

Louis Stokes Alliance for Minority Participation Research Programs
UMBC & University System of Maryland
lsamp.umbc.edu

U-RISE Program
National Institute of General Medical Sciences (NIGMS) at the NIH
urise.umbc.edu

McNair Scholars
U.S. Department of Education TRIO Program
mcnair.umbc.edu

Meyerhoff Scholarship Program
Supported by a network of institutional partners and friends
meyerhoff.umbc.edu

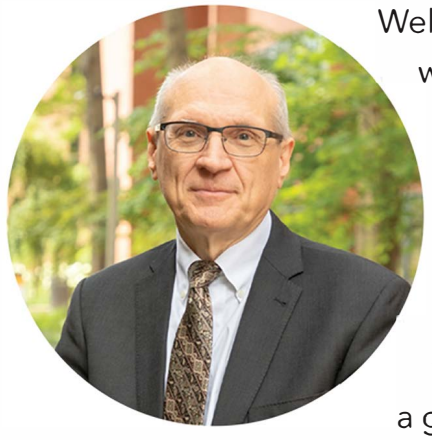
National Institute on Drug Abuse
irp.nida.nih.gov

STEM BUILD 2.0 at UMBC
NIH Common Fund and NIGMS
stembuild.umbc.edu

Translational Life Science Technology
shadygrove.umbc.edu/program/translational-life-science-technology

NSF Research Experience & Mentoring
betenbaugh.jhu.edu/REM.html

Message from the Dean



Welcome to the 2023 UMBC Summer Undergraduate Research Fest, which is hosted annually by the College of Natural and Mathematical Sciences. 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.

While some projects are the result of independent arrangements, many have been made possible by grants or other funds dedicated to encouraging undergraduate research. 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 welcome you to our SURF event and encourage you to view the outstanding works of our presenters and interact with these remarkable students.

Congratulations and best wishes for a successful event,

William R. LaCourse, Ph.D.
Dean and Professor of Chemistry
College of Natural and Mathematical Sciences

PARTICIPATING FACULTY & POSTDOC MENTORS

Songon An
UMBC
Chemistry and Biochemistry

Joseph Bennett
UMBC
Chemistry and Biochemistry

Charles Bieberich
UMBC
Biological Sciences

Lee Blaney
UMBC
Chemical, Biochemical and Environmental Engineering

Rachel Brewster
UMBC
Biological Sciences

Maria Cambraia Guimaro
UMBC
College of Natural and Mathematical Sciences

Steven Caruso
UMBC
Biological Sciences

Zhiyuan Chen
UMBC
Information Systems

Abu-Zaher Faridee
UMBC
Information Systems

Ankit Goel
UMBC
Mechanical Engineering

Erin Green
UMBC
Biological Sciences

Christopher Hennigan
UMBC
Chemical, Biochemical and Environmental Engineering

Kathleen Hoffman
UMBC
Mathematics & Statistics

Nele Hollmann
UMBC
Chemistry and Biochemistry

Tyler Josephson
UMBC
Chemical, Biochemical and Environmental Engineering

Lisa Kelly
UMBC
Chemistry and Biochemistry

Andrei Khodak
Princeton University
Mechanical Engineering

Erin Lavik
UMBC
Chemical, Biochemical and Environmental Engineering

Tara LeGates
UMBC
Biological Sciences

Margaret MacDonald
US Army DEVCOM CBC
Chemistry

Elaine MacDougall
UMBC
English

Brea Manuel
UMBC
Chemistry and Biochemistry

Jan Marchant
UMBC
Chemistry and Biochemistry

Mark Marten
UMBC
Chemical, Biochemical and Environmental Engineering

Stuart Martin
University of Maryland, Baltimore
Department of Pharmacology, Department of Physiology

Stephen Miller
UMBC
Biological Sciences

Kevin Omland
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Biological Sciences

Achuth Padmanabhan
UMBC
Biological Sciences

Phyllis Robinson
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Biological Sciences

Zeev Rosenzweig
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Chemistry and Biochemistry

Nirmalya Roy
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Information Systems

Aaron Smith
UMBC
Chemistry and Biochemistry

Michelle Starz-Gaiano
UMBC
Biological Sciences

Michael Summers
UMBC
Chemistry and Biochemistry

Ali Tokay
UMBC
Geography and Environmental Systems

Ramana Vinjamuri
UMBC
Computer Science & Electrical Engineering

Fernando Vonhoff
UMBC
Biological Sciences

Jianwu Wang
UMBC
Information Systems

Kwai Wong
University of Tennessee, Knoxville
Computer Science & Electrical Engineering

Roberto Yus
UMBC
Computer Science & Electrical Engineering

Poster Session Assignments:

Last Name	First Name	Abstract/Poster Presentation Title	Session I or Session II	Poster Board #
Abisamra	Elea-Maria	TUNING THE DISRUPTIVE INTERACTIONS OF MXENES AND PHOSPHOLIPID VESICLES THROUGH SURFACE MODIFICATIONS	Session 2	7
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Agbere	Fariha	Discovering Equations for Simple Acids Dissociation	Session 2	41
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Ahmed	Fairine	NATIVE CELL MEMBRANES AS A PLATFORM FOR STRUCTURAL BIOLOGY IN NEUROSCIENCE	Session 2	71
Ajibade	Tolulope	COMPARING SIMILAR INTEGRASE PROTEINS IN DIFFERENT PHAGES TO EVALUATE THE PRESENCE OF HORIZONAL GENE TRANSFER	Session 1	49
Akinbamowo	Dipo	EXPLORING THE FATE OF RNA IN MOLONEY MURINE LEUKEMIA VIRUS	Session 1	65
Appiah	Christopher	UNVEILING THE FASCINATING WORLD OF PENDULUMS: AN ANALYSIS VIA INCORPORATING DESIGN, SIMULATION, AND MODELING	Session 1	24
Arizpe-vega	Juan	MULTI-MODLE UNSUPERVISED VARIATIONAL AUTOENCODER FRAMEWORK FOR ARTIFACT DETECTION	Session 2	64
Atolagbe	Gloria	A STUDY ON TECHNOLOGY ACCEPTANCE TO SUPPORT PERSONAL DECISION-MAKING ON A COLLEGE CAMPUS	Session 1	18
Azhar	Shahabal	Investigating the role of mod and elys gene in collective cell migration	Session 2	62
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Bajwah	Abdullah	PTEN REACTIVATION IN A MOUSE MODEL OF PROSTATE CANCER	Session 1	75
Barnett	Samuel	NICOTINE-INDUCED ASSOCIATIVE LEARNING IN CAENORHABDITIS ELEGANS	Session 2	10
Barry	Kaylee	INVESTIGATING INFLUENCE OF TRIMERIZATION ON SELECTIVITY OF THE CES DIMER BY USING A TRITRANSMEMBRANE FUSION-PROTEIN	Session 2	57
Bentsil	Angel	PROTEIN OPTIMIZATION OF HIV-1 MYRISTOYLATED MATRIX FOR FUTURE MEMBRANE BINDING STUDIES	Session 1	37
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Birenzvige	Joshua	AN AB-INITIO INVESTIGATION OF VARIOUS SULPHATES ON A CALCITE SURFACE USING DENSITY FUNTIONAL THEORY	Session 2	27

Boehlert	Kellie	INVESTIGATING THE ROLE OF DIMERIZATION AND CAP SEQUESTRATION IN SELECTIVE PACKAGING	Session 1	60
Bolima	Nelanne	ANALYSIS OF ASPERGILLUS NIDULANS STRAIN BRANCHING PATTERNS TO DETERMINE IMPACT ON MYCELIAL MATERIAL MECHANICAL PROPERTIES.	Session 1	30
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Willis	Lindsay	PROTEIN OPTIMIZATION OF HIV 1 MYRISTOLATED MATRIX FOR FUTURE MEMBRANE BINDING STUDIES	Session 1	37
Woodson	Sophia	AN EXPLORATORY STUDY OF MMWAVE RADAR FOR OBJECT DETECTION AND CLASSIFICATION	Session 2	29

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ABSTRACTS

Listed Alphabetically by Presenter's Last Name:

A

TUNING THE DISRUPTIVE INTERACTIONS OF MXENES AND PHOSPHOLIPID VESICLES THROUGH SURFACE MODIFICATIONS

Elea-Maria Abisamra[1]; Swapnil Ambade[2], Kushani Mendis[2], and Zeev Rosenzweig[2]
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MXenes are recently discovered 2D nanomaterials with a high metal-like electrical conductivity. MXenes are composed of the following formula, Mn+1XnTx (n=1, 2 or 3), whereby the 'M' symbolizes a transition metal, the 'X' usually represents carbon or nitrogen, and 'T' illustrates the functional groups etched onto its surface during the MAX phase. Though MXenes have a high potential for application in energy storage and biomedical engineering, their degradation in biological systems requires further analysis to determine their long-term effects on biological systems and environmental sustainability. The current project aims to determine the antimicrobial activity of MXenes and to tune this activity through surface chemistry modifications. We are looking primarily for ligands that would enable tuning the antimicrobial activity of MXenes while inhibiting surface oxidation of MXenes in aqueous media. As a part of this project, we carried out experiments to better understand the interactions between MXene nanosheets and phospholipid vesicles (liposomes), which serve as a model for bacterial cell membranes, and the impact of surface modifications with phosphonic amine derivatives on the strength of these interactions and on other functional properties of MXenes. Fluorescence-based liposome lysis assays and complementary methods are used to determine the impact of MXenes with different surface functionalities on liposomes of various phospholipid compositions. In line with the CSN research goals, understanding the interactions between unmodified and surface-modified MXenes and phospholipid membranes is vital to developing environmentally benign synthetic nanoparticles with minimal adverse impact on living organisms in the environment.

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STRUCTURAL STUDIES OF AN HIV-1 PACKAGING INHIBITOR THAT TARGETS THE VIRAL RNA

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Treatments for HIV-1 target various aspects of its viral life cycle to terminate reproduction of new virions. However, due to its retroviral nature, as well as social implications that prevent patients from receiving consistent regimens, the HIV-1 virus rapidly mutates to resist current treatments. To

compensate, we aim to determine the structural makeup of the virus's proteins and RNA to identify alternative targets for novel treatment. The HIV-1 viral RNA is selectively packaged for virion assembly via interactions between the nucleocapsid (NC) of the virus's Gag Polyproteins and the Core Encapsidation Signal (CES) of the viral RNA. A region of CES, the Psi Stem-loop (PST), has multiple high-affinity binding sites for NC, which specifically binds to the PST via non-Watson-Crick base paired guanosines. We hypothesize that this labile nature of the viral RNA facilitates the RNA-protein interaction. A quinolinium derivative compound NSC260594 (NSC) has been recently identified to potentially inhibit NC binding to the PST. We aim to understand the implications of this binding on the structure of the viral RNA. To learn the molecular mechanism of this inhibition, I am conducting nuclear magnetic resonance (NMR) studies of both the PST and the PST bound to NSC to investigate, by comparison, how the structure of the viral RNA is potentially altered, or stabilized, when bound to NSC. Furthermore, I will perform gel studies comparing NC and NSC binding to the PST to determine the binding affinity of NSC to the PST in the presence and absence of NC. By understanding the RNA's binding preferences, we can determine how effective NSC is for inhibition of genome packaging for new virions. The results of this project may lead to future use of NSC as a novel treatment for the HIV-1 virus.

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Discovering Equations for Simple Acids Dissociation

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Zeolites, widely used microporous crystals, serve as valuable adsorbents across diverse industries due to their unique TO4 building block, where T is primarily silicon (Si). Brønsted acid zeolites, formed by the replacement of Si by elements like aluminum (Al) or phosphorus (P), exhibit acid functionality, enhancing their catalytic and adsorptive capabilities. We aim to study interactions in zeolite adsorption, particularly in Brønsted acid zeolites, but we face challenges in finding affordable and reliable methods. Density Functional Theory (DFT) is known for providing accurate data, but it can be costly, especially for large-scale systems. In contrast, molecular mechanics force fields are available for simulations, but they have not been well-established for studying acid-base interactions in Brønsted acid zeolites. To address this, we are exploring the development of transferable and reliable force fields tailored for acid-base interactions with the help of symbolic regression, which allows us to derive functional forms of interaction potentials from potential energy surface scan data. In our poster, we will present our methodology and findings, showcasing how symbolic regression can potentially help bridge the gap between accurate but expensive DFT calculations and more accessible force field simulations. Our proposed approach could open up exciting new methods for conducting efficient and accurate studies of zeolite adsorption.

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SYNTHESIS AND ANALYSIS OF SPHERICAL GOLD NANOPARTICLES

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Prostate cancer, the second leading cause of cancer in American males, poses a major threat to a large community. While conventional chemotherapy treatment for cancer at the metastatic stage can effectively kill tumor cells, this treatment also produces several side effects, namely hair loss, nausea, and extreme fatigue due to the distribution of drugs throughout the entire body. Therefore, the Daniel Lab proposes a solution that administers chemotherapeutics in a more targeted form; the use of functionalized gold nanomaterials, which act as carriers for chemotherapeutics and imaging agents through surface modification with dendrons. As opposed to other nanomaterials, gold nanoparticles are biocompatible, highly stable, have a tunable size and shape, a high surface area to volume ratio, and are cost efficient. My current project is to synthesize spherical gold nanoparticles of approximately 20 nm in diameter. These gold nanoparticles are synthesized using the Turkevich-Frens method, involving the reduction of chloroauric acid (HAuCl4) with trisodium citrate (Na3C6H5O7). After synthesis, these nanoparticles are analyzed using DLS (dynamic light scattering) and UV-VIS (ultraviolet visible spectroscopy) to determine the diameter of the nanoparticles and the wavelength of light that causes the LSPR phenomenon (localized surface plasmon resonance) to occur, respectively. Resultantly, based on the Z-average value, spherical nanoparticles with a size of 18.34 nm (DLS) and an absorbance of 518.0 nm (UV-VIS) were produced. The proceeding steps in the process will include synthesis of gold nanorattles; a core, void, and porous shell structure produced through galvanic replacement with silver metal, to which dendrons will be attached. These structures have a much higher loading capacity for all functionalities and due to cage structure, the NIR absorption can be applied, enhancing the efficacy of the treatment through photothermal therapies.

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NATIVE CELL MEMBRANES AS A PLATFORM FOR STRUCTURAL BIOLOGY IN NEUROSCIENCE

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Information processing in the brain requires the coordinated activity of billions of synaptic proteins, which collectively act to mediate synaptic transmission and facilitate high cognitive functions. Dysfunction of synaptic proteins is linked to numerous neurological disorders, including Schizophrenia, Alzheimer's Disease, and ALS. A detailed structural understanding of synaptic proteins is necessary for the development of therapeutics targeting diverse neurological conditions; however, classical structural biology techniques require protein purification, which often places the target proteins in an artificial environment, altering the polarization and biological complexity of native cell membranes required for proper function. It has been shown that isolating cell membranes natively anchors integral proteins for structural analysis; however, a method for synaptic protein production in membranes has not been established. We hypothesized that we could use native membranes to isolate synaptic proteins for structural determination. We

therefore developed a methodology for isolating cell membranes to ultimately characterize a detailed protein structure through a high-resolution imaging technique, cryo-electron microscopy (cryo-EM). We explored various approaches, leveraging chemicals that stimulate isolation of cell membrane components. We refined these approaches to achieve particle sizes suitable for data analysis. In a 600-micrograph dataset, we achieved a 55% rate of images with membranes of the desired size, along with the proteins of interest. In the future, we will use cryo-EM images to compare structures of purified synaptic proteins to those that we solve in native cell membranes. Collectively, these advances will enhance our understanding of synaptic protein structure and aid in the development of more effective therapeutics.

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Comparing Similar Integrase Proteins in Different Phages to Evaluate the Presence of Horizontal Gene Transfer

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The integrase protein, an integral part of the temperate life cycle, was investigated for elements of divergent evolution within temperate phages. The integrase protein from *Gordonia* phages ClubL and Oneup (cluster CQ) were phylogenetically examined with 15 actinobacteriophages of various clusters carrying integrases classified into seven different phams and compared to a proteomic tree produced of the same phages. As would be expected, when entire proteomes were examined, the phages assorted by cluster and host infected. When the integrase was investigated phylogenetically, however, evidence of horizontal gene transfer was found in bacteriophages, with phages of different clusters forming different clades in several instances. Two cases of note are pham 98453, which is found in Bantam (cluster DL) as well as phages ClubL and OneUp (CQ1 and CQ2), and pham 96094 is found in phages Lucky10 (DH) and Horus (DN1). The presence of an identical integrase gene in genetically different phages suggests horizontal gene transfer as the mechanism. It appears likely that the gene was picked up by an ancestor of ClubL and OneUp prior to their divergence as the integrases of Bantam and OneUp appear to be more closely related than the integrases of OneUp and ClubL's despite their being in the same cluster.

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EXPLORING THE FATE OF RNA IN MOLONEY MURINE LEUKEMIA VIRUS

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The moloney murine leukemia virus (MoMuLv), a virus that causes leukemia and neurological diseases within rodentia, has been studied since the 1950s to act as a model to further understand the underlying mechanisms of all retroviruses due to its easy use. Our laboratory mainly focuses on the human immunodeficiency virus type-1 (HIV-1), most particularly the segment of the HIV-1 RNA genome important for viral replication, known as the 5'-Leader (5'L). The 5'L exists in two conformations: the dimeric conformation adapted by 5'-capped RNAs beginning with one guanosine (Cap1G) in which the cap is sequestered, and the monomeric conformation adapted by 5'-capped RNAs beginning with two or three guanosines (Cap2G and Cap3G respectively) where our cap is exposed. We refer to viruses containing these different beginning sites as having transcriptional start site heterogeneity. Inversely, MoMuLv contains a unique transcription start site, meaning the virus consists of only one start site, Cap1G. It has been shown that the 5'L can still adopt a dimeric or monomeric form. In this work, we aim to explore what drives RNA packaging versus translation in a retrovirus that contains only unique start sites. We suspect that MoMuLv's genome fate is driven by dimerization dependent cap sequestration and hypothesize that dimerization is catalyzed by the nucleocapsid (NC) domain of the retroviral Gag polyprotein. We plan to explore the behavior of MoMuLv's genome in vitro for both monomeric and dimeric RNA, by focusing on cap sequestration and exposure. Through electrophoretic mobility shift assays (EMSA), we can assess whether the cap is sequestered or exposed, which we will further confirm using nuclear magnetic resonance (NMR). In HIV-1, we know that dimerization is driven by transcriptional start site heterogeneity, but in MLV we will explore if dimerization is NC-dependent, which we will later practice in vivo. Our work will provide more information on the mechanisms of retroviruses with unique start sites, and hopefully allow answers on how to stop replication of all retroviruses.

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MULTI-MODEL UNSUPERVISED VARIATIONAL AUTOENCODER FRAMEWORK FOR ARTIFACT DETECTION

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Non-invasive sensor technologies offer an unprecedented opportunity for longitudinal and continuous monitoring of physiological and cognitive functions, enabling researchers to examine temporal changes and patterns in real-world settings. However, despite the non-invasive nature of commercially available wearable sensors, the presence of artifacts, including noise, motion artifacts, ambient interference, and physiological artifacts, can significantly impact the accuracy and interpretability of the collected data, especially in real-world settings. Therefore, effective artifact detection and correction methods are crucial for enhancing the robustness and validity of the sensed data. We focus on the challenges and advancements in multimodal artifact detection and improving the performance for downstream tasks (emotion recognition, cognitive assessment, etc.). In this work, we propose an end-to-end unsupervised variational autoencoder (VAE) framework to detect artifacts in Electroencephalogram (EEG) data by learning the underlying data distribution of the data.

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A STUDY ON TECHNOLOGY ACCEPTANCE TO SUPPORT PERSONAL DECISION-MAKING ON A COLLEGE CAMPUS

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The research looks at undergraduate students' willingness to accept a technology that uses an individual's connection to the WiFi to inform users on the occupancy of a given place or classroom on a university cam- pus. Such an application has everyday uses such as finding an optimal study location, as well as the potential to be appropriated for crises such as the COVID-19 pandemic when social distancing was necessary to re- duce the spread of the disease. Phase 1 of the survey was conducted in the previous year to investigate undergraduate students' response to such an application in the late stages of the pandemic when pandemic fatigue was high. The second phase of the survey is currently underway and fo- cuses on whether undergraduates would use this type of application to inform their everyday decision-making on campus now that the threat of the pandemic has dwindled. Additionally, it asks the undergraduate stu- dents how they would like the application to appear (i.e., maps, tables, or cards). By the end of this research, we expect to understand the opinions of the undergraduate students regarding the application and their percep- tions of the ethical issues behind this type of application. If we find that undergraduate students would use such an application in their decision-making processes, we will be moving to the next stage of development (i.e., actually building an app).

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Investigating the role of *modulo* and *elys* gene in collective cell migration

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The investigation of border cell migration is imperative for understanding animal development, and may help in gaining valuable insight into metastasis, inflammatory diseases, immune response, and embryogenesis. The Starz-Gaiano laboratory focuses on investigating a migratory group of cells called the border cell cluster. Border cells detach from an epithelium and migrate collectively during *Drosophila melanogaster* oogenesis. Border cell migration serves as an efficient model system to study migration in vivo as the migrating cells can be manipulated genetically and the migration can be imaged in live or fixed tissues with relative ease. The genes of interest I am working on are *Elys* and*modulo (mod)*. Both Elys and Mod are transcription factors that were identified in a screen of proteins that interact with Mind Bomb 2 (Mib2) which is a ubiquitin ligase. Our lab previously showed that Mib2 is important for migration and thus, I hypothesize that modifying *mod* and *Elys* levels in border cells will result in delayed border cell migration. To test this, I am using RNA interference in a cell type-specific pattern to reduce the expression levels of these two genes in the border cells and am examining potential changes in cell migration using microscopy. Understanding the role of *mod* and *Elys* in border cell migration will give us valuable insights into the migratory process and could be applied to the broader context of human development and/or disease.

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B

EFFICACY OF PHAGE ENZYME TOOLS WHEN DETERMINING PHAGE CLUSTERS

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Bacteriophages are a type of virus that infects bacteria. Bacteriophage genomes are very diverse. Genetically similar phages are grouped in clusters, with more similar phages grouped into subclusters. Bacteriophage clusters and subclusters are identified through sequencing. But with a restriction enzyme digest the cluster or subcluster can be predicted with a program, Phage Enzyme Tools (PET 2.0). Is PET 2.0 effective with its predictions? We investigated the accuracy of PET 2.0 cluster predictions with data from restriction digests. PET 2.0 is a tool used to aid in the identification of bacteriophage clusters and subclusters, specifically ones we had identification on but wanted to see how PET would identify it. The program works by comparing the results from completed digestion patterns of an unknown phage to simulated digests produced from a database of sequenced phages. We have looked at twelve previously sequenced bacteriophages and ran them through two methods in hopes of finding out how effective one is based on the other. Out of the twelve bacteriophages we chose, none of the sequenced clusters and subclusters matched the predicted clusters and subclusters of PET 2.0. This suggests that PET 2.0 should only be viewed as a prediction and further analysis can be done to verify the cluster or subcluster of the phage.

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PTEN REACTIVATION IN A MOUSE MODEL OF PROSTATE CANCER

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With recent clinical successes of immune checkpoint inhibitors (ICI), immunotherapy has become the standard of cancer treatment. However, due to factors including insufficient tumor immunogenicity and an immunosuppressive tumor microenvironment, ICI suffer from a limited rate of anti-tumor responses for many cancers, including prostate cancer (PCa). Thus, in order to improve these anti-tumor responses, while avoiding the serious side effects of traditional treatments, it became integral to develop of a strategy to exploit immune cell death effectively and synergize it with current ICI. The use of therapeutic mRNA, paired with cytosolic delivery by nanoparticles, had shown promise to improve the cytosolic delivery of various RNA agents. In this project, we proposed to explore whether NP co-delivery of PTEN mRNA induced anti-tumor immune responses in a genetically engineered mouse model of PCa. To achieve this goal, we evaluated the anti-tumor efficacy of PTEN mRNA as well as its combination with anti-PD-1 immunotherapy in the immunocompetent BMPC mouse model of PCa. We also evaluated the in-vivo safety of this combination treatment. We expected that the NP co-delivery strategy could be expanded to

other tumor suppressors and adjuvants, which benefits cancer immunotherapy research and development of novel and effective cancer therapies.

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NICOTINE-INDUCED ASSOCIATIVE LEARNING IN *CAENORHABDITIS ELEGANS*

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Children who observe parents smoking are more likely to smoke when they are older due to associative learning. Associative learning is when two unrelated elements (sounds, smells, objects, emotions, etc.) become connected in the brain through conditioning. These associations can result in learned behaviors. Smoking can be a learned behavior and creates positive reinforcement, which induces a perpetuating cycle. Smoking before/during/after meals may encourage learned behaviors through association. Nicotine, the main addictive chemical in tobacco products, is an alkaloid that occurs naturally in some plants in low quantities. Nicotine can modulate associative learning in the wormlike nematode *Caenorhabditis elegans* a small soil-dwelling nematode that has similar neurological pathways implicated in associative learning compared to mammals. In this study, the associative relationship between food and nicotine is investigated. A chronic exposure assay was conducted using concentrations of 0.01mM and 0.1mM. An acute exposure tolerance assay was performed for nicotine concentrations between 100-1000mM. Concentrations of 250mM and 500mM were selected as effective concentrations and are used in pre-exposure to facilitate associative learning. A chemotaxis assay was used to measure the propensity of the non- or pre-exposed *C.elegans* to move toward *Escherichia coli*. Our preference indexes indicated that *C. elegans* had the same propensity to move toward their food after acute and chronic pre-exposure to nicotine compared to the control. Nicotine's appetitive suppressive effects were not observed in higher concentrations indicating a learned association or adaptation. Future studies could investigate metabolized nicotine levels and the genomic and neurological events that trigger learned behaviors from nicotine exposure in *C.elegans*.

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INVESTIGATING INFLUENCE OF TRIMERIZATION ON SELECTIVITY OF THE CES DIMER BY USING A TRITRANSMEMBRANE FUSION-PROTEIN

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The retrovirus HIV-1 creates new virions by packaging its dimeric genomic RNA (gRNA) and exporting it from the host cell. To find new treatments for HIV-1, it's important to structurally understand how the virus selectively packages its own gRNA. Previous studies have found that one of the HIV-1 viral proteins, the Gag poly-protein, contains a Nucleocapsid (NC) domain that predominantly binds to a region in the 5' UTR of the genome called the Core Encapsidation Signal (CES). Gag is translocated to the plasma membrane of the host cell where the protein packages and thereby exports the gRNA. To investigate which structural features allow Gag to specifically select for the gRNA over other cellular RNAs, we are studying the binding interactions between Gag, CES, and the cell membrane. The main goal of this project is to investigate whether trimerization is a factor that influences selectivity for the CES dimer. Previous work used a GCN4 fusion protein, a trimeric coiled-coil domain that is fused to the Gag protein via a GS linker. We are now incorporating another fusion protein called the tritransmembrane protein (triTM). This protein is designed, similar to GCN4, to trimerize at the N-terminus of CA-SP1-NC, but the key difference is that triTM additionally binds to the cell membrane. This allows to have a more realistic study to understand the process of RNA packaging where we can investigate interactions between Gag and the gRNA in the presence of a lipid bilayer in form of a nanodisc. We will replicate previous binding studies of GCN4 and gRNA using triTM to additionally understand if not only trimerization, but assembly at the plasma membrane, influences selectivity towards the CES dimer. The ultimate goal will be to obtain a high-resolution image of this protein-RNA complex bound to a lipid bilayer using cryogenic electron microscopy.

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PROTEIN OPTIMIZATION OF HIV-1 MYRISTOYLATED MATRIX FOR FUTURE MEMBRANE BINDING STUDIES

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Human Immunodeficiency Virus (HIV) is a retrovirus. Like all retroviruses, it encodes for a Gag polyprotein that helps direct the assembly of the virus particles in the host cells. The beginning of this Gag polyprotein house the Matrix protein which has an N terminal myristoyl group which is instrumental in anchoring it and the entire Gag complex to the plasma membrane which is the beginning of the assembly process that also directs envelope glycoproteins to these viral assembly sites. We are looking at the protein optimization of the HIV myristoylated Matrix protein to do assembly experiments using a nanodisc model to mimic the plasma membrane. Our vector exists in the pET Duet plasmid which allows expression of both the HIVMA protein and the

codon optimized N-myristoyltransferase enzyme (NMT). This is a co- translational process that is mediated by the first six amino acids at the N-terminal of the protein referred to as the myristoyl signal (MGARAS). The myristoyl group attachment consists of a 14 Carbon Fatty acid chain that gets anchored in the hydrophobic layer of the membrane. During transport, this group is sequestered in the protein folded structure. Once in contact with the membrane, this group pops out to anchor it to the plasma membrane. This process is referred to as the myristoyl switch. Some of the challenges faced in purifying the myristoylated matrix are due to the protein being extremely pH dependent. At lower pH's, the myristoyl group is exposed and aggregates to be precipitated out in solution. To optimize protein purification, we use different buffer conditions with a range of pHs. Our findings indicate that the myristoylated Matrix is sequestered at a pH of 7, allowing us to further optimize the expression and purification of this protein.

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AN AB-INITIO INVESTIGATION OF VARIOUS SULFATES ON A CALCITE SURFACE USING DENSITY FUNCTIONAL THEORY

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Art conservation scientists have identified that ancient Egyptian limestone artifacts can degrade at faster rates than previously observed, linking this degradation to the presence of surface salts. Calcite, a major mineral component of limestone, can protonate or decarboxylate in different chemical environments altering the surface structure. This study attempts to assist art conservationists and scientists by understanding the effects of salt adsorption of calcite by using plane-wave Density Functional Theory (DFT) to model the interactions of various sulfate adsorbates on the surface of calcite. A calcium terminated surface and a proton terminated surface were used to model the difference between conditions found in a vacuum and normal conditions on earth respectively. The results of these calculations indicate strong and favorable adsorption of sulfate containing compounds onto both calcium and proton terminated surfaces. This study will assist conservationists in their attempt to desalinate limestone surfaces to prevent further degradation of artifacts.

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INVESTIGATING THE ROLE OF DIMERIZATION AND CAP SEQUESTRATION IN SELECTIVE PACKAGING

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The HIV-1 lifecycle requires its RNA to serve dual purpose: as a messenger RNA and as genomic RNA. To dictate the function of the RNA, HIV-1 utilizes heterogenous transcription start sites, producing RNAs beginning with either 1 (Cap1G) or 3 (Cap3G) guanosines. The number of guanosines dictates the structure of the untranslated region of the genome, the 5'-Leader—a region essential to the regulation of translation, splicing, and packaging. Cap3G RNAs are monomeric, hiding Gag binding sites and exposing the 5'-cap, enabling eIF4E binding which allows it to serve as a messenger RNA. Cap1G, on the contrary, adopts a dimeric structure where polyA is stacked with TAR, allowing the dimerization initiation site (DIS) to be available for dimerization, while simultaneously sequestering the 5'-cap. Cap1G's structure will ensure high affinity binding of Gag to allow HIV-1 packaging. Previous literature suggests the stability of polyA is the primary determinant of the selective packaging HIV-1 RNA. Based on competitive packaging assays between wild type HIV and various mutants designed to either disrupt or stabilize the polyA, they hypothesize that polyA stability dictates selective packaging. However, our work has yielded alternative results, where it was deduced that stable polyA mediates cap sequestration—a process we deem essential to efficient HIV-1 packaging. Our project aims to conclude whether cap sequestration is a dominant regulator for packaging. We plan to further explore these mutants from a series of EMSAs with eIF4E, a cap binding protein, in order to evaluate the exposure of the cap to see if these results dictate their packaging tendencies. We also plan to use NMR to visualize the exact effects of the mutations on structure. Successful completion of our work will help identify the dominant features of selective packaging of the HIV-1 genome.

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ANALYSIS OF ASPERGILLUS NIDULANS STRAIN BRANCHING PATTERNS TO DETERMINE IMPACT ON MYCELIAL MATERIAL MECHANICAL PROPERTIES

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Global reliance on plastic and other non-renewable materials has begun to raise concerns regarding long term effects on public health. Consequently, global research efforts are now concentrating on plastic-mitigation strategies to reduce the overall detrimental effects of prolonged plastic use. One promising strategy is the use of filamentous fungi to create materials with properties similar to those of plastic (and other traditional, non-renewable materials), as a sustainable, biodegradable alternative to plastic. We call these mycelial materials. We hypothesize that mycelial-material mechanical properties can be modified by altering fungal phenotype (e.g., increased/decreased hyphal branching), and that this can be accomplished through genetic modification. To test this hypothesis, we studied various strains of the model fungus *Aspergillus nidulans* to quantify hyphal branching rates. To carry out experiments, a branching assay was employed to compare the branching patterns of *Aspergillus nidulans* mutants and control strains. These strains will eventually be used to make mycelial material, to determine if degree of hyphal branching correlates with mechanical properties of the resultant material. The eventual results will provide valuable insights into the development of strong and stable mycelial materials, supporting the progression of sustainable alternatives to plastic-based materials.

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INVESTIGATING THE RELATIONSHIP BETWEEN SUBCLUSTER AND HOST PREFERENCE IN BACTERIOPHAGES

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Superbugs are strains of bacteria and microorganisms that have adapted to become multidrug resistant. While science is searching for ways to counteract these recurring diseases, we look to phage therapy as a potential solution. Phage therapy is a developing form of treatment where phages are selected to target and kill bacterial infections. Bacteriophages are viruses that infect bacterial hosts. In this study, we compared host range data of myoviruses to determine if they had similar host preference. We analyzed nine bacteriophages characterized through the Phage Hunters program belonging to Cluster C. All nine phages were plated against the four bacterial hosts to determine host range similarities and infectivity. Host range data was plotted on a Venn diagram and cross compared to genetic data from a genomic dot plot and phylogenetic tree. Using a dot plot, we viewed the alignment of genetic sequences between all nine bacteriophages. We created a phylogenetic tree using VICTOR to display lines of evolutionary descent and relatedness between phages regardless of subcluster. Cross analyzing host preference and genetic identity provided us a better understanding of a correlation between the two. After comparing host preference and genetic alignment between phages, we found a relationship between host range and subcluster. Previous studies reinforce this point. However, results from our experiment are not conclusive as extensive research and a larger sample size is required to validate our study. Therefore, we can suggest that a relationship between host range and cluster exists. Bacteriophages are important to medical use as prior studies have shown that when phages of genetic relation are combined into a “phage cocktail", they can effectively suppress and eliminate disease. Further experimentation on this subject is important as use of genetically related phages may strengthen the power of phage therapy.

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Impacts of pH and salt concentration on uptake of per- and polyfluoroalkyl substances (PFAS) by anion-exchange membranes

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Per- and polyfluoroalkyl substances (PFAS) are contaminants of emerging concern that are present in water resources around the country. The Environmental Protection Agency recently

proposed strict regulations to protect Americans from PFAS-contaminated drinking water. Due to temporal variation in PFAS concentrations, grab samples are not representative of average PFAS levels in surface water. To address this challenge, we developed a prototype Passive Sampler comprised of an anion-exchange membrane. The goal is to enable PFAS adsorption to the membrane, and then use equilibrium relationships to back-calculate the time-averaged concentrations of 19 PFAS in a water source. We were particularly interested in examining whether the solution pH and salt content would affect PFAS uptake. These research questions were addressed by calculating the selectivity coefficients of 19 PFAS against chloride, a common background ion in water; note, the selectivity coefficients are the equilibrium constants for the ion-exchange reaction. In general, the selectivity coefficients demonstrated a clear trend with chain length, with long-chain PFAS being preferentially adsorbed by the membrane due to electrostatic interactions (PFAS head) and hydrophobic interactions (PFAS tail); for similar reasons, the long-chain PFAS also demonstrated greater adsorption to the containers. We hypothesized that the selectivity coefficients for PFAS that primarily exist as anions would not be sensitive to solution pH. PFOSA was the only compound that exhibited different selectivity coefficients when the pH was increased from 5.0 to 9.0. This outcome was attributed to the acid dissociation constant of PFOSA (pKa = 6.24), which caused a fraction of PFOSA to be neutral at lower pH and therefore not available to interact with the anion-exchange membrane. We hypothesized that the higher salt concentrations would cause salting-out phenomena that increase the selectivity coefficients for PFAS over chloride. The results confirmed this hypothesis. These findings will allow us to develop a universal calibration of the anion-exchange membrane-based passive sampler for use in different water quality conditions. Ultimately, our goal is to deploy the passive sampler to ensure accurate and time-averaged concentrations of PFAS in drinking water supplies to protect public health.

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DETERMINING A HIGH-RESOLUTION STRUCTURE FOR MYRISTOYLATED MATRIX BOUND TO THE PLASMA MEMBRANE

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HIV (Human Immunodeficiency Virus) is a retrovirus that directly infects host cells by binding to CD-4 receptors of the cell surface. Following binding, the virus injects its viral genetic material and enzymes into the host cell where viral RNA (vRNA) is reverse transcribed into DNA and integrated into the host's genome. This genomic integration allows the expression of several important viral proteins- one being the Gag polyprotein which is composed of four main domains: matrix (MA), capsid (CA), nucleocapsid (NC), and P6. This analysis will be focusing on MA and an important post-translational modification of the protein called myristoylation in which a fatty acid known as a myristoyl group is covalently linked to MA. This post-translational modification is responsible in targeting Gag to the host's lipid plasma membrane, which initiates viral assembly and the formation of new virions. The goal of this study is to understand the interaction of the myristoyl group with the host cell's plasma membrane in more detail. In doing so, we aim to determine a high-resolution structure of myristoylated MA (myrMA) bound to PIP-2 in the lipid membrane. This will be done through simulating a phospholipid bilayer using NW-9 nano discs. These nano discs allow the proteins to bind and form a small enough complex to determine binding interactions and a high-resolution structure using NMR (Nuclear Magnetic Resonance) spectroscopy.

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INVESTIGATING THE MOLECULAR INTERACTIONS BETWEEN MONOMERIC HIV-1 RNAS AND CAP-DEPENDENT TRANSLATIONAL MACHINERY, EIF4E

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HIV-1, also known as the human immunodeficiency virus type-1, has persisted since the 1980s and affects over 39 million people worldwide. HIV-1 can progress into the autoimmune deficiency syndrome (AIDS) if not treated. Current treatments include a drug cocktail consisting of inhibitors that target multiple steps of the viral replication cycle. However, due to the copious amount of drugs needed to combat the high viral mutation rates and drug resistance, many patients experience numerous painful and disruptive side effects; leading us to find a treatment that targets areas less susceptible to mutations. Our laboratory focuses on investigating a highly conserved segment of the HIV-1 RNA genome known as the 5′-Leader (5′-L) because it is known to control many viral functions such as translation, packaging, assembly, and splicing. The HIV-1 5′-L exists in equilibrium between two conformations: a monomer and a dimer, due to transcriptional start site heterogeneity. The monomer begins with two or three guanosines at the 5′-end and will also have a 5′-cap - this serves as mRNA that will translate to HIV viral proteins. The dimer is packaged and begins with one guanosine and also has a 5′-cap that is sequestered. Our group focuses on investigating the interactions of the monomeric 5′-L with translation machinery such as the protein eIF4E. We designed and purified two 5′-capped RNA oligos called Cap3G-TAR-F1-C57 and Cap3G-TAR-F1-U64 to determine if structural elements of the RNAs affect eIF4E binding. To study the binding interactions of these RNAs to eIF4E, we conduct electrophoretic mobility shift assays (EMSAs). Qualitatively, the two RNAs bind to eIF4E with similar binding affinities but we need to introduce a quantitative approach to understand how the different structural elements of the two RNAs affect eIF4E recruitment. Next, we used isothermal titration calorimetry (ITC) that measures the changes in thermodynamics parameters as two molecules are binding. Our ITC data reveals that both RNAs bind tightly to eIF4E (nM affinity) and bind tighter than the 5′-cap alone. However, the Cap3G-TAR-F1-U64 binds slightly weaker than the Cap3G-TAR-F1-C57 RNA oligo, suggesting that the additional residues are inhibiting some of the binding interactions. Our data reveals that structural elements of our RNAs can affect recruitment and binding of eIF4E and we aim to further explore this by mutating segments of our RNA oligos and determine their effects on eIF4E binding.

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C

INVESTIGATING THE RELATIONSHIP BETWEEN SUBCLUSTER AND HOST PREFERENCE IN BACTERIOPHAGES

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Superbugs are strains of bacteria and microorganisms that have adapted to become multidrug resistant. While science is searching for ways to counteract these recurring diseases, we look to phage therapy as a potential solution. Phage therapy is a developing form of treatment where phages are selected to target and kill bacterial infections. Bacteriophages are viruses that infect bacterial hosts. In this study, we compared host range data of myoviruses to determine if they had similar host preference. We analyzed nine bacteriophages characterized through the Phage Hunters program belonging to Cluster C. All nine phages were plated against the four bacterial hosts to determine host range similarities and infectivity. Host range data was plotted on a Venn diagram and cross compared to genetic data from a genomic dot plot and phylogenetic tree. Using a dot plot, we viewed the alignment of genetic sequences between all nine bacteriophages. We created a phylogenetic tree using VICTOR to display lines of evolutionary descent and relatedness between phages regardless of subcluster. Cross analyzing host preference and genetic identity provided us a better understanding of a correlation between the two. After comparing host preference and genetic alignment between phages, we found a relationship between host range and subcluster. Previous studies reinforce this point. However, results from our experiment are not conclusive as extensive research and a larger sample size is required to validate our study. Therefore, we can suggest that a relationship between host range and cluster exists. Bacteriophages are important to medical use as prior studies have shown that when phages of genetic relation are combined into a “phage cocktail", they can effectively suppress and eliminate disease. Further experimentation on this subject is important as use of genetically related phages may strengthen the power of phage therapy.

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NICOTINE-INDUCED ASSOCIATIVE LEARNING IN *CAENORHABDITIS ELEGANS*

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Children who observe parents smoking are more likely to smoke when they are older due to associative learning. Associative learning is when two unrelated elements (sounds, smells, objects, emotions, etc.) become connected in the brain through conditioning. These associations can result in learned behaviors. Smoking can be a learned behavior and creates positive reinforcement, which induces a perpetuating cycle. Smoking before/during/after meals may encourage learned behaviors through association. Nicotine, the main addictive chemical in tobacco products, is an alkaloid that occurs naturally in some plants in low quantities. Nicotine can modulate associative

learning in the wormlike nematode *Caenorhabditis elegans* a small soil-dwelling nematode that has similar neurological pathways implicated in associative learning compared to mammals. In this study, the associative relationship between food and nicotine is investigated. A chronic exposure assay was conducted using concentrations of 0.01mM and 0.1mM. An acute exposure tolerance assay was performed for nicotine concentrations between 100-1000mM. Concentrations of 250mM and 500mM were selected as effective concentrations and are used in pre-exposure to facilitate associative learning. A chemotaxis assay was used to measure the propensity of the non- or pre-exposed C.*elegans* to move toward *Escherichia coli*. Our preference indexes indicated that C. *elegans* had the same propensity to move toward their food after acute and chronic pre-exposure to nicotine compared to the control. Nicotine's appetitive suppressive effects were not observed in higher concentrations indicating a learned association or adaptation. Future studies could investigate metabolized nicotine levels and the genomic and neurological events that trigger learned behaviors from nicotine exposure in C.*elegans*.

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Unraveling the Role of Sugar Modifications in Guiding Border Cell Migration

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Cell migration plays a crucial role in the development and homeostasis of multicellular organisms. It can occur during tissue repair or in metastastic cancer, thus providing significant insights into human health and disease. A strong model organism, *Drosophila melanogaster* (fruit flies), has emerged as an indispensable model system for studying cell migration due to its well-characterized genetics and powerful imaging tools. This study focuses on border cells, a collectively migrating cell population regulated by signaling pathways, which migrate to the oocyte during oogenesis, playing a pivotal role in fertilization of the developing egg. The oocyte within the egg chamber secretes proteins that act as guidance cues for border cells during migration. Heparan sulfate proteoglycans have sugar modifications that are essential for their function. Since glycoproteins can alter diffusion, we want to examine this modification for guidance proteins. To test this, we will use RNA interference to inhibit a gene encoding a sugar modification enzyme called *sugarless*. We will then assess if manipulating sugar modifications on glycoproteins disable interactions with guidance cues and affect border cell migration, by using antibody labeling combined with microscopy techniques. This will provide valuable insights into the need for some sugar modifications for proteins involved in border cell signaling during migration towards the oocyte. Leveraging Drosophila as a model organism from continued research in this field promises to reveal complexities of cell migration, fostering potential advancement in therapeutic strategies for various diseases.

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EFFECTS OF LISINOPRIL ON THE MOTOR NETWORK OF AGING DROSOPHILA WITH THE ABSENCE OF APP-LIKE PROTEIN

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Alzheimer's disease (AD) neuropathology is shown to be caused by the cleavage of the amyloid precursor protein (APP) at the β and sites, leading to the overproduction of $A\beta_{42}$ peptides in neuronal tissues and the formation of neuritic plaques. These aggregates result in observable cognitive and motor decline due to neurodegeneration. Using *Drosophila melanogaster* as a model for studying AD has become common practice due to the presence of an APP homolog, APP-Like (APPL), showing high levels of conservation at the structural and functional levels. The human angiotensin-converting enzyme (ACE) is closely associated with high blood pressure or hypertension and physical decline in older adults. ACE inhibitors (ACEi), like Lisinopril, are prescribed for hypertension. While medications like Lisinopril have been shown to mitigate the symptoms of cognitive and motor decline, there is a disparity in their effectiveness. In this study, we explored the beneficial effects of Lisinopril on the motor functions of flies mutant for *appl*. We conducted climbing and flight performance assays to measure the speed, endurance, and reaction time of the flies. We also used a wild-type genotype (w^{1118}) as a control to compare our results. The flies were tested at 2, 10, and 30 days old. Our results indicate that *appl*-mutant flies had poor performance in comparison to the control flies. In comparison to the *appl*-mutant flies with no medication, those treated with Lisinopril show better performance overall. These results suggest there is great potential for ACEi to counter neurodegenerative symptoms related to *appl*-mutant flies and AD.

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INVESTIGATING HYDROGEL DESALINATION OF EGYPTIAN LIMESTONE OBJECTS USING NMR-MOUSE SPECTROSCOPY

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Soluble salts contained within Egyptian limestone objects are a major challenge for the Cultural Heritage field. Fluctuations in humidity during storage can cause these salts to dissolve, migrate, and recrystallize leading to delamination, flaking, and general loss of structural stability of the object. While full submersion into water has been used as a successful treatment approach, especially fragile objects require a gentler method, such as use of a poultice or gel to draw out the salts. This project monitors and evaluates the efficacy of a 3% agarose hydrogel treatment for desalination using a Profiler NMR-MOUSE spectrometer. This portable, non-invasive analytical technique affords in-situ depth profile measurements of the stone and hydrogel throughout treatment to observe the egress of salt water from stone to gel and T_2 (spin-spin) relaxation experiments to track changes in the salinity in the stone over the course of the treatment. Preliminary data shows a decrease in T_2* decay time of water in the stone over 5 days, indicative of a lower concentration of salt after treatment, suggesting the time needed for the agarose hydrogel to desalinate the stone. The use of two different organic polymer consolidants, B-72 and Tetraethyl orthosilicate (TEOS), and their effect on the desalination process were also investigated. In addition, ICP-MS, SEM-EDX, and a series of microchemical tests were employed to analyze the salt composition of powder which had delaminated from three Egyptian limestone objects found in the Walters Art Museum's collection. Quantitative evidence of Na^+, K^+, and Mg^{2+}

cations were found in each sample in addition to the likely presence of phosphates, sulfates, and chlorides. This project advanced knowledge of the use of agarose hydrogels in the desalination of fragile objects and shows the utility of interdisciplinary collaboration in the Cultural Heritage field.

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D

The Impact of Nitrates and Phosphates on the Surface of Calcite: A First-Principles Analysis of Calcium Carbonate

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Art provides us with historical insight into the cultures of those who came before us. Art is intrinsic to human history and as time passes, natural materials tend to degrade. In order to retain that history, the field of art conservation science investigates the preservation of artwork and objects important to cultural heritage through nondestructive methods designed to clean, preserve, and occasionally repair these objects. Currently, the presence of salts has contributed to the degradation of limestone statues. Salts in solution can permeate stone statues and recrystallize, causing structural instabilities which can lead to cracks and crumbling of the limestone over time. The mineral calcite is a major component of limestone, and here we use computational chemistry, more specifically density functional theory, to create atomistic models of different salt adsorbates on two different calcite surface terminations. Specifically, we are looking at interactions between nitrate and phosphate salts on a calcium terminated calcite surface and a proton terminated surface to determine how salt adsorbates behave across different chemical environments. Overall, our evidence suggests that phosphate salts adhere more strongly to calcite surfaces than nitrate salts and that both types of salt interact more weakly with proton terminated surfaces than with metal terminated surfaces.

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PROTEIN OPTIMIZATION OF HIV-1 MYRISTOYLATED MATRIX FOR FUTURE MEMBRANE BINDING STUDIES

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Human Immunodeficiency Virus (HIV) is a retrovirus. Like all retroviruses, it encodes for a Gag polyprotein that helps direct the assembly of the virus particles in the host cells. The beginning of this Gag polyprotein house the Matrix protein which has an N terminal myristoyl group which is instrumental in anchoring it and the entire Gag complex to the plasma membrane which is the beginning of the assembly process that also directs envelope glycoproteins to these viral assembly sites. We are looking at the protein optimization of the HIV myristoylated Matrix protein to do assembly experiments using a nanodisc model to mimic the plasma membrane. Our vector exists in the pET Duet plasmid which allows expression of both the HIVMA protein and the codon optimized N-myristoyltransferase enzyme (NMT). This is a co- translational process that is mediated by the first six amino acids at the N-terminal of the protein referred to as the myristoyl signal (MGARAS). The myristoyl group attachment consists of a 14 Carbon Fatty acid chain that gets anchored in the hydrophobic layer of the membrane. During transport, this group is sequestered in the protein folded structure. Once in contact with the membrane, this group pops out to anchor it to the plasma membrane. This process is referred to as the myristoyl switch. Some of the challenges faced in purifying the myristoylated matrix are due to the protein being extremely pH dependent. At lower pH's, the myristoyl group is exposed and aggregates to be precipitated out in solution. To optimize protein purification, we use different buffer conditions with a range of pHs. Our findings indicate that the myristoylated Matrix is sequestered at a pH of 7, allowing us to further optimize the expression and purification of this protein.

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THE EFFECTS OF LIFELONG NICOTINE CONSUMPTION ON GROWTH AND REPRODUCTION IN *CAENORHABDITIS ELEGANT*

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Nicotine and cigarette usage in the household affects children in many ways. The contact with nicotine products during childhood has been linked to stunted growth and issues in development of

proper reproductive health. Usage of nicotine also directly affects many hormones in the body, reducing fertility and ability for females to conceive. Usage of tobacco products are at an all time high in minors with e-cigarettes and vapes being specifically targeted to them, and reported as the highest used product by the youth since 2014. In order to test observed stunting and decrease in fertility of those consuming nicotine, the model organism *Caenorhabditis elegans* was used. This nematode has remarkably similar genomic parallels to humans, including their nicotine attraction and addiction. C. *elegans* have an extremely fast life cycle and contain two sexes, male and the self replicating hermaphrodites which represent 99.99% of the population. Two different concentrations of nicotine were tested, 0.04mM and 0.2mM, to gauge whether the level of consumption will also determine stunting and fertility. Wild type C. *elegans* were synchronized to the embryo stage and transferred to lifelong exposure plates +/- various nicotine concentrations. A microscope digital camera and ImageJ were used to record and measure their growth, respectively, from 24-96h after synchronization. Experiments confirmed stunted growth in the nicotine exposed worms and this difference gets more pronounced between the L3 and adult stages of development. Brood size for each nicotine concentration was also recorded, and decreased egg laying in those exposed to nicotine was observed. Our data indicates that a higher concentration of nicotine in lifelong exposure generates a higher impact in growth and reproduction, showing a concentration-dependent effect.

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E

EFFICACY OF PHAGE ENZYME TOOLS WHEN DETERMINING PHAGE CLUSTERS

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Bacteriophages are a type of virus that infects bacteria. Bacteriophage genomes are very diverse. Genetically similar phages are grouped in clusters, with more similar phages grouped into subclusters. Bacteriophage clusters and subclusters are identified through sequencing. But with a restriction enzyme digest the cluster or subcluster can be predicted with a program, Phage Enzyme Tools (PET 2.0). Is PET 2.0 effective with its predictions? We investigated the accuracy of PET 2.0 cluster predictions with data from restriction digests. PET 2.0 is a tool used to aid in the identification of bacteriophage clusters and subclusters, specifically ones we had identification on but wanted to see how PET would identify it. The program works by comparing the results from completed digestion patterns of an unknown phage to simulated digests produced from a database of sequenced phages. We have looked at twelve previously sequenced bacteriophages and ran them through two methods in hopes of finding out how effective one is based on the other. Out of the twelve bacteriophages we chose, none of the sequenced clusters and subclusters matched the predicted clusters and subclusters of PET 2.0. This suggests that PET 2.0 should only be viewed as a prediction and further analysis can be done to verify the cluster or subcluster of the phage.

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EXAMINING LEARNED ASSOCIATIONS BETWEEN CONTEXTUAL CUES AND STRESS-INDUCING EXPERIENCES

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Our response to stressful situations is essential to our survival. The ability to associate stress-inducing stimuli with surrounding contextual information allows organisms to make better decisions in the future that keeps them out of harm's way. However, it remains unclear how the brain brings this information together to properly guide behavior. To gain insight into this process, we used a behavioral paradigm where mice learn to associate contextual cues with aversive stimuli (conditioned place aversion (CPA)). Since this paradigm is typically used to evaluate pharmacological compounds, we first sought to determine whether the same effect could be elicited with a stress-inducing aversive stimulus. Using physical restraint as the aversive stimulus, we conditioned the mice using an arena in which two chambers, connected by a small corridor, can be distinguished by contextual cues. Comparing time spent in the chambers before and after conditioning, we initially found that restraint induced CPA. However, repeating this experiment in a separate group of mice failed to reproduce this result. We will be repeating these experiments using foot shock as the aversive stimulus to determine whether it is more effective at inducing CPA. To determine what brain regions may be responsible for mediating this behavior, we measured cFos expression in mice that were restrained in the CPA chamber. Mice restrained in their home cage as well as those with free access to their cage or the CPA arena served as controls. cFos is an immediate early gene where expression can serve as a proxy for brain activity, allowing us to determine the brain regions that are specifically activated during restraint context pairing. We focused on quantifying cells in the hippocampus, nucleus accumbens, and amygdala due to their prominent roles in contextual learning and memory, motivated behaviors, and fear. Our findings will be important in understanding the neurobiological basis of stress and aversion with implications for how we understand stress-related neuropsychiatric disorders.

Support for this research was provided by a grant to UMBC from the Howard Hughes Medical Institute through the Driving Change Initiative, the EDUCATE Program at UMBC through the National Institute on Drug Abuse (NIDA/NIH) under award R25 DA 051338, and funding from the UMBC Startup Package.

EXPRESSION TESTING OF FEOD, A NOVEL SINGLE-PASS TRANSMEMBRANE PROTEIN OF THE FEO SYSTEM

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The ferrous iron transport (Feo) system is the most prevalent ferrous iron (Fe^{2+}) importer found in the bacterial domain. The canonical Feo system found in the model organism *Escherichia coli* is tripartite and comprises two cytosolic proteins (FeoA and FeoC) as well as a polytopic, multi-pass

transmembrane protein (FeoB). However, in many bacteria, FeoC is not present, ostensibly suggesting its lack of functional conservation. Recently, the our lab has uncovered genomic data fin several bacterial *feo* operons suggesting the presence of a new predicted single-pass transmembrane protein, which we have termed "FeoD". The predicted amino acid sequence reveals the presence of several Cys residues, including a CxxC motif that commonly binds [Fe-S] clusters. As [Fe-S] cluster are also present in a number of FeoC proteins, and genomic data suggest that FeoC and FeoD are mutually exclusive, we propose that these two distinct proteins may have analogous functions. However, the biophysical characterization of FeoD is unrealized. To begin, we cloned the *feoD* genes from a number of pathogenic and commensal bacterial organisms and inserted these genes into commonly-used plasmids for recombinant protein expression. Before being able to analyze the structure and function of this FeoD, we undertook extensive expression testing to be able to determine the optimal conditions for overproduction of FeoD. The work presented here shows that expression of a maltose-binding protein (MBP) fusion to the single-pass *Streptococcus thermophilus* FeoD results in good accumulation of this fusion construct under certain conditions. These results provide a promising starting point for the future characterization of this small, novel membrane protein.

This research is funded by the Arnold & Mabel Beckman Foundation through the Beckman Scholars program at UMBC

EXAMINING THE EFFECT OF LOCATION ON PHAGES' BACTERIAL HOST PREFERENCE

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Bacteriophages, also known as phages, are viruses that infect bacterial hosts. Phages make up the majority of the organisms within the biosphere. They reproduce using a bacterial host's cellular machinery and are specific for certain hosts. Scientists are studying the use of phages to discover a variety of therapeutic treatments for pathogenic bacterial infections. We are determining if *Streptomyces* phages from the same ten-mile radius have similar host ranges.We hypothesize that phages isolated from the same region will infect the same number of hosts. Using archived phage data from the UMBC phage hunters spanning from the years 2019-2022, we were able to gauge how the numerous phages infected four strains of bacteria, *S. diastatochromogenes, S. griseus, S. mirabilis,* and *S. scabiei*. The phages were organized in 10-mile increments from the center of Baltimore ranging up to 40 miles. The phages were then categorized by how many bacterial strains they infected (n = 0-4). We found that the phages were not evenly distributed in their respective regions, as the majority of phages were collected in the 0-10 mile radius from Baltimore. We also found that phages from each region infected a different average number of bacteria hosts. This data suggests that phages in certain locations possess similar characteristics influencing their bacterial host preference. This is significant to phage therapy research as it is important to use similar phages to ensure that your results are repeatable, which is hard to achieve due to the vast amount of phages in the world. With further research, we can potentially infer that phages from similar areas have similar characteristics.

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.

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NICOTINE-INDUCED ASSOCIATIVE LEARNING IN *CAENORHABDITIS ELEGANS*

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Children who observe parents smoking are more likely to smoke when they are older due to associative learning. Associative learning is when two unrelated elements (sounds, smells, objects, emotions, etc.) become connected in the brain through conditioning. These associations can result in learned behaviors. Smoking can be a learned behavior and creates positive reinforcement, which induces a perpetuating cycle. Smoking before/during/after meals may encourage learned behaviors through association. Nicotine, the main addictive chemical in tobacco products, is an alkaloid that occurs naturally in some plants in low quantities. Nicotine can modulate associative learning in the wormlike nematode *Caenorhabditis elegans* a small soil-dwelling nematode that has similar neurological pathways implicated in associative learning compared to mammals. In this study, the associative relationship between food and nicotine is investigated. A chronic exposure assay was conducted using concentrations of 0.01mM and 0.1mM. An acute exposure tolerance assay was performed for nicotine concentrations between 100-1000mM. Concentrations of 250mM and 500mM were selected as effective concentrations and are used in pre-exposure to facilitate associative learning. A chemotaxis assay was used to measure the propensity of the non- or pre-exposed *C.elegans* to move toward *Escherichia coli*. Our preference indexes indicated that *C. elegans* had the same propensity to move toward their food after acute and chronic pre-exposure to nicotine compared to the control. Nicotine's appetitive suppressive effects were not observed in higher concentrations indicating a learned association or adaptation. Future studies could investigate metabolized nicotine levels and the genomic and neurological events that trigger learned behaviors from nicotine exposure in *C.elegans*.

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F

DECODING HAND MOVEMENTS FROM ELECTROMYOGRAPHIC SIGNALS TOWARDS A NEAR-NATURAL PROSTHESIS

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Stroke, Injuries, diabetes, cardiovascular diseases and amniotic band syndrome are a few unfortunate situations that have caused approximately 50 million people in the world to have a limb amputated currently. Over the years, new technological advancements have allowed missing limbs to be replaced by mechanical prosthetic limbs that act as assistive devices, but do not offer the full range of motion and sophistication to make one's day-to-day life natural. The aim of the Vinjamuri Lab is to study Brain-Machine Interfaces (BMIs) that can be used for upper limb prosthetics. The specific aim of this project is to create a computational neuroscience model using machine learning that can synthesize electromyography (EMG) signals from forearm muscle groups, and predict diverse hand movements based on EMG. This model is an algorithm based on classification, meaning that it reads muscle data that relates to a specific hand gesture or "class," and the numerical data for these classes are what the predictions are based on. The Classification Learner application within MATLAB was used to train a model that can effectively differentiate EMG signals from the fist hand gesture or a flat hand gesture. To test this model, the Hiwonder Robotic Hand was coded using the Arduino Support Package feature in MATLAB, to actuate the fingers to a predicted position based on the classification model. The accuracy of the model currently is 100% effective at differentiating between the fist and flat hand positions in real-time, which validates the coded model. Future aims are to apply this model to a more complex hand to create a more efficient myoelectric prosthetic.

This research was supported by the National Science Foundation (CAREER Award HCC-2053498), the Meyerhoff Scholars Program at UMBC, and the Howard Hughes Medical Institute.

CHARACTERIZING THE RELATIONSHIP BETWEEN THE CONSERVATION OF MINOR TAIL PROTEINS AND HOST RANGE IN *STREPTOMYCES* BACTERIOPHAGES

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Previously sequenced genomes of *Streptomyces* bacteriophages demonstrate that there are many unknown variables that affect the host range of an individual phage. There are multiple proteins, including the minor tail protein (MTP), that a bacteriophage uses to identify hosts it is able to infect. The purpose of this research was to characterize the relationship between bacteriophages that share related minor tail proteins and their respective host ranges. We used data previously collected by UMBC Phage Hunters to identify and compare MTP amino acid sequences of phages through phamerator. A group of three similar MTPs that repeat throughout the cluster were isolated based on this data and used to create a phylogenetic tree that compares divergence between the MTPs between phages. This data was compared to both a phylogenetic tree of whole genomes from the same phages and their host ranges. Host range was evaluated based on any infection of the host bacteria. When MTPs from these three families were found, the bacteriophage was also able to infect a minimum of two bacterial strains. Based on this data, we have determined that the minor tail protein may serve a role in determining host range, but other factors are also important. This approach shows that it is more likely that phages develop specialization for fewer bacterial strains over time. Developing broader recognition for multiple

bacterial strains seems unlikely because there are clumps of phages that infect multiple with one branch that infects less. The simplest assumption based on the data is that phages that infect fewer types of bacteria develop this trait individually and show less similarity to other host specific phages. This research could inform individualized studies of phages for future use in phage therapy and support the need for future collection of bacteriophage host range data.

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G

CHARACTERIZING THE DIMERIZATION INTERFACE OF LABILE DIMERS

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Like nearly all retroviruses, Human Immunodeficiency Virus (HIV) requires dimerization of its genomic RNA, a pivotal step for packaging, reverse transcription, and other cellular processes. Dimerization is initialized by a region of psuedopalindromic sequence in HIV's 5' genomic RNA in the 5' untranslated region called the Dimerization Initiation Sequence (DIS). While the precise mechanism of dimerization is not fully known, the current established model suggests a two-step process involving the formation of a kissing dimer which is formed by the loop-loop interaction of two DIS regions, followed by an extended dimer, formed by the conversion of intramolecular stems into intermolecular helices. Different strains of HIV-1 have been studied inorder to ensure the conservation of this proposed dimerization mechanism. Notably, diverse strains of HIV-1 have been found to show distinct liabilities, which corresponds to their kinetics under gel electrophoresis. Our electrophoretic dimerization assays reveal that MAL is labile, as it falls apart on a gel while Nl43 is non labile as it runs as a dimer. We hypothesize that this difference in kinetics is due to MAL forming a kissing dimer compared to NL43's extended dimer. Previous investigations using Nuclear Magnetic Resonance (NMR) spectroscopy have confirmed that NL43 adopts an extended dimer conformation. In contrast, there are no solved structures for large labile dimers. Building on this, we aim to employ smaller fragments of labile dimers to comprehensively characterize the dimerization interface of the 5' leader of labile dimers. Success in this endeavor will allow us to characterize the conserved interface of different labile dimers, and even the dimerization interface of other labile retroviruses.

This research was funded by the NIAID U54150470 grant and the Howard Hughes Medical Institute at UMBC

EXAMINING THE EFFICIENCY AND CAPACITY FOR EFFECTIVE NANOCAPSULE SYNTHESIS

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In drug delivery, one of the main goals is to achieve high efficacy and limit or eliminate undesired side effects. Nanocapsules, a type of nanoparticle consisting of a core that can enclose drugs, may serve to meet these needs with their various properties that allow such control in drug delivery. Acriflavine, a topical antiseptic and antibacterial agent, is one drug that benefits from being encapsulated as it allows for extended release when compared to free acriflavine which is physically too small to act long term within the body. An analysis of drug loading, release, and accumulation was performed with acriflavine. Its uptake into polyurethane nanocapsules was recorded and then characterized to determine the average size of nanocapsules within the batch and its reproducibility. Polyurethane nanocapsules were utilized as it was previously found to be advantageous to poly(lactic-co-glycolic acid) (PLGA) based nanocapsules for its comparative lack of complement activation, better degradability and on-demand delivery potential. Ultimately, the objective is to test nanocapsule synthesis efficiency while ensuring stability and a high yield of the nanocapsules with the encapsulated drug. This serves as a preliminary step to in vivo or in vitro models that intend to utilize encapsulated drugs.

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EXAMINING THE EFFECT OF GENETIC COMPENSATION IN THE *CHLAMYDOMONAS* TAG PATHWAY

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Understanding the relationship between the environment and algae creates the possibility of a sustainable and cheaper energy source. Under environmental stress, algae produce the lipid triacylglycerol (TAG) which is a source of energy and protection against the build up of toxic chemicals. This lipid is of interest due to its easy conversion into biofuel. Previous studies showed that, surprisingly, when some TAG genes were knocked out, other TAG-related genes became highly expressed and the amount of TAG produced remained the same or increased. The goal of this study is to see if genetic compensation occurs in the TAG pathway when 2 TAG mutations are present. This will be done by analyzing the double mutant *dgtt1 pdat1* in *Chlamydomonas reinhardtii*. The genes *PDAT1* and *DGTT1* are responsible for the majority of TAG production. These genes work in 2 separate pathways: acyl CoA independent (*PDAT1)* and acyl CoA dependent (*DGTT1)*. To examine expression of TAG genes related to *dgtt1* and *pdat1* in the double mutant, *C.reinhardtii* was cultivated in a phosphorus-deficient medium to induce TAG gene expression. Then we measured gene expression of TAG-related genes *DGTT2*, *DGTT3*, and *PDG1* using RT qPCR. Data coming from this study will determine if genetic compensation occurs in the TAG pathway and how it would affect TAG production in the double mutant. Studying how TAG-related genes are expressed when homologs are defective should shine light on algal TAG regulation that can be used to improve biofuel production.

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EXAMINING THE EFFECT OF LOCATION ON PHAGES' BACTERIAL HOST PREFERENCE

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Bacteriophages, also known as phages, are viruses that infect bacterial hosts. Phages make up the majority of the organisms within the biosphere. They reproduce using a bacterial host's cellular machinery and are specific for certain hosts. Scientists are studying the use of phages to discover a variety of therapeutic treatments for pathogenic bacterial infections. We are determining if *Streptomyces* phages from the same ten-mile radius have similar host ranges.We hypothesize that phages isolated from the same region will infect the same number of hosts. Using archived phage data from the UMBC phage hunters spanning from the years 2019-2022, we were able to gauge how the numerous phages infected four strains of bacteria, *S. diastatochromogenes, S. griseus, S. mirabilis,* and *S. scabiei*. The phages were organized in 10-mile increments from the center of Baltimore ranging up to 40 miles. The phages were then categorized by how many bacterial strains they infected (n = 0-4). We found that the phages were not evenly distributed in their respective regions, as the majority of phages were collected in the 0-10 mile radius from Baltimore. We also found that phages from each region infected a different average number of bacteria hosts. This data suggests that phages in certain locations possess similar characteristics influencing their bacterial host preference. This is significant to phage therapy research as it is important to use similar phages to ensure that your results are repeatable, which is hard to achieve due to the vast amount of phages in the world. With further research, we can potentially infer that phages from similar areas have similar characteristics.

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BIOPHYSICAL CHARACTERIZATION OF BQSR, THE RESPONSE REGULATOR OF PSEUDOMONAS AERUGINOSA'S TWO-COMPONENT SYSTEM, BQSR/S

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Pseudomonas aeruginosa (*Pa*) is a ubiquitous and opportunistic Gram-negative bacterium most renowned for infecting late-stage Cystic Fibrosis (CF) patients. It can grow either as planktonic or as biofilm, complex microbial structures capable of providing an advantageous protective quality that causes bacteria living within a biofilm to be highly resistant to antimicrobial therapies. Studies have unearthed a novel two-component signal transduction system (BqsR/S) that regulates biofilm formation/decay in *P. aeruginosa* through extracellular Fe^{2+}, which is present throughout each stage of infection in CF sputum and constitutes a large portion of the iron pool present in advanced stages of lung function failure. Despite their importance, neither of these proteins have been structurally characterized, and the details of how and to what extent these proteins interact with Fe^{2+} remains unsolved. *Pa*BqsR has been identified as a cytosolic response regulator that binds to DNA and is capable of altering transcription.

To explore the structural and biophysical properties of *Pa*BqsR, *Pa*BqsR has partially been characterized via NMR structural techniques, and the structure of the N-terminal domain of *Pa*BqsR has been solved via X-ray crystallography. Additionally, generating a homology model using

AlphaFold identifies two Lewis-basic regions that may hold an affinity for Lewis acids such as Fe^{2+}, Mn^{2+}, Co^{2+}, or Zn^{2+}. To determine the metal-binding capabilities *Pa*BqsR to these metals, *in vitro* metal-loading experiments have been performed. In the future, the stoichiometry of metal-bound *Pa*BqsR using ICP-MS will be explored as well as attempts to crystallize the metal-replete *Pa*BqsR. Furthermore, because *Pa*BqsR binds to DNA, unearthing the stoichiometry and thermodynamics of DNA binding by conducting electrophoretic mobility shift assays (EMSA) and isothermal titration calorimetry (ITC) is of interest. Ultimately, this work will reveal essential properties of *Pa*BqsR that could serve as a foundation for potential novel antibiotics to target biofilms of antibiotic-resistant pathogens.

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SYNTHESIS OF AMINE TERMINATED MXENE THIN FILM VIA AN EPICHLOROHYDRIN CROSSLINKING TO A GLASS SUPPORT

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MXenes are a newly emerging family of 2D nanomaterials that is growing at a rapid pace. They are hydrophilic, conductive, thermally stable, and biocompatible. These physiochemical properties make them effective when used in a variety of applications, such as energy storage, catalysis, and biosensing. MXenes physiochemical properties can be altered though surface modifications to tune their chemical and functional properties. This study aims to prepare an amine modified Ti3C2 MXene thin film on a glass support. We are studying the impact of amine charge density of amine-modified MXene films on the antimicrobial properties of MXene films. We are also testing the membrane disruption properties of amine-modified MXene films using phospholipid vesicles (liposomes) as a model system.

Support for this research was provided by the Meyerhoff Scholars Program.

H

EFFECTS OF CELL-BASED PROTEIN INTERACTIONS ON PARTICULATE MATTER TOXICITY

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Particulate matter (PM) are liquid or solid microscopic particles suspended in the air. PM forms as a result of natural occurrences, such as the wildfires of western Canada this summer, and anthropogenic sources such as industrial activity and diesel use. Fine particulate matter or PM 2.5, defined as particles having a diameter $\leq$ 2.5 µm, has been associated with various health effects and has been reported to have caused 4.2 million premature deaths in 2019 according to the WHO. However, little is known about the mechanisms through which PM is harmful to human

health. Oxidative stress is considered one of the mechanisms of toxicity and occurs when the amount of reactive oxygen species (ROS) in the body exceeds the amount of antioxidants, causing damage to DNA, lipids, proteins, cells, and tissues. Oxidative Potential (OP), defined as the capability of particles to generate ROS, is considered a method to measure the potential of a particle to cause oxidative stress in the body. Though Oxidative Potential is commonly used as a standalone method of estimating oxidative stress, it fails to consider the role of direct protein interactions and therefore may not be an accurate measure of toxicity. In this study, we directly measured the effects of PM on key proteins as well as the effect of proteins on oxidative potential in acellular and cellular in vitro activity assays. Our results suggest that protein interactions with PM in cells may result in reactions of greater complexity that need to be accounted for when quantifying oxidative potential and PM toxicity. Further research needs to be done to elucidate these mechanisms.

Support for this research was provided by the National Science Foundation (2050728).

EFFECTS OF LISINOPRIL ON THE MOTOR NETWORK OF AGING DROSOPHILA WITH THE ABSENCE OF APP-LIKE PROTEIN

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Alzheimer's disease (AD) neuropathology is shown to be caused by the cleavage of the amyloid precursor protein (APP) at the β and sites, leading to the overproduction of $A\beta_{42}$ peptides in neuronal tissues and the formation of neuritic plaques. These aggregates result in observable cognitive and motor decline due to neurodegeneration. Using *Drosophila melanogaster* as a model for studying AD has become common practice due to the presence of an APP homolog, APP-Like (APPL), showing high levels of conservation at the structural and functional levels. The human angiotensin-converting enzyme (ACE) is closely associated with high blood pressure or hypertension and physical decline in older adults. ACE inhibitors (ACEi), like Lisinopril, are prescribed for hypertension. While medications like Lisinopril have been shown to mitigate the symptoms of cognitive and motor decline, there is a disparity in their effectiveness. In this study, we explored the beneficial effects of Lisinopril on the motor functions of flies mutant for *appl*. We conducted climbing and flight performance assays to measure the speed, endurance, and reaction time of the flies. We also used a wild-type genotype (w^{1118}) as a control to compare our results. The flies were tested at 2, 10, and 30 days old. Our results indicate that *appl*-mutant flies had poor performance in comparison to the control flies. In comparison to the *appl*-mutant flies with no medication, those treated with Lisinopril show better performance overall. These results suggest there is great potential for ACEi to counter neurodegenerative symptoms related to *appl*-mutant flies and AD.

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CORRELATING GENOMIC MINOR TAIL PROTEIN CONTENT ON HOST RANGE EFFICIENCY IN *STREPTOMYCES* PHAGES

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Bacteriophages, or phages, are viruses that infect bacteria, needing a host bacterium to reproduce and grow. Phages are currently studied as potential treatments for bacterial infections. Through genetic engineering, scientists can produce phages with desirable genes that are valuable in therapeutic applications. A bacteriophage's host range is the scope of bacteria a phage can infect; the minor tail protein (MTP) is an integral part of its infection process and is coded in the phage's genome. This study aimed to find a correlation between the amount of genes coding MTPs in a *Streptomyces* phage's genome and its relation to host range efficiency. We hypothesized that the higher the proportion of the genome encoding MTPs, the more hosts it can successfully infect. To determine host range efficiency, phages were exposed to different bacteria to test for successful infections. The number of successful host infections indicated a higher host range efficiency. A genome mapping program was used to observe the MTP content in each phage, and host range data was referenced from data previously collected by UMBC students. No significant correlation was found when comparing the percentage of genes encoding MTPs in a phage's genome and the number of infected hosts; this indicates no significant correlation between a phage's genomic MTP proportion and its ability to infect hosts. Using the insight gained from this study, further research can be done to study the correlation between tape measure proteins and host range efficiency. It would be beneficial to sequence more phages and complete more host range efficiency assays for a larger data set and more confident conclusions in the future.

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EXPLORING THE FATE OF RNA IN MOLONEY MURINE LEUKEMIA VIRUS

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The moloney murine leukemia virus (MoMuLv), a virus that causes leukemia and neurological diseases within rodentia, has been studied since the 1950s to act as a model to further understand the underlying mechanisms of all retroviruses due to its easy use. Our laboratory mainly focuses on the human immunodeficiency virus type-1 (HIV-1), most particularly the segment of the HIV-1 RNA genome important for viral replication, known as the 5'-Leader (5'L). The 5'L exists in two conformations: the dimeric conformation adapted by 5'-capped RNAs beginning with one guanosine (Cap1G) in which the cap is sequestered, and the monomeric conformation adapted by 5'-capped RNAs beginning with two or three guanosines (Cap2G and Cap3G respectively) where our cap is exposed. We refer to viruses containing these different beginning sites as having transcriptional start site heterogeneity. Inversely, MoMuLv contains a unique transcription start site, meaning the virus consists of only one start site, Cap1G. It has been shown that the 5'L can still adopt a dimeric or monomeric form. In this work, we aim to explore what drives RNA packaging versus translation in a retrovirus that contains only unique start sites. We suspect that MoMuLv's genome fate is driven by dimerization dependent cap sequestration, and hypothesize that dimerization is catalyzed by the nucleocapsid (NC) domain of the retroviral Gag polyprotein. We plan to explore the behavior of MoMuLv's genome in vitro for both monomeric

and dimeric RNA, by focusing on cap sequestration and exposure. Through electrophoretic mobility shift assays (EMSA), we can assess whether the cap is sequestered or exposed, which we will further confirm using nuclear magnetic resonance (NMR). In HIV-1, we know that dimerization is driven by transcriptional start site heterogeneity, but in MLV we will explore if dimerization is NC-dependent, which we will later practice in vivo. Our work will provide more information on the mechanisms of retroviruses with unique start sites, and hopefully allow answers on how to stop replication of all retroviruses.

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INVESTIGATING HYDROGEL DESALINATION OF EGYPTIAN LIMESTONE OBJECTS USING NMR-MOUSE SPECTROSCOPY

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Soluble salts contained within Egyptian limestone objects are a major challenge for the Cultural Heritage field. Fluctuations in humidity during storage can cause these salts to dissolve, migrate, and recrystallize leading to delamination, flaking, and general loss of structural stability of the object. While full submersion into water has been used as a successful treatment approach, especially fragile objects require a gentler method, such as use of a poultice or gel to draw out the salts. This project monitors and evaluates the efficacy of a 3% agarose hydrogel treatment for desalination using a Profiler NMR-MOUSE spectrometer. This portable, non-invasive analytical technique affords in-situ depth profile measurements of the stone and hydrogel throughout treatment to observe the egress of salt water from stone to gel and T_2 (spin-spin) relaxation experiments to track changes in the salinity in the stone over the course of the treatment. Preliminary data shows a decrease in T_2* decay time of water in the stone over 5 days, indicative of a lower concentration of salt after treatment, suggesting the time needed for the agarose hydrogel to desalinate the stone. The use of two different organic polymer consolidants, B-72 and Tetraethyl orthosilicate (TEOS), and their effect on the desalination process were also investigated. In addition, ICP-MS, SEM-EDX, and a series of microchemical tests were employed to analyze the salt composition of powder which had delaminated from three Egyptian limestone objects found in the Walters Art Museum's collection. Quantitative evidence of Na^+, K^+, and Mg^{2+} cations were found in each sample in addition to the likely presence of phosphates, sulfates, and chlorides. This project advanced knowledge of the use of agarose hydrogels in the desalination of fragile objects and shows the utility of interdisciplinary collaboration in the Cultural Heritage field.

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Gregory Bailey, Senior Objects Conservator, and Katharine Shulman, Graduate Intern from the Walters Art Museum, and thanks to Dr. Cynthia Niedermaier, Molecular Characterization and Analysis Complex Facility Manager at UMBC and Dr. Tagide deCarvalho, Director of the Keith. R. Porter Imaging Facility (KPIF) at UMBC.

CHARACTERIZING THE ROLE OF ZINC FINGER PROTEIN 217 (ZNF217) IN OVARIAN CARCINOGENESIS

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Ovarian Cancer is the fifth leading cause of cancer-associated death in women in the United States. Due to the absence of reliable early diagnostic markers, the majority of patients continue to be diagnosed with metastatic disease. To improve clinical outcomes, we need to address existing knowledge gaps in our understanding of factors that drive ovarian cancer progression and drug resistance. ZNF217 is a transcription factor located at chromosomal region 20q13.2 which is frequently amplified in many human cancers, including ovarian. Consistently, ZNF217 mRNA is overexpressed in epithelial ovarian cancer and is negatively correlated with 5-year survival outcomes. Despite this connection, little is known about the role of ZNF217 in the development of epithelial ovarian cancer. Previous work in the Padmanabhan lab has demonstrated that high levels of ZNF217 are associated with an increase in metastasis and tumor volume in xenograft models of ovarian cancer. To explore whether ZNF217 depletion represents a viable therapeutic strategy, I have cloned ZNF217 shRNA into an inducible lentiviral expression vector. I then sent the DNA construct for sequencing to confirm the shRNA was in the PLKO-TetOn vector. My future work will use this DNA for lentiviral transduction of ovarian cancer cells. ZNF217 knockdown will be induced by doxycycline and confirmed by Western blot. Once confirmed, I will inject $1x10^7$ cells intraperitoneally in 5-week-old immunodeficient mice. Doxycycline will be administered via water bottle after 3 weeks once tumors are established to induce ZNF217 knockdown.

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VISUALIZING SINGLET OXYGEN PRODUCTION OF DIFFERENT MOF CATALYSTS

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Chemical warfare agents (CWAs) are extremely toxic weapons of mass destruction and are synthesized to incapacitate their targets. Among CWAs, sulfur mustard is a notorious nerve gas that is designed to burn skin and induce acute respiratory distress. Metal-organic frameworks (MOFs) are porous crystalline materials that have demonstrated promising results within CWA decontamination. NU-1000, a commonly used MOF containing zirconium nodes and functionalized

tetra-(benzoic acid) pyrene linkers, has been shown to generate singlet oxygen in the presence of UV and blue light, which successfully oxidized sulfur mustard's stimulant 2-chloroethyl ethyl sulfide (2-CEES). Our research aims to quantify singlet oxygen generation from different NU-1000 MOFs using fluorescent singlet oxygen probes, 1,3-diphenylisobenzofuran (DPBF) and 9,10-anthracenediyl-bis (methylene) dimalonic acid (ABDA). Through absorbance and fluorescence spectroscopies, changes in the singlet oxygen probe's properties could be visualized and used to quantify the production of singlet oxygen that is photosensitized by the NU-1000 MOFs. Our research has identified the limitations of these probes for quantifying the photocatalytic production of singlet oxygen from the NU-1000s. DPBF is not photostable but was capable of detecting singlet oxygen with the inclusion of simultaneous control experiments. In the case of ABDA, the four carboxylate groups adsorbed to the MOF, creating false degradation patterns. As the result of this work, esterified ABDA derivatives are proposed as efficient and selective probes of singlet molecular oxygen produced upon irradiation of MOF materials.

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Demonstration of Genetic Compensation in *Volvox Carteri*

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Volvox carteri is a green alga that serves as a model organism for investigating developmental mechanisms and their evolution. It contains 2 cell types (somatic & germ), which are differentiated by the gene *regA*. When *regA* is mutated, all cells become germ cells. *regA*-related genes *rlsA, rlsB,* and *rls*C are also believed to mediate differentiation but their functions are unknown. An *rlsA* mutant is not defective for cell differentiation suggesting that upregulation of related genes might occur to compensate for the loss of *rlsA*. To test this idea, we are using CRISPR to create *rlsB*and *rls*C mutants and possibly double and triple mutants to understand the relationship between *rls* genes and if *Volvox* exhibits genetic compensatory mechanisms. We are introducing Cas9 and single-guide RNA (sgRNA) plasmids via a method of transformation known as particle bombardment. In this method, we precipitate DNA onto gold and launch it at high speeds at *Volvox* early embryos. We aim to bombard using 4 plasmids targeting different regions of the *rlsB* and *rls*C genes. Using antibiotic markers in our plasmids we can find survivors that take up the plasmids, which we then sequence to confirm mutants have been made. As the experiment is ongoing results will be reported at the conference.

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I

RADAR SNOWFALL ESTIMATION IN SOUTHERN NEW ENGLAND

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Meteorologists often quantify snow through its water equivalent. The amount of water within a snowflake can dramatically alter how much snow accumulates in a storm. Wet snow through a Nor'easter and dry snow through a cold frontal passage result in very different accumulation at the same snow intensity. Weather radars measure the return power from falling snowflakes, called reflectivity (Ze), and require a power law relationship to estimate the snow water equivalent rate (SWER). These relationships depend on the size, concentration, fall speed, and mass of the falling snowflakes. This study derives empirical relationships between the measured radar reflectivity and estimated SWER utilizing ground measurements in Southern New England. The field study was conducted under NASA's Global Precipitation Measurement mission ground validation program during the winter of 2021-22. The key objective of this study is to provide the relevant SWER(Ze) relationship to create an accurate ground-based snowfall mapping for evaluating the spaceborne snowfall retrieval algorithms. This study derived and evaluated event-by-event, synoptic, density, and snowflake habit based SWER(Ze) relationships. The synoptic based SWER(Ze) relationships have potential to be used by National Weather Service for estimates of falling snow and related hydrological forecasting.

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J

DETERMINING THE ROLE OF AZIN1 IN PROSTATE CANCER METASTASIS IN A MOUSE MODEL

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Prostate cancer (PCa) is the second leading cause of cancer death in American men. The current treatment paradigm, while effective early on, remains largely ineffective against aggressive PCa. To address the challenges in treating lethal PCa, robust models are critically needed to study the disease initiation, progression, as well as platforms to test novel therapeutics. The gain of the proto-oncogene *MYC* and the loss of the tumor suppressor *PTEN*are highly prevalent in lethal PCa. Combined overexpression of human *MYC* and genetic deletion of *Pten*, specifically in the mouse prostate, promote highly aggressive PCa initiation and progression in the model termed BMPC. However, the machinery engaged during metastasis remains unknown. Recent studies have implicated AZIN1, a critical regulator of the polyamine biosynthesis pathway, in promoting cancer progression. We hypothesize that amplification of AZIN1 in our recently-derived primary BMPC PCa cell lines will enhance their proliferative and metastatic potential both *in vitro* and *in vivo*. To test this, we have developed and introduced a doxycycline-inducible lentiviral *Azin1* overexpression plasmid into our BMPC cell line, and are assessing changes in growth and metastatic potential. To examine the role of AZIN1 *in vivo*, we plan to perform orthotopic injections of the transduced BMPC cell line into immunocompetent, syngeneic mice. We will monitor and compare tumor growth in cohorts of tumor-bearing mice with or without overexpression of *Azin1*, and upon endpoint dissection we will determine frequency and extent of metastasis by anatomic and histologic analyses. Investigating the role of AZIN1 in mouse PCa progression and metastasis will strengthen our understanding of its potential as a therapeutic target.

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INVESTIGATING THE MOLECULAR INTERACTIONS BETWEEN MONOMERIC HIV-1 RNAS AND CAP-DEPENDENT TRANSLATIONAL MACHINERY, EIF4E

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HIV-1, also known as the human immunodeficiency virus type-1, has persisted since the 1980s and affects over 39 million people worldwide. HIV-1 can progress into the autoimmune deficiency syndrome (AIDS) if not treated. Current treatments include a drug cocktail consisting of inhibitors that target multiple steps of the viral replication cycle. However, due to the copious amount of drugs needed to combat the high viral mutation rates and drug resistance, many patients experience numerous painful and disruptive side effects; leading us to find a treatment that targets areas less susceptible to mutations. Our laboratory focuses on investigating a highly conserved segment of the HIV-1 RNA genome known as the *5′*-Leader (*5′*-L) because it is known to control many viral functions such as translation, packaging, assembly, and splicing. The HIV-1 *5′*-L exists in equilibrium between two conformations: a monomer and a dimer, due to transcriptional start site heterogeneity. The monomer begins with two or three guanosines at the *5′*-end and will also have a *5′*-cap - this serves as mRNA that will translate to HIV viral proteins. The dimer is packaged and begins with one guanosine and also has a *5′*-cap that is sequestered. Our group focuses on investigating the interactions of the monomeric *5′*-L with translation machinery such as the protein eIF4E. We designed and purified two *5′*-capped RNA oligos called Cap3G-TAR-F1-C57 and Cap3G-TAR-F1-U64 to determine if structural elements of the RNAs affect eIF4E binding. To study the binding interactions of these RNAs to eIF4E, we conduct electrophoretic mobility shift assays (EMSAs). Qualitatively, the two RNAs bind to eIF4E with similar binding affinities but we need to introduce a quantitative approach to understand how the different structural elements of the two RNAs affect eIF4E recruitment. Next, we used isothermal titration calorimetry (ITC) that measures the changes in thermodynamics parameters as two molecules are binding. Our ITC data reveals that both RNAs bind tightly to eIF4E (nM affinity) and bind tighter than the *5′*-cap alone. However, the Cap3G-TAR-F1-U64 binds slightly weaker than the Cap3G-TAR-F1-C57 RNA oligo, suggesting that the additional residues are inhibiting some of the binding interactions. Our data reveals that structural elements of our RNAs can affect recruitment and binding of eIF4E and we aim to further explore this by mutating segments of our RNA oligos and determine their effects on eIF4E binding.

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NICOTINE-INDUCED ASSOCIATIVE LEARNING IN *CAENORHABDITIS ELEGANS*

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Children who observe parents smoking are more likely to smoke when they are older due to associative learning. Associative learning is when two unrelated elements (sounds, smells, objects, emotions, etc.) become connected in the brain through conditioning. These associations can result in learned behaviors. Smoking can be a learned behavior and creates positive reinforcement, which induces a perpetuating cycle. Smoking before/during/after meals may encourage learned behaviors through association. Nicotine, the main addictive chemical in tobacco products, is an alkaloid that occurs naturally in some plants in low quantities. Nicotine can modulate associative learning in the wormlike nematode C*aenorhabditis elegans* a small soil-dwelling nematode that has similar neurological pathways implicated in associative learning compared to mammals. In this study, the associative relationship between food and nicotine is investigated. A chronic exposure assay was conducted using concentrations of 0.01mM and 0.1mM. An acute exposure tolerance assay was performed for nicotine concentrations between 100-1000mM. Concentrations of 250mM and 500mM were selected as effective concentrations and are used in pre-exposure to facilitate associative learning. A chemotaxis assay was used to measure the propensity of the non- or pre-exposed C.*elegans* to move toward *Escherichia coli*. Our preference indexes indicated that C. *elegans* had the same propensity to move toward their food after acute and chronic pre-exposure to nicotine compared to the control. Nicotine's appetitive suppressive effects were not observed in higher concentrations indicating a learned association or adaptation. Future studies could investigate metabolized nicotine levels and the genomic and neurological events that trigger learned behaviors from nicotine exposure in C.*elegans*.

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K

THE INFLUENCE OF PKA PHOSPHORYLATION ON MELANOPSIN G-PROTEIN SIGNALING

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Melanopsin is a visual pigment found in intrinsically photosensitive retinal ganglion cells (ipRGCs) in the retina. Light stimulation of melanopsin regulates the pupillary light reflex, circadian rhythm, and sleep regulation. Light stimulation of melanopsin in ipRGCs drives calcium influx into these cells, depolarizing the cell and eliciting action potentials. However, when melanopsin is phosphorylated by protein kinase A (PKA), downstream calcium signaling is downregulated. Other GPCRs have shown differential G-protein signaling after PKA phosphorylation, with some having their primary G-protein switched to another family, such as the adrenergic receptor B_2AR switching from $G_s$signaling to G_i. Here we hypothesize that PKA phosphorylation of melanopsin will alter its G-protein signaling in HEK293 cells. To test our hypothesis, we used immunohistochemistry to confirm expression and membrane localization of a melanopsin mutant that cannot be phosphorylated by PKA. Next, we used a BRET based G-protein signaling assay to compare wildtype melanopsin signaling to that of the PKA mutant melanopsin. We expect to

see reduced Gq signaling as a result of phosphorylation by PKA for wildtype melanopsin, but not for the PKA mutant melanopsin. Additionally, we will determine if the PKA mutant melanopsin has altered G-protein signaling compared to wildtype melanopsin in the absence of PKA phosphorylation. Our results show that the mutant melanopsin expresses at similar levels on the membrane of HEK cells. In conclusion, these assays will illuminate forms of regulation that control melanopsin signaling *in vitro* and give clues to how melanopsin signaling is regulated *in vivo*.

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CHARACTERIZING THE MECHANISM OF HIV-1 GENOME DIMERIZATION

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HIV-1 like nearly every retrovirus has a dimeric genome, directly involved reverse transcription, and recombination. Dimerization is mediated within the 5' leader–a highly conserved region of the genome responsible for regulating processes such as packaging, splicing, and translation. Within the 5' leader there exists multiple domains serving different functions, and dimerization is mediated by a hairpin named the DIS, a stem loop that contains a 6-nucleotide palindromic sequence that enables it to dimerize. In cell evidence suggests that multi-step dimerization occurs because as viruses mature the dimer becomes more resistant to denaturation. Current proposals suggest a two-step mechanism where the DIS palindrome leads to a loop-loop kissing dimer before gradually maturing into a duplex structure which possesses increased intermolecular base-pairing. This maturation process would need to overcome a large thermodynamic barrier to occur; however, this mechanism is poorly characterized. In previous literature it was proposed that internal bulges within the DIS stem may destabilize it to allow the transition from a kissing complex to an extended duplex. By using NMR relaxation dispersion, they discovered mutants within the stem that reduces the ability of the RNA to transition from kissing to duplex thus suggesting a possible relationship between the bulges of the stem to the maturation of the RNA. However, their study was conducted on a monomeric 32 nucleotide sequence of the DIS which ignores the context of the full leader which is known to have long range interactions with the DIS. Therefore, to properly understand the regulatory properties of transient states the mutation will be inserted into both MAL and NL43 and run on an agarose native gel in both TB and TBM conditions (either Tris-Borate or Tris-Borate Magnesium condition respectively).

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DIGITAL STORYTELLING: WELL-BEING AND LAO AMERICAN INITIATIVE

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The Lao American community is a vibrant and culturally rich group that has faced significant challenges such as facing high rates of low income (and poverty), maintaining relationships, and connecting to their cultural community in their tumultuous environment. Limited studies have explored the Lao American population. Lao Americans have been largely left out of research studies, educational curriculums, and narratives. There is a lack of awareness and acknowledge of the existence of the Lao-American population, resulting in scarce and inadequate resources for the continually expanding population of Lao-Americans. This project highlights the importance of community-based services such as reusing items in empowering and supporting individuals and communities. The project's aim is to document and share the story of one of my initiatives as a Lao American leader of this secondhand exchange (preowned clothing and item redistribution) in hopes to bridge the cultural gap. This project also explores the potential benefits of digital storytelling to address unique needs and promote the holistic well-being of the Lao American community.

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INVESTIGATING THE RELATIONSHIP BETWEEN SUBCLUSTER AND HOST PREFERENCE IN BACTERIOPHAGES

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Superbugs are strains of bacteria and microorganisms that have adapted to become multidrug resistant. While science is searching for ways to counteract these recurring diseases, we look to phage therapy as a potential solution. Phage therapy is a developing form of treatment where phages are selected to target and kill bacterial infections. Bacteriophages are viruses that infect bacterial hosts. In this study, we compared host range data of myoviruses to determine if they had similar host preference. We analyzed nine bacteriophages characterized through the Phage Hunters program belonging to Cluster C. All nine phages were plated against the four bacterial hosts to determine host range similarities and infectivity. Host range data was plotted on a Venn diagram and cross compared to genetic data from a genomic dot plot and phylogenetic tree. Using a dot plot, we viewed the alignment of genetic sequences between all nine bacteriophages. We created a phylogenetic tree using VICTOR to display lines of evolutionary descent and relatedness between phages regardless of subcluster. Cross analyzing host preference and genetic identity provided us a better understanding of a correlation between the two. After comparing host preference and genetic alignment between phages, we found a relationship between host range and subcluster. Previous studies reinforce this point. However, results from our experiment are not conclusive as extensive research and a larger sample size is required to validate our study. Therefore, we can suggest that a relationship between host range and cluster exists. Bacteriophages are important to medical use as prior studies have shown that when phages of genetic relation are combined into a “phage cocktail", they can effectively suppress and eliminate disease. Further experimentation on this subject is important as use of genetically related phages may strengthen the power of phage therapy.

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THE EFFECTS OF HIGH SUGAR DIETS IN THE BEHAVIOR OF *CAENORHABDITIS ELEGANT*

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With excessive amounts of added sugar in processed foods, heart diseases and obesity rates continue to be the largest health concerns in the United States. Glucose and fructose are some of the most common sugars in processed foods while erythritol is a commonly used sugar alternative. In previous studies, a high sugar diet correlated with preference and slower locomotion. In this study, these three sugars were examined at different concentrations to test their individual effects after lifelong exposure on the behavior of *Caenorhabditis elegans*.These small nematodes are used in a plethora of scientific studies due to their convenience and similar genetic functions shared with humans. It was hypothesized that lifelong exposure to sugar will cause a development in preference to sugar and decrease their general mobility. Wild type C. *elegans* were synchronized to the embryo stage and grown in plates with increasing concentrations of glucose, fructose and erythritol. A chemotaxis assay was performed to measure sugar preference of the nematodes that were lifelong exposed to the sugars. The worms developed in a glucose and erythritol environment showed a higher preference for that particular sugar than the non-exposed worms. However, fructose-exposed worms demonstrated a lower preference to the sugar at lower concentrations. This data suggests that prolonged sugar consumption from the embryonic stages may lead to developed preference to that sugar in adulthood. To measure the change in motility, a thrashing assay was performed. The nematodes exposed to fructose depicted an increase in motility in all tested concentrations. Surprisingly, the erythritol-treated worms showed a decrease in motility with a sudden increase at the highest tested concentration. Our data suggests that the preference of C. *elegans* differ by the source and concentration of sugar. However, there was no correlation observed in the concentration of sugar and their behavior.

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GRAPH NEURAL NETWORKS FOR PREDICTION OF GENE-AUTOIMMUNE DISORDER ASSOCIATIONS

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Autoimmune disorders (ADs), triggered by the body's immune system erroneously attacking healthy cells, present a significant global health burden. Despite the continuous and rapid growth in the number of ADs worldwide, specifically within industrialized societies, the causes of the biological phenomena are relatively unknown. Only a small proportion of the relevant genes have been identified to date, leaving our understanding of the genetic underpinnings of these diseases incomplete. The lack of knowledge severely stalls and hinders the development of treatment options. Traditional methods for gene discovery, like genome-wide association studies (GWAS), demand significant commitments in terms of time, labor, and finance. We propose a novel model to predict gene-autoimmune disease associations with Graph Neural Networks (GNNs). We created a heterogeneous graph structure with a convolutional framework from the non-Euclidean data available from Gene & Autoimmune Disease Association Database (GAAD), Kyoto Encyclopedia of Gene and Genomes (Kegg), and Online Mendelian Inheritance in Man (OMIM). Through this structure, we are able to predict undiscovered gene-autoimmune disease associations with an accuracy of about 80%.

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L

PARAMETER SENSITIVITY, IDENTIFIABILITY, AND ESTIMATION METHODS APPLIED TO IN VIVO HIV

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Mathematical models of biological systems depend on many parameters. Parameter sensitivity, parameter identifiability, and parameter estimation are tools that measure and quantify the role of these parameters in these models. We surveyed the literature for different mathematical and statistical techniques associated with each parameter tool. Parameter sensitivity describes how varying a model's parameters affects the observable outputs. Sensitivity was determined by computing the partial rank correlation coefficients using two different sample methods to thoroughly explore the parameter space: Latin hypercube sampling and Sobol sequences. Parameter identifiability explores whether the model's parameters can be uniquely identified from observable experimental data. Applying a differential algebra approach, we first determine whether a set of parameters are structurally identifiable with respect to sample observable data without noise. If the model was shown to be structurally identifiable, Monte Carlo simulations are applied to determine if the parameters can be estimated through stochastic observable data. Once the model is shown to be identifiable for a given parameter set, parameter estimation methods were applied to determine the numerical value of each parameter. These estimations were computed using simulated annealing and the Nelder-Mead algorithm in conjunction with Sobol sequences. These methods for sensitivity, identifiability, and estimation were tested on a simple example of *in vivo* HIV dynamics focused on the total CD4+ T-cell count and total viral load.

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THE EFFECTS OF HIGH SUGAR DIETS IN THE BEHAVIOR OF *CAENORHABDITIS ELEGANT*

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With excessive amounts of added sugar in processed foods, heart diseases and obesity rates continue to be the largest health concerns in the United States. Glucose and fructose are some of the most common sugars in processed foods while erythritol is a commonly used sugar alternative. In previous studies, a high sugar diet correlated with preference and slower locomotion. In this study, these three sugars were examined at different concentrations to test their individual effects after lifelong exposure on the behavior of *Caenorhabditis elegans*.These small nematodes are used in a plethora of scientific studies due to their convenience and similar genetic functions shared with humans. It was hypothesized that lifelong exposure to sugar will cause a development in preference to sugar and decrease their general mobility. Wild type C. *elegans* were synchronized to the embryo stage and grown in plates with increasing concentrations of glucose, fructose and erythritol. A chemotaxis assay was performed to measure sugar preference of the nematodes that were lifelong exposed to the sugars. The worms developed in a glucose and erythritol environment showed a higher preference for that particular sugar than the non-exposed worms. However, fructose-exposed worms demonstrated a lower preference to the sugar at lower concentrations. This data suggests that prolonged sugar consumption from the embryonic stages may lead to developed preference to that sugar in adulthood. To measure the change in motility, a thrashing assay was performed. The nematodes exposed to fructose depicted an increase in motility in all tested concentrations. Surprisingly, the erythritol-treated worms showed a decrease in motility with a sudden increase at the highest tested concentration. Our data suggests that the preference of C. *elegans* differ by the source and concentration of sugar. However, there was no correlation observed in the concentration of sugar and their behavior.

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COMPREHENSIVE ANALYSIS OF THE *ASPERGILLUS NIDULANS* KINASE DELETION LIBRARY FOR INCREASED SEPTATION UNDER CELL WALL STRESS

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Filamentous fungi are both important human pathogens and are used prevalently in the bioprocess industry to produce valuable products. In both cases, the cell wall plays an important role. For example, in pathogens it can impact virulence and in bioprocessing productivity. To regulate their cell-wall structure, fungi rely on complex signaling pathways, composed of signaling proteins such as kinases. The objective in this study was to investigate the contribution of protein kinases from Aspergillus nidulans in the fungal response to cell-wall stress. By determining which protein kinases (in various signaling pathways) affect cell wall integrity and respond to cell wall stress, we will identify potential targets for new antifungal drugs. Previous research in our lab has shown (i) that cell-wall stress leads to increased levels of septation and (ii) that genetic mutations which reduce septation lead to more susceptible strains. We hypothesize that other, as yet unknown, kinases are involved in wall-stress-induced septation and survival. To test this hypothesis, we screened the A. nidulans kinase deletion library (98 strains), each lacking a specific kinase. We conducted experiments on each of the library strains under two conditions: one group was treated with micafungin, a cell-wall perturbant, at the 12-hour mark, while the other remained undisturbed. After 16 hours, we captured images of the fungi and measured the quantity of septa formed as well as the overall projected area (to measure growth). By assessing the extent of growth and septation, we are able infer the involvement of each kinase in responding to cell-wall stress.

Support for this research was provided by the National Science Foundation, through awards 2050728 and 2006189.

ADDRESSING VIEW INVARIABILITY IN SEASHIP DETECTION WITH A FEDERATED LEARNING MODEL

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Addressing the issue of view invariability in training models for object detection within a federated learning environment poses a formidable challenge. The presence of multiple datasets with diverse vantage points complicates object detection, as the angle of observation significantly impacts the model's ability to identify objects accurately. The existing literature reveals a discrepancy in the granularity of leveling strategies employed for annotated datasets, impeding effective model training with the current datasets. To ensure meaningful training, the adoption of clustering techniques and feature extraction becomes imperative, enabling the model to recognize objects from various perspectives. To overcome this challenge, we propose the implementation of clustering techniques and feature extraction. Our approach involves leveraging ship image datasets, including ABOShips, Seaships by RoboFlow, and the VIS Offshore and VIS Onshore images from the Singapore Maritime Dataset. Clustering will be performed based on the outcomes of a feature extraction algorithm. To facilitate our research, we will utilize the FedML

framework, a platform for Federated Learning, which allows us to simulate a server and multiple clients by connecting multiple edge devices. To address the issue, we are developing a specific server aggregation strategy. We intend to replace the conventional federated averaging model with a tailored aggregation technique. The strategy will be practically deployed, involving real robots such as the Jackal UGV, to test its effectiveness. In summary, our formal plan entails utilizing clustering techniques, feature extraction, and ship image datasets to tackle the challenges of view invariability in object detection training within a federated learning environment. Through the employment of the FedML framework and the development of a specialized server aggregation strategy, we aim to enhance model performance and enable effective deployment in real-world scenarios.

This research was partly supported through a Research Experience for Undergraduates (REU) funded by National Science Foundation grant #2050999 and Army National Lab grant #W911NF2120076.

M

Comparing Similar Integrase Proteins in Different Phages to Evaluate the Presence of Horizontal Gene Transfer

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The integrase protein, an integral part of the temperate life cycle, was investigated for elements of divergent evolution within temperate phages. The integrase protein from *Gordonia* phages ClubL and Oneup (cluster CQ) were phylogenetically examined with 15 actinobacteriophages of various clusters carrying integrases classified into seven different phams and compared to an proteomic tree produced of the same phages. As would be expected, when entire proteomes were examined, the phages assorted by cluster and host infected. When the integrase was investigated phylogenetically, however, evidence of horizontal gene transfer was found in bacteriophages, with phages of different clusters forming different clades in several instances. Two cases of note are pham 98453, which is found in Bantam (cluster DL) as well as phages ClubL and OneUp (CQ1 and CQ2), and pham 96094 is found in phages Lucky10 (DH) and Horus (DN1). The presence of an identical integrase gene in genetically different phages suggests horizontal gene transfer as the mechanism. It appears likely that the gene was picked up by an ancestor of ClubL and OneUp prior to their divergence as the integrases of Bantam and OneUp appear to be more closely related than the integrases of OneUp and ClubL's despite their being in the same cluster.

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THE INVESTIGATION OF THE EFFECTS OF STRESS AND ALCOHOL TOLERANCE IN *CAENORHABDITIS ELEGANT*

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Stress, anything that challenges the body's ability to function in its usual fashion, is a significant cause of decreased lifestyle quality. This can cause migraines, fatigue, anxiety, or depression in adults, leading people to find ways to cope. One common coping mechanism is alcohol consumption which can turn into excessive drinking or alcoholism, a chronic disease that accounts for one in five deaths in adults between 20-49 years old in the United States. National stress levels and alcohol consumption are at an all-time high. To investigate this relationship, a research experiment was conducted using C*aenorhabditis elegans*, a small, cost-effective and maintainable nematode that has many gene counterparts in humans. Wild type worms were introduced to different stress factors being either heat at 30 °C, starvation, or a combination of both and underwent acute or chronic exposure to ethanol. These experiments explore whether stress can affect their response to ethanol and if ethanol consumption has any effect on how the worms react to stress. The worm's tolerance to ethanol was measured by a thrashing assay after acute and chronic exposure to ethanol. It was found that prolonged stress enabled most worms to robustly deal with ethanol compared to their controls. Starving had a higher impact in the increase of tolerance to ethanol in the acute exposure, while the combination of heat and starving displayed the highest increase on the chronic group. Our data indicates that long term stressors could generate a higher tolerance to ethanol which could be related to a future development of alcohol dependence.

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AN APPROACH TO CAMERA-BASED CONTACT-LESS BREATHING RATE MONITORING

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Respiratory rate (RR), measured by breaths per minute, is one of the four human vital signs. It is recommended to check the RR pattern regularly as it provides early signs of various common cardio-vascular diseases across different age groups. To facilitate a ubiquitous contactless RR monitoring system, we propose to use off-the-shelf video cameras to monitor RR instead of using special pressure-based wearables. We aim to capture the breathing-induced body parts (shoulder, abdomen, chest) movement via a regular video camera and design a robust video

processing mechanism to track the spatiotemporal movements to infer breathing rate from video. In developing such a system, we plan to collect a large RR dataset to train and validate contactless RR methods and develop a lightweight robust approach to extract RR from the input video for ubiquitous contactless RR applications. Firstly, we aim to collect quality RR datasets from diverse subjects by considering realistic situations like low RR, high RR, exercise, force RR, natural RR, variance in clothes, lighting conditions, backgrounds, different RR-induced body components, and body posture. In this study, we will make our data open source to validate RR methods and attract wider research. Secondly, we will create a spatiotemporal model to localize the RR-induced body parts and track their subtle temporal movement due to RR to infer the underlying breathing rate. Currently, we are exploring edge detection and edge movement tracking by calculating their volumetric changes and edge-energy shifts, which are more computationally efficient than their data-hungry deep-learning-based video processing counterparts. In the future, we also plan to develop data-efficient deep-learning approaches to learn breathing rates from video automatically.

I would like to thank the NSF REU for funding this research experience.

DYNAMICS OF CHAOS: A COMPARATIVE ANALYSIS OF CHAOTIC BEHAVIOR IN COMPLEX NONLINEAR SYSTEMS

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This abstract provides a comprehensive overview of my research on chaotic systems, explicitly analyzing their chaotic behavior as complex nonlinear dynamical systems. In my research, I thoroughly examined the chaotic behavior of various systems, including the Single pendulum, Double pendulum, Lorenz system and other nonlinear ordinary differential equations (ODEs). By carrying out thorough examination of their trajectories and sensitivity to initial conditions, my goal was to obtain valuable insights and understanding into the enchanting world of chaotic dynamics and its effects in complex nonlinear systems.

The art of modeling chaotic systems consists of identifying regularities in a system and then creating a mathematical process that emulates, to a limited degree, these properties. Although chaotic systems comprise the transition between solvable and near-solvable systems, they are studied using the tools of mathematical analysis. Numerical simulations were conducted using MATLAB and its inbuilt ode45 solver to model these chaotic systems and understand their sensitivity to initial conditions and their butterfly effect. Numerically simulating chaotic systems creates a whole understanding of how these systems are deterministic in nature and how limited predictability in chaotic systems is. For example, in the Lorenz system, I found out that no point in space is ever visited more than once by the same trajectory. If it happens then the trajectory will be predictable. Furthermore, no two trajectories will ever intersect. If it happens, they will merge into the same path giving the same outcome whereas they had different initial conditions. Through mathematical modeling and numerical simulations, a system is characterized as chaotic when it is topologically transitive, sensitive to initial conditions and has dense periodic orbits. In summary, analyzing chaotic systems has provided me with a deeper understanding of complex nonlinear systems that exhibit chaotic behavior. After conducting numerous simulations on several chaotic systems, it is fascinating to observe how they possess deterministic nature yet remain unpredictable, and how chaos can emerge from seemingly simple ordinary differential equations.

I would like to extend my appreciation to Dr Ankit Goel, ECLL research lab, and UMBC Mechanical Engineering Department for their vital support in my research on chaotic systems. Their guidance and resources have been priceless. Gratitude also extends to my peers for their contributions and discussions.

INVESTIGATING THE BINDING INTERACTIONS AND STRUCTURE OF THE HIV-1 REV PROTEIN AND REV RESPONSE ELEMENT

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The human immunodeficiency virus (HIV) requires its full-length or partially spliced viral RNA to be exported from the nucleus to the cytoplasm for translation or packaging into new virions. It is therefore essential for the unspliced viral RNA to exit the nucleus, however, host quality control mechanisms prevent this. Instead HIV regulates the export of its incompletely spliced RNA through production of an accessory protein, Rev, which enters the nucleus and oligomerizes on the Rev response element (RRE), a landmark on these viral RNAs. This complex is then exported via the host Crm-1 pathway. The RRE is a highly conserved region of the viral RNA which contains multiple high affinity binding sites for Rev. The previously characterized Rev binding sites on the RRE include purine rich bulges in stem-1A, stem-2B, and the stem 2 junction site. We aim to characterize the binding interactions between Rev and the RRE, with the ultimate goal of determining the complete structure of the Rev-RRE complex. To have an in-depth understanding of Rev-RRE interactions, we initially used a Rev peptide and a stem-1A RNA oligo, a truncated part of the RRE, then conducted our studies using electrophoretic mobility shift assays (EMSAs). We also created a series of mutants by removing certain features of stem-1, such as its purine rich bulge, to assess their importance for Rev binding. Based on our results, we believe there are multiple Rev binding sites on stem-1 other than the purine rich bulge. Our current and future work includes creating a Rev mutant that prevents aggregation for additional binding studies with the RRE. A thorough understanding of this interaction could pave the way for the development of targeted therapies against HIV.

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COMPREHENSIVE ANALYSIS OF THE *ASPERGILLUS NIDULANS* KINASE DELETION LIBRARY FOR INCREASED SEPTATION UNDER CELL WALL STRESS

Feonil G. Limiac[12]; Raina B. Miller[13]; Rianna S. Minter[14]; Greeshma Tarimala[15]; Joshua K. Dayie[6]; Meredith E. Morse[6]; Alexander G. Doan[6]; Mark R. Marten[6]
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Filamentous fungi are both important human pathogens and are used prevalently in the bioprocess industry to produce valuable products. In both cases, the cell wall plays an important role. For example, in pathogens it can impact virulence and in bioprocessing productivity. To regulate their cell-wall structure, fungi rely on complex signaling pathways, composed of signaling proteins such as kinases. The objective in this study was to investigate the contribution of protein kinases from Aspergillus nidulans in the fungal response to cell-wall stress. By determining which protein kinases (in various signaling pathways) affect cell wall integrity and respond to cell wall stress, we will identify potential targets for new antifungal drugs. Previous research in our lab has shown (i) that cell-wall stress leads to increased levels of septation and (ii) that genetic mutations which reduce septation lead to more susceptible strains. We hypothesize that other, as yet unknown, kinases are involved in wall-stress-induced septation and survival. To test this hypothesis, we screened the A. nidulans kinase deletion library (98 strains), each lacking a specific kinase. We conducted experiments on each of the library strains under two conditions: one group was treated with micafungin, a cell-wall perturbant, at the 12-hour mark, while the other remained undisturbed. After 16 hours, we captured images of the fungi and measured the quantity of septa formed as well as the overall projected area (to measure growth). By assessing the extent of growth and septation, we are able infer the involvement of each kinase in responding to cell-wall stress.

Support for this research was provided by the National Science Foundation, through awards 2050728 and 2006189.

N

UNVEILING THE FASCINATING WORLD OF PENDULUMS: AN ANALYSIS VIA INCORPORATING DESIGN, SIMULATION, AND MODELING

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This abstract provides a brief overview of my research, performing simulations on developed models. Including extensive exploration of pendulum systems undertaken, and focusing on the design, simulation, and analysis using Simscape and Gazebo. This abstract provides a complete and concise showcasing of the application by performing advanced simulation techniques to gain valuable insights into the behavior and characteristics of the diverse pendulum models. In this research, we focus on different types of pendulums, including compound, simple, railing, and double pendulums. These pendulums were designed and modeled in SolidWorks. Subsequently, the SolidWorks models were transferred into Gazebo in the form of URDFs, with extreme attention given to detailing all joints involving revolute, fixed, and prismatic while incorporating both aerodynamic and dynamic features. This includes considering gravity, air friction as well as the height and weight of the model. The dimensions were described using a coordinate system, defining the exact axis of rotation or motion. Gazebo is a simulator that implies a real-world environment and features on the model aiding in a better understanding of the behavior of the motion. Compared to working with Simscape, Gazebo is much different, Gazebo offers a complete environment in which the model can be interacted with other similar models. However,

Simscape also known as Simulink does not imply the environmental features like air friction and pressure of the wind. While in Simscape we can imply the trajectory as well as joint features which help to understand the mechanism of the model. Gazebo as well as Simscape provide us with a thorough graphical reading which helps us understand the motion and the effect of different scenarios acting on that model. The inclusion of limits and restrictions makes the simulation much more in-depth. Restraining a certain angle from which the pendulum experiences a free fall makes it a lot easier to understand the motion of the pendulum. That's why we restrain each model with a given angular limit. In summary, this review underscores the significance of pendulum motion in both theoretical and practical domains, which helps us understand the motion of the Pendulum with the influence of gravitational force on the velocity as well as overall acceleration which eventually make the pendulum come to a complete stop. We also figure out how the time rate frame differs with the shape, size, and weight of the pendulum. The double pendulum helps us study chaos in both experimental and numerical ways. It also helps us demonstrate various studies of mechanisms and restoring energy.

I want to express my sincere gratitude to Dr. Ankit Goel, ECLL research lab, and UMBC Mechanical Engineering Department for their incredible guidance and support. Their commitment throughout the research on pendulum research was impeccable. I sincere gratitude to my peer fellows for their immense help and contribution to the research project.

CORRELATING GENOMIC MINOR TAIL PROTEIN CONTENT ON HOST RANGE EFFICIENCY IN *STREPTOMYCES* PHAGES

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Bacteriophages, or phages, are viruses that infect bacteria, needing a host bacterium to reproduce and grow. Phages are currently studied as potential treatments for bacterial infections. Through genetic engineering, scientists can produce phages with desirable genes that are valuable in therapeutic applications. A bacteriophage's host range is the scope of bacteria a phage can infect; the minor tail protein (MTP) is an integral part of its infection process and is coded in the phage's genome. This study aimed to find a correlation between the amount of genes coding MTPs in a *Streptomyces* phage's genome and its relation to host range efficiency. We hypothesized that the higher the proportion of the genome encoding MTPs, the more hosts it can successfully infect. To determine host range efficiency, phages were exposed to different bacteria to test for successful infections. The number of successful host infections indicated a higher host range efficiency. A genome mapping program was used to observe the MTP content in each phage, and host range data was referenced from data previously collected by UMBC students. No significant correlation was found when comparing the percentage of genes encoding MTPs in a phage's genome and the number of infected hosts; this indicates no significant correlation between a phage's genomic MTP proportion and its ability to infect hosts. Using the insight gained from this study, further research can be done to study the correlation between tape measure proteins and host range efficiency. It would be beneficial to sequence more phages and complete more host range efficiency assays for a larger data set and more confident conclusions in the future.

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Numerical Analysis of a Fully-Developed MHD Free Surface Flow

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This abstract presents the analysis of liquid-metal flow on plasma facing components of future fusion devices, which serve as a protective layer and energy exhaust. Computational fluid dynamics (CFD) methods are utilized to simulate the behavior of electrically conductive liquids in complex geometries and strong magnetic fields. The study compares data obtained from numerical simulations using a customized CFD code, CFX from ANSYS, with an analytical solution developed at Princeton Plasma Physics Laboratory. The CFX code is adapted for magnetohydrodynamic (MHD) problems, incorporating transport equations for magnetic field components and the Poisson equation for electric potential. The simulations closely match the analytical solutions across a range of Hartmann numbers and wall conductance ratios, demonstrating the effectiveness of the implemented approach.

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PERFORMANCE ANALYSIS OF HETEROGENEOUS NETWORKS FOR ROBOTIC NAVIGATION

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During disaster recovery, it is imperative to take the assistance of robots to navigate hostile terrains. Robots can autonomously make application-oriented decisions and send data (such as images) to human personnel for decision-making. Communication in a disaster-struck environment can be challenging with the destruction of communication infrastructure or lack thereof. Establishing satellite-based communication can be a costly affair. The requirement for wireless networks in far-reach areas led to the inception of LoRa (Long-Range) networks, which leverage Chirp Spread Spectrum (CSS) technology for long-range communication over low bandwidth. Thus, devices equipped with LoRa can communicate small chirps of data over a long-range, making them power efficient to sustain their battery life for a longer duration. Per regulations, in the United States LoRa exists on the 902-928Mhz band with power restrictions. LoRaWAN is a WAN protocol built on top of LoRa, which has typically been used to transmit small amounts of data from low-power sensor networks. In this project, we first set up a LoRaWAN network to interface and interact with UAVs and UGVs. We then analyze the performance of LoRaWAN

network on varying workloads and monitor the computation and communication power consumption of a bot while employing the LoRa network. We further explore the possibility of transmitting image data over the LoRaWAN network. We leverage the low bandwidth of LoRaWAN to send feature representatives of the images (rather than sending raw image data) that can be processed at an edge node for object classification applications. To lay down a path for decision-making (selecting the best possible network) in a heterogeneous network environment, we compare sending images and feature representatives of the raw images over WiFi via MQTT (as proposed by previous works) and LoRaWAN. We analyze the performance (delay and power consumption) of WiFi and LoRaWAN given varying workloads.

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The Impact of Nitrates and Phosphates on the Surface of Calcite: A First-Principles Analysis of Calcium Carbonate

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Art provides us with historical insight into the cultures of those who came before us. Art is intrinsic to human history and as time passes, natural materials tend to degrade. In order to retain that history, the field of art conservation science investigates the preservation of artwork and objects important to cultural heritage through nondestructive methods designed to clean, preserve, and occasionally repair these objects. Currently, the presence of salts has contributed to the degradation of limestone statues. Salts in solution can permeate stone statues and recrystallize, causing structural instabilities which can lead to cracks and crumbling of the limestone over time. The mineral calcite is a major component of limestone, and here we use computational chemistry, more specifically density functional theory, to create atomistic models of different salt adsorbates on two different calcite surface terminations. Specifically, we are looking at interactions between nitrate and phosphate salts on a calcium terminated calcite surface and a proton terminated surface to determine how salt adsorbates behave across different chemical environments. Overall, our evidence suggests that phosphate salts adhere more strongly to calcite surfaces than nitrate salts and that both types of salt interact more weakly with proton terminated surfaces than with metal terminated surfaces.

This work was performed as part of the Baltimore SCIART Program, which is supported by the Andrew W. Mellon Foundation under Award 41500634. All calculations were performed using the UMBC HPCF. The acquisition of equipment for the HPCF is partially supported by the NSF, whose support we gratefully acknowledge, and which requires the following notice: This material is based upon work supported by the NSF under the MRI grants CNS-0821258, CNS-1228778, and OAC-1726023, and the SCREMS grant DMS-0821311.

Researching the role of Hoxb13 in suppressing prostate cancer in the mouse model

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Prostate cancer is the second most lethal cancer in men. Although disease risk is most closely associated with age, there are a few hereditary gene variants that contribute to disease initiation and progression. HOXB13 is a homeobox protein that plays a role in prostate epithelium development. Two Hoxb13 variants have been identified that coincide with an increased risk of prostate cancer. To study the role of HOXB13 in prostatic carcinogenesis we used the transgenic Hi-Myc mouse prostate cancer model, which overexpresses the human oncogene MYC in a prostate-specific manner, crossed with Hoxb13 knockout mice. We observed a significant decrease in tumor initiations in mice carrying deleted Hoxb13 allele. Our results suggest that Hoxb13 contributes to the transcriptomic changes that permit transformation in MYC-driven prostate cancer.

This research is supported and funded by URA

IDENTIFYING ECTOPIC SYNAPSES IN NEUROMUSCULAR JUNCTIONS OF DROSOPHILA LARVAE CARRYING CANDIDATE AUTISM GENES MANIPULATIONS

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Autism spectrum disorder (ASD) is a neurodevelopmental disorder that results in lifelong management and interventions. An estimate of 1 in every 36 children are diagnosed with autism in the United States, which raises a need for the continual study in this field. This condition has a broad range of severity and can include deficits in social interaction, repetitive behaviors and limited interests, sensory hypersensitivity, abnormal speech tone or rhythm, and other diagnoses that may interfere with the ability to function in life. Synaptic elimination, a process through which ectopic synapses on off-target partners are eliminated during neuronal development, has been linked to several neurodevelopmental disorders including autism, as it is essential for the maintenance of the plasticity of the central nervous system. There are over 100 candidate genes that are associated with the development of autism, and for my project I analyzed the effects of knocking down the Drosophila genes USP8 and Prosap, which prevent protein degradation and regulate synapse formation respectively. I set out to identify ectopic synapses at the neuromuscular junctions in abdominal muscles 6 and 7 in the manipulated Drosophila larvae to determine how it compares to the control larvae. I dissected the larvae as fillet preparations, leaving only the brain, and counted the number of ectopic synapses in the immunostained neuromuscular junctions. This project contributes to the ongoing goal of understanding the process of synaptic elimination in Drosophila larvae associated with these candidate autism genes to provide translational research.

This research project is funded by the U-RISE Program at the University of Maryland, Baltimore County (UMBC).

CHARACTERIZING THE DISTRIBUTION OF GADD45B, A CANDIDATE MEDIATOR OF HYPOXIA-ADAPTATION

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Oxygen fulfills a critical role in cellular respiration, and when it becomes limited a change in metabolic priorities occurs. In the absence of oxygen (or even in normal developing tissues where oxygen is limited), Hif represents a key upstream factor in orchestrating adaptive responses. Hif-

1a is ubiquitously expressed and may contribute more towards upregulation of glucose transport and glycolysis. Hif-2a is restricted to specific tissues, and it may drive transcription of genes involved in red blood cell production (erythropoiesis) and formation of blood vessels (angiogenesis). Zebrafish can withstand anoxia & hypoxia for hours at a time, and they furthermore represent a model for regenerative responses. Following hypoxia, reoxygenation is a damaging process that contributes to damage in stroke victims. Growth arrest and DNA-damage inducible 45 beta (Gadd45b) is a gene which has been implicated in stress-responsive expression in hematopoietic stem cells, which can give rise to all blood cell lineages. Members of the gadd45 gene family have been implicated in regulating HSC differentiation, and specifically in terminal differentiation of myeloid cells. The main focus of my research is to examine the role of gadd45b in the circulatory system. This gene was identified as transcriptionally up-regulated in low oxygen, suggesting that it plays a role in hypoxia adaptation. To identify the cells in which gadd45b is up-regulated, I performed immunolabeling using an antibody against gadd45b using Tg(fli1:EGFP) transgenic embryos, in which endothelial cells are GFP-positive, Gadd45b. This analysis revealed that Gadd45b is localized in the hematopoietic stem cell (HSC) niche that extends along the anterior-posterior axis of the embryo, Interestingly, exposure to anoxia or anoxia followed by a period of re-oxygenation triggers the exit of Gadd45b-positive cells from the HSC niche into circulation. In the future, I plan to knock down gadd45b to test its function in the blood lineage.

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O

CONTRIBUTION OF PHOSPHOGLUCOSE ISOMERASE AND PHOSPHOGLYCERATE MUTASE 1 TO GLUCOSOME FORMATION IN HUMAN CELLS

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Glucosome is a multi-enzyme complex that diverts glucose flux between glycolysis and building block biosynthesis (i.e., the pentose phosphate pathway and serine biosynthesis) in human cells. Glucosome is composed of at least four rate-limiting enzymes from glycolysis and gluconeogenesis: phosphofructokinase (PFK), fructose bisphosphatase, pyruvate kinase (PK), and phosphoenolpyruvate carboxykinase (PEPCK). Based on high-content imaging assays as well as mathematical modeling approaches, we have proposed that glucose flux is regulated by glucosomes in an assembly size-dependent manner. However, the current understanding of the glucosome composition does not explain the mechanism behind the size-dependent functions of glucosome yet. We hypothesize that non-rate limiting enzymes in the pathway, like phosphoglucose isomerase (PGI) and phosphoglycerate mutase 1 (PGAM1), would play an important role in directing glucose flux through glucosome assemblies in human cells. PGI catalyzes glucose-6-phosphate (G6P) to fructose-6-phosphate (F6P) whereas PGAM1 catalyzes 3-phosphoglycerate (3PG) to 2-phosphoglycerate (2PG). Their substrates (i.e., G6P and 3PG) are used as starting metabolites for the pentose phosphate pathway and serine biosynthesis, respectively. In this work, we have constructed a fusion protein of PGI and PGAM1 with a monomeric enhanced green fluorescent protein (mEGFP). Through molecular cloning techniques, we have successfully constructed two plasmids that express mEGFP-PGI and mEGFP-PGAM1 in

mammalian cells. Both recombinants will be used in fluorescent live-cell imaging to evaluate the localization of PGI and PGAM1 to see if they colocalize with glucosome assemblies in living human cells. Our results would lead us to explore the metabolic roles they would play in the function of glucosome in human cells.

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SSAR: BUILDING SCALABLE MICRO-ACTIVITY RECOGNITION VIA LIMITED SUPERVISION

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Wearable-based technology for human activity recognition is prevalent in today's society. Recently, deep learning algorithms have enabled us to develop scalable data-driven algorithms. Such algorithms can help advocate for transferring the knowledge of complex human motions to downstream tasks via activity recognition, skill assessment, etc. However, these models lack labeled data- one of the key challenges for downstream tasks. This work tackles the challenge of scarce labeled samples encountered in the activity recognition task. This work proposes ***SSAR***, a self-trained, semi-supervised learning framework (SSL) that can effectively discern and classify human activities through leveraging pseudo labels. The motivation for utilizing a proxy label method like pseudo labels is to propagate labels from labeled data to predict labels for unlabeled data with minimal expert supervision. We utilize a CNN-based learning framework to learn the robust representation from labeled data and leverage the learned knowledge to the unlabeled data for detecting micro-complex activities. Lastly, we evaluate the proposed framework using two publicly available datasets: ***Badminton Activity Recognition*** (BAR) and ***WISDM***, by computing four evaluation metrics: ***F1-score, recall, precision*** and ***accuracy***.

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SMYD3 INHIBITION USED TO IDENTIFY AND BLOCK MAIN METASTATIC PATHWAYS WITHIN PROSTATE CANCER

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Aberrant lysine methylation of histone and non-histone proteins mediated by deregulated lysine methyltransferases (KMT) and lysine demethylases (KDM) has been associated with numerous malignancies. SMYD3, a member of the SMYD family of lysine methyltransferases, is overexpressed in multiple cancers including prostate cancer. Increased expression levels of SMYD3 in prostate cancer cells promotes survival, migration, invasion, and metastasis, indicating that it plays a significant role in prostate carcinogenesis. However, the molecular and the biochemical mechanisms that regulate substrate identification and lysine methyltransferase activity of SMYD3 remain undefined. We hypothesize that SMYD3 has a preferred substrate through which it facilitates development and progression of malignancy. In prostate cancer cells, using

subcellular fractionation and immunofluorescence we found SMYD3 to be primarily localized in the cytoplasm. Interestingly, preliminary data indicates that subcellular localization of SMYD3 changes when nuclear export is blocked, suggesting that localization of SMYD3 is under tight regulation. In order to determine how SMYD3 subcellular localization is regulated, our goal is to study the contribution of different regions of the proteins. Structurally, SMYD3 contains a conserved SET domain, which catalyzes methylation, a zinc finger MYND domain, a cysteine rich post-SET domain and a TPR-like region comprising C-terminal domain (CTD). Through immunofluorescent imaging, we aim to define the role of the different domains of SMYD3 in regulating its localization.

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The Role of Heparan Sulfate Proteoglycans in Mediating Cell Migration in Drosophila Egg Chambers

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Investigating cell migration is essential to understanding metastatic cancers, immune responses, embryogenesis, and wound repair, which can lead to novel therapeutics for metastatic cancer and mechanisms to enhance the immune system and tissue repair. The Starz-Gaiano laboratory examines migratory patterns of the border cell cluster in *Drosophila melanogaster* oogenesis. In this system, the cluster detaches from the anterior of the egg chamber and travels between nurse cells, toward the oocyte. Signaling molecules, such as Platelet Derived Growth Factor and Vascular Endothelial Growth Factor-related Factor 1 (PVF1), guide this migration, which attracts the cluster to travel toward the oocyte. PVF1 binds to a receptor tyrosine kinase on border cells, which signals the cells to move toward the oocyte. We predict that heparan sulfate proteoglycans (HSPGs) on the nurse cell surfaces regulate the diffusion of PVF1. I hypothesize that the enzymes that make HSPG are necessary to formulate the correct spatial distribution of PVF1. By disrupting the gene expression for glycosylation enzymes using RNA interference, we can investigate the effects of HSPGs on the migratory timeline. This alteration is expected to alter the molecule's distribution and may alter the cluster's migration as compared to wild type. Additionally, to help visualize the microscopic processes occurring within an egg chamber, we are developing a protocol for expansion microscopy, which effectively expands the egg chambers to improve imaging of smaller structures. After preserving the sample in a chemical gel, we incubate the egg chambers in water to allow them to expand while maintaining their structural integrity. We have seen egg chambers expand over two times their size, and others have reported up to ten times expansion. Overall, we aim to discern the effect of HSPGs on growth factor dispersal, which controls border cell cluster migration and better characterize egg chamber development with novel imaging techniques.

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P

THE EFFECTS OF HIGH SUGAR DIETS IN THE BEHAVIOR OF *CAENORHABDITIS ELEGANT*

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With excessive amounts of added sugar in processed foods, heart diseases and obesity rates continue to be the largest health concerns in the United States. Glucose and fructose are some of the most common sugars in processed foods while erythritol is a commonly used sugar alternative. In previous studies, a high sugar diet correlated with preference and slower locomotion. In this study, these three sugars were examined at different concentrations to test their individual effects after lifelong exposure on the behavior of *Caenorhabditis elegans*.These small nematodes are used in a plethora of scientific studies due to their convenience and similar genetic functions shared with humans. It was hypothesized that lifelong exposure to sugar will cause a development in preference to sugar and decrease their general mobility. Wild type C. *elegans* were synchronized to the embryo stage and grown in plates with increasing concentrations of glucose, fructose and erythritol. A chemotaxis assay was performed to measure sugar preference of the nematodes that were lifelong exposed to the sugars. The worms developed in a glucose and erythritol environment showed a higher preference for that particular sugar than the non-exposed worms. However, fructose-exposed worms demonstrated a lower preference to the sugar at lower concentrations. This data suggests that prolonged sugar consumption from the embryonic stages may lead to developed preference to that sugar in adulthood. To measure the change in motility, a thrashing assay was performed. The nematodes exposed to fructose depicted an increase in motility in all tested concentrations. Surprisingly, the erythritol-treated worms showed a decrease in motility with a sudden increase at the highest tested concentration. Our data suggests that the preference of C. *elegans* differ by the source and concentration of sugar. However, there was no correlation observed in the concentration of sugar and their behavior.

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MULTIMODAL DOMAIN ADAPTATION FOR HUMAN ACTIVITY RECOGNITION: A SURVEY

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Human Activity Recognition is a subset field in Artificial Intelligence that interprets human motion using computer vision, sensors, audio, and other signals to identify, detect, classify, and predict movements/activities. The applications of HAR are plentiful – human motion tracking can be useful in the healthcare field, computer vision proves to be useful in surveillance, and motion sensors are widely used in entertainment, specifically gaming. However, there are some limitations in the field of HAR and gaps in the available literature. The main limitation of HAR is the lack of labeled data available for researchers to use and implement – deep learning models, which are the

prominent architectures, require a copious volume of data to improve the performance of those models. Since collecting and labeling data is costly and time-consuming, researchers bypassing this constraint is a prominent part of the available literature. Domain adaptation - a transfer learning technique that allows researchers to leverage the learned knowledge from existing labeled dataset use datasets to annotate an unlabeled dataset resulting in more viable data. Multimodal domain adaptation utilizes data with multiple modalities, including text, image, and sound. Multimodal domain adaptation is important because it mitigates the problem that is insufficient data, while also improving deep learning models by learning from multiple modalities. Domain adaptation, in general, reduces the data requirements of models, which reduces operational expenditures. In this survey, we review the current literature on Multimodal Domain Adaptation for Human Activity Recognition, the techniques used to mitigate the problems, and the datasets used in these papers. We also find unacknowledged gaps in the current literature and propose researching those gaps.

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Comparing Similar Integrase Proteins in Different Phages to Evaluate the Presence of Horizontal Gene Transfer

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The integrase protein, an integral part of the temperate life cycle, was investigated for elements of divergent evolution within temperate phages. The integrase protein from *Gordonia* phages ClubL and Oneup (cluster CQ) were phylogenetically examined with 15 actinobacteriophages of various clusters carrying integrases classified into seven different phams and compared to an proteomic tree produced of the same phages. As would be expected, when entire proteomes were examined, the phages assorted by cluster and host infected. When the integrase was investigated phylogenetically, however, evidence of horizontal gene transfer was found in bacteriophages, with phages of different clusters forming different clades in several instances. Two cases of note are pham 98453, which is found in Bantam (cluster DL) as well as phages ClubL and OneUp (CQ1 and CQ2), and pham 96094 is found in phages Lucky10 (DH) and Horus (DN1). The presence of an identical integrase gene in genetically different phages suggests horizontal gene transfer as the mechanism. It appears likely that the gene was picked up by an ancestor of ClubL and OneUp prior to their divergence as the integrases of Bantam and OneUp appear to be more closely related than the integrases of OneUp and ClubL's despite their being in the same cluster.

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CHARACTERIZING THE RELATIONSHIP BETWEEN THE CONSERVATION OF MINOR TAIL PROTEINS AND HOST RANGE IN *STREPTOMYCES* BACTERIOPHAGES

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Previously sequenced genomes of *Streptomyces* bacteriophages demonstrate that there are many unknown variables that affect the host range of an individual phage. There are multiple proteins, including the minor tail protein (MTP), that a bacteriophage uses to identify hosts it is able to infect. The purpose of this research was to characterize the relationship between bacteriophages that share related minor tail proteins and their respective host ranges. We used data previously collected by UMBC Phage Hunters to identify and compare MTP amino acid sequences of phages through phamerator. A group of three similar MTPs that repeat throughout the cluster were isolated based on this data and used to create a phylogenetic tree that compares divergence between the MTPs between phages. This data was compared to both a phylogenetic tree of whole genomes from the same phages and their host ranges. Host range was evaluated based on any infection of the host bacteria. When MTPs from these three families were found, the bacteriophage was also able to infect a minimum of two bacterial strains. Based on this data, we have determined that the minor tail protein may serve a role in determining host range, but other factors are also important. This approach shows that it is more likely that phages develop specialization for fewer bacterial strains over time. Developing broader recognition for multiple bacterial strains seems unlikely because there are clumps of phages that infect multiple with one branch that infects less. The simplest assumption based on the data is that phages that infect fewer types of bacteria develop this trait individually and show less similarity to other host specific phages. This research could inform individualized studies of phages for future use in phage therapy and support the need for future collection of bacteriophage host range data.

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Q

ELUCIDATING THE MOLECULAR NATURE OF THE MONOMERIC HIV-1 RNA GENOME AND THE CELLULAR CAP-DEPENDENT TRANSLATION INITIATION PROTEIN, EIF4E

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The human immunodeficiency virus type-1 (HIV-1) has globally impacted over 39 million people and has drastic impacts on an individual's immune system. HIV-1 patients are treated with a drug cocktail that targets multiple aspects of the viral replication cycle; however, all of these drugs target HIV proteins that are susceptible to mutations and can lead to drug resistance. Our laboratory's research focuses on investigating highly conserved regions of the HIV-1 RNA genome

such as the 5′-Leader (5′-L). This segment of the RNA genome controls multiple functions such as translation, packaging, and assembly. The 5′-L exists in equilibrium between two conformers - a monomer that serves as mRNA to translate into viral proteins and a dimer that serves as gRNA to serve as genomic material for the next virion. One unique structural difference between the two conformations is that the monomer has an exposed 5′-cap whereas the dimer has a sequestered 5′-cap, preventing cap-dependent translation machinery, such as eIF4E, from interacting with the dimer. While it is well known that cap-dependent translation serves as the primary mechanism for HIV-1 genome translation, the molecular binding interactions between 5′-capped RNAs and eIF4E remains unknown.

One particular RNA construct of interest is known as Cap3G-Mini-TPUD - this consists of a portion of the TAR hairpin, polyA region, and the U5:DIS stabilized by a loop - as the entire 5′-L is difficult to study through nuclear magnetic resonance (NMR) spectroscopy. I purified the RNA and used a novel DNA splint binding technique to add the 5′-cap. Next, I optimized buffer conditions to study the binding interactions between eIF4E and Cap3G-Mini-TPUD through EMSAs. We aim to collect ITC data to quantitatively understand the binding affinity of this RNA-protein complex and determine if residues of the RNA affect eIF4E recruitment.

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R

ISOLATING THE ROLE OF POLY-A STRUCTURE IN SELECTIVE PACKAGING

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In HIV-1 replication, RNA transcripts are required to serve multiple functions, both as genomic RNA and as messenger RNA. The untranslated region of the genome, called the 5'-Leader, is found to regulate this function, specifically influenced by heterogeneous transcription start site usage. RNAs beginning with one guanosine (cap1G) can dimerize and be packaged to serve as genetic material for the progeny virus, while RNAs beginning with three guanosines are monomeric and act as messenger RNA. Prior literature argued that dimerization propensity regulates selective packaging of Cap1G over Cap3G RNAs. Cap1G's Poly-A forms a hairpin structure which exposes the DIS binding site, allowing it to dimerize, whereas cap3G's extra guanosines bind to the base of the Poly-A, disrupting its hairpin stem, and causing it to refold into a structure which sequesters the DIS binding site, impeding dimerization. Due to new research regarding a dimeric but poorly packaged mutant, our work instead proposes an alternate feature to regulate packaging: sequestration of the 5'-cap. Upon structural analysis via NMR, the Poly-A hairpin was determined to contain bulges persistent across HIV-1 group M. Stabilization of the Poly-A hairpin in Cap3G RNA through removal of these bulges prevents unwinding of the stem and maintains a dimeric structure despite the start site. This mutant dimerizes and, according to Isothermal Titration Calorimetry, binds nucleocapsid like other competitively packaged RNAs. However, in-cell packaging assays demonstrate poor competitive packaging of this mutant. This

finding instead supports our hypothesis that removal of the bulges uniquely exposes the 5'-cap which prevents packaging, and the increase in dimerization propensity does not improve packaging. Prior results suggesting that dimerization drives packaging overlook a key feature intrinsic to the Cap1G dimeric structure: its sequestration of the 5'-cap. This work highlights the structure and makeup of the Poly-A region as a critical regulator of both monomer-dimer equilibrium and RNA fate.

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EXPLORING THE FATE OF RNA IN MOLONEY MURINE LEUKEMIA VIRUS

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The moloney murine leukemia virus (MoMuLv), a virus that causes leukemia and neurological diseases within rodentia, has been studied since the 1950s to act as a model to further understand the underlying mechanisms of all retroviruses due to its easy use. Our laboratory mainly focuses on the human immunodeficiency virus type-1 (HIV-1), most particularly the segment of the HIV-1 RNA genome important for viral replication, known as the 5'-Leader (5'L). The 5'L exists in two conformations: the dimeric conformation adapted by 5'-capped RNAs beginning with one guanosine (Cap1G) in which the cap is sequestered, and the monomeric conformation adapted by 5'-capped RNAs beginning with two or three guanosines (Cap2G and Cap3G respectively) where our cap is exposed. We refer to viruses containing these different beginning sites as having transcriptional start site heterogeneity. Inversely, MoMuLv contains a unique transcription start site, meaning the virus consists of only one start site, Cap1G. It has been shown that the 5'L can still adopt a dimeric or monomeric form. In this work, we aim to explore what drives RNA packaging versus translation in a retrovirus that contains only unique start sites. We suspect that MoMuLv's genome fate is driven by dimerization dependent cap sequestration, and hypothesize that dimerization is catalyzed by the nucleocapsid (NC) domain of the retroviral Gag polyprotein. We plan to explore the behavior of MoMuLv's genome in vitro for both monomeric and dimeric RNA, by focusing on cap sequestration and exposure. Through electrophoretic mobility shift assays (EMSA), we can assess whether the cap is sequestered or exposed, which we will further confirm using nuclear magnetic resonance (NMR). In HIV-1, we know that dimerization is driven by transcriptional start site heterogeneity, but in MLV we will explore if dimerization is NC-dependent, which we will later practice in vivo. Our work will provide more information on the mechanisms of retroviruses with unique start sites, and hopefully allow answers on how to stop replication of all retroviruses.

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THE IMPACT OF CHLORIDES ON THE SURFACE OF CALCITE: A DENSITY FUNCTIONAL THEORY ANALYSIS OF CALCIUM CARBONATE

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It is well known in art conservation science that salts, specifically chlorides, are a problem for calcite artifacts. It has been well documented that chlorides are highly corrosive so there is a vested interest in understanding the impacts on the surface of calcite and understanding if chlorides can viably be removed or if it would be harmful to the piece to remove them in the first place. This project used computational chemistry to understand the interactions between calcite surfaces and various chloride salts to aid conservation scientists in seeking alternatives to traditional desalination techniques. Plane-wave density-functional theory (DFT) provides a cost-effective avenue to accurately assess the strength of interactions between molecules and surfaces, yielding adsorption energies and the atomistic response of a surface to different small molecules. We probed two different surfaces of calcite; a calcium-terminated surface and a proton-terminated surface. Our analysis suggests that chloride will adsorb to both surfaces and in multiple configurations, however, chlorides exposed to a hydrogen-terminated surface are potentially more likely to be removable.

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EXAMINING LEARNED ASSOCIATIONS BETWEEN CONTEXTUAL CUES AND STRESS-INDUCING EXPERIENCES

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Our response to stressful situations is essential to our survival. The ability to associate stress-inducing stimuli with surrounding contextual information allows organisms to make better decisions in the future that keeps them out of harm's way. However, it remains unclear how the brain brings this information together to properly guide behavior. To gain insight into this process, we used a behavioral paradigm where mice learn to associate contextual cues with aversive stimuli (conditioned place aversion (CPA)). Since this paradigm is typically used to evaluate pharmacological compounds, we first sought to determine whether the same effect could be elicited with a stress-inducing aversive stimulus. Using physical restraint as the aversive stimulus, we conditioned the mice using an arena in which two chambers, connected by a small corridor, can be distinguished by contextual cues. Comparing time spent in the chambers before and after conditioning, we initially found that restraint induced CPA. However, repeating this experiment in a separate group of mice failed to reproduce this result. We will be repeating these experiments using foot shock as the aversive stimulus to determine whether it is more effective at inducing CPA. To determine what brain regions may be responsible for mediating this behavior, we measured cFos expression in mice that were restrained in the CPA chamber. Mice restrained in their home cage as well as those with free access to their cage or the CPA arena served as controls. cFos is an immediate early gene where expression can serve as a proxy for brain activity, allowing us to determine the brain regions that are specifically activated during restraint context pairing. We focused on quantifying cells in the hippocampus, nucleus accumbens, and amygdala due to their prominent roles in contextual learning and memory, motivated behaviors, and fear. Our findings will be important in understanding the neurobiological basis of stress and aversion with implications for how we understand stress-related neuropsychiatric disorders.

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S

STRUCTURAL BASIS AND MECHANISM OF HIV-1 GENOME PACKAGING

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The Human Immunodeficiency Virus type 1 (HIV-1) is a retrovirus that depletes CD4+ cells, weakening the host immune system resulting in Acquired Immunodeficiency Syndrome (AIDS). Current antiviral therapies target proteins of HIV-1 that are inclined to high mutation rates. A greater understanding of the structure of HIV-1 is necessary to target a more conserved region. During viral genome packaging, two copies of the genomic viral RNA form a dimer and bind with Gag polyproteins (Gag). Genomic recognition is a highly conserved process and a promising drug target. Mutagenesis studies of selective HIV-1 packaging determined the minimal packaging unit for HIV-1, referred to as the Core Encapsidation Signal (CES) that exhibits native-like dimerization, nucleocapsid (NC) binding, and packaging efficiency. Keane et al. determined the three-dimensional structure of CES. The central finding was that the splice donor (SD) region does not form a hairpin, instead forming long range base pair interactions into a tandem-3-way junction and is sequestered. However, this work primarily focused on the monomeric form of the NL4-3 strain of HIV-1, where a GAGA mutation in the Dimer Initiation Site (DIS) prevented dimerization. Our project focuses on the MAL strain of HIV-1 to determine the structure of the native, non-mutated packing signal. Utilizing an enzyme, TGK, which can extend RNA using a DNA oligo for segmental labeling, addressing limitations in structurally characterizing the dimeric CES the NL4-3 strain researchers faced. This segmental labeling technique allows for unambiguous Nuclear Magnetic Resonance (NMR) signal assignment by selectively eliminating signals from any desired half of the entire CES sequence. Our next goal will be to characterize the RNA and Gag interactions important for nucleocapsid (NC) binding, genome selection, and selective packaging. Overall, understanding the conserved region advances HIV antiviral therapies.

Special acknowledgment to Dr. Summer and mentor Brian Grossman for all their support on this project. Additionally, an extended gratitude to the HHMI for their grants funding the research.

STRUCTURAL CHARACTERIZATION OF THE HIV-1 REV RESPONSE ELEMENT USING NMR SPECTROSCOPY

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The Rev Response Element (RRE) is a conserved segment of the human immunodeficiency virus (HIV) RNA genome and plays a crucial role in replication, particularly in the export of unspliced and partially spliced viral RNAs from the nucleus to the cytoplasm. The RRE interacts with an HIV accessory protein called Rev, which facilitates binding to the viral RNA and subsequent nuclear export. The RRE is over 350 nucleotides in size, has highly structured RNA elements, and contains multiple stem-loops and bulges. In solution, RRE exists in equilibrium between two conformations containing either 4 or 5 stem loops. We have introduced stabilizing mutations into the RRE sequence to study each of these conformers in isolation (4SLm and 5SLm respectively). Understanding the structural characteristics and dynamics of the RRE is essential for unraveling its functional mechanisms and have a better understanding of the binding interactions between the RRE and Rev. We study the structure and dynamics of the two different mutants using nuclear magnetic resonance (NMR) spectroscopy. We will describe our attempts to generate RRE RNAs of various lengths up to 358 nucleotides in both 4SLm and 5SLm via cloning and mutagenesis experiments.

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PROTEIN OPTIMIZATION OF HIV-1 MYRISTOYLATED MATRIX FOR FUTURE MEMBRANE BINDING STUDIES

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Human Immunodeficiency Virus (HIV) is a retrovirus. Like all retroviruses, it encodes for a Gag polyprotein that helps direct the assembly of the virus particles in the host cells. The beginning of this Gag polyprotein house the Matrix protein which has an N terminal myristoyl group which is instrumental in anchoring it and the entire Gag complex to the plasma membrane which is the beginning of the assembly process that also directs envelope glycoproteins to these viral assembly sites. We are looking at the protein optimization of the HIV myristoylated Matrix protein to do assembly experiments using a nanodisc model to mimic the plasma membrane. Our vector exists in the pET Duet plasmid which allows expression of both the HIVMA protein and the codon optimized N-myristoyltransferase enzyme (NMT). This is a co- translational process that is mediated by the first six amino acids at the N-terminal of the protein referred to as the myristoyl signal (MGARAS). The myristoyl group attachment consists of a 14 Carbon Fatty acid chain that gets anchored in the hydrophobic layer of the membrane. During transport, this group is sequestered in the protein folded structure. Once in contact with the membrane, this group pops out to anchor it to the plasma membrane. This process is referred to as the myristoyl switch. Some of the challenges faced in purifying the myristoylated matrix are due to the protein being

extremely pH dependent. At lower pH's, the myristoyl group is exposed and aggregates to be precipitated out in solution. To optimize protein purification, we use different buffer conditions with a range of pHs. Our findings indicate that the myristoylated Matrix is sequestered at a pH of 7, allowing us to further optimize the expression and purification of this protein.

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Predictive Fluorescence Analytics: Evaluating Deep Learning Tools Applied to Excitation-Emission Matrix Analysis

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The excitation emission matrix (EEM) is a spectroscopic technique used to analyze the fluorescence properties of a sample. The use of EEM helps monitor the quality of bodies of water, by measuring the presence of organic matter or pollutants in the water. The modern form of analyzing Excitation Emission matrix is Parallel Factor Analysis (PARAFAC). This method is time consuming; integrating machine learning in this process can be used to minimize error, and accelerate data analysis. Convolutional Neural Networks (CNN) are capable of identifying complex patterns in images and classifying them. CNN takes an image input and uses different layers to understand features and complex patterns. In this study, we investigate the applicability of a CNN model from the literature (Ren 2022)on our data, which spanned a different range of emissions and excitation wavelengths compared to that used in training and testing the literature model. To evaluate the model's performance, we compared its analysis of our EEM data with our original PARAFAC analysis. The findings from this study shed light on the model's suitability for inferring EEM components and its potential utility as a versatile analytical tool in diverse research and practical applications.

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DOES TTLL11-INDUCED TUBULIN GLUTAMYLATION ENHANCE METASTATIC PHENOTYPES TO PROMOTE BREAST CANCER METASTASIS IN VITRO AND IN VIVO?

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Triple negative breast cancer (TNBC) is known to metastasize very quickly. TNBC cells disseminate from primary tumor cells and can enter the bloodstream, where these cells are termed circulating tumor cells (CTCs). The CTCs may then attach to the endothelial lining of the blood vessels and invade or extravasate into nearby tissue. Once in a distant tissue, the TNBC cells may either remain dormant or begin to grow as metastatic cancer. Given the harsh environment of the bloodstream and heterogeneity of CTCs, this can lead to poor prognosis and higher risk of metastatic relapse for breast cancer patients. Therefore, it is critical to elucidate cellular

mechanisms that promote the metastatic cascade to develop targeted drug therapies to inhibit and/or prevent metastasis.

To understand the metastatic potential of TNBC, the Martin lab has focused on the cytoskeletal components of the cells along with post translational modifications that affect the rate of metastasis. Metastatic breast cancer cells can have cytoskeletal membrane protrusions, also identified as microtenticles (McTN), caused by microtubule hyper stabilization. This is caused by the imbalance of microtubule growth overcoming the inward forces of the actin cortex. Microtubules are composed of polymerized alpha and beta tubulin heterodimers which are critical for cell structure and division. Post translational modifications on either tubulin heterodimer can enhance McTN growth and encourage cellular invasion and attachment during metastasis. Glutamylation on the C-terminus of alpha tubulin is a specific post translational modification that leads to microtubule stabilization and possible cellular invasion and reattachment. Tubulin tyrosine-like ligase (TTLL11) is a glutamylase that causes this modification and has implications in inducing breast cancer metastasis. The aim for the current project is to determine if expression of TTLL11-induced tubulin glutamylation promotes metastatic phenotypes in triple negative breast cancer cells in vitro and in vivo.

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DATA-ENABLED COMPUTATIONAL CHEMISTRY TO BETTER UNDERSTAND WATER QUALITY

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We will use a combination of crystallographic database mining, density functional theory (DFT) simulations, and tabulated thermodynamic data to uncover the release profiles of Pb from complex solids in water to better understand the atomistic processes that occur in water distribution systems at different pH values and concentrations. In order to do that, we have to know how to correctly utilize DFT, which is a quantum mechanical modeling method used to compute and investigate the electronic structure of many-body systems, in particular atoms, molecules, and condensed phases. For my project, I will focus on model systems that are known, smaller bulk materials such as lead oxides, carbonates, and phosphates. I would start with known structures that come from crystallographic databases to use as the input for my DFT calculations. Then, they would be modified by investigating exchange-correlation functionals and the addition of a Hubbard U to minimize errors in the calculations. Doing this can address any of the drawbacks of local and semi-local exchange-correlation functionals, while still ensuring computational efficiency. I would then specify the molecular or crystal structure of the system using 3D coordinates followed by geometry optimization which I would have obtained by using a DFT software called quantum ESPRESSO. After obtaining these results, I can analyze the results and interpret the obtained electronic structure and properties in the context of the systems I am studying to then create realistic surfaces and compute the thermodynamics of ion release from those surfaces for a wide range of pH values.

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THE ROLE OF ANCHOR GENE IN ALCOHOL DISORDERS IN A *DROSOPHILA* KNOCKDOWN MODEL

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Alcohol use disorder (AUD) is an illness characterized by an impaired ability to stop or regulate alcohol usage despite negative social, career, or health effects. AUD can range from mild to severe and is considered a neurological condition. Genetics influence the risk of developing AUD. However, the specific genes causing AUD have not yet been fully identified. Due to its function in reward processing, habit development, and biased decision-making, a brain region known as the dorsolateral striatum (DLSt) has been shown to be an area of interest in studying alcohol use disorder (AUD). In vertebrates, GPR155 is a marker of the DLSt, meaning it is uniquely expressed in the DLSt as opposed to other regions of the striatum. In order to rapidly and efficiently characterize its behavioral role, we studied the *Drosophila* homolog, anchor. The molecular function of the Anchor gene is unknown. We studied the behavioral responses of *Drosophila* to ethanol using a pan-neuronal anchor model and tested olfactory attraction to ethanol in a two-choice paradigm. We also measured ethanol-induced sedation. We hypothesized that a *Drosophila* model with pan-neuronal anchor knockdown would affect ethanol-induced sedation and olfactory ethanol attraction. Specifically, we found that male and female anchor knockdown flies sedate more slowly compared to genetic controls. Additionally, preliminary data shows that preference was reversed in both male and female anchor knockdown flies compared to genetic controls. The future directions of the study will entail cell-specific knockdown experiments to determine Anchor's function in controlling ethanol-related behaviors in other cell populations. We also seek to investigate other ethanol-related behaviors, confirm findings using a GPR155 deletion mice model, and identify the pattern of Anchor expression in the brain. This study will help us understand the role of Anchor in alcohol-related behaviors and identify potential areas of ethanol-induced reactions.

This research was partially funded by the USM LSAMP program, supported by NSF LSAMP Award # 2207374."

INVESTIGATING HOW THE STRUCTURAL ELEMENTS OF THE HIV-1 5′-LEADER AFFECT BINDING OF THE CELLULAR CAP BINDING PROTEIN, EIF4E

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The acquired immunodeficiency syndrome is caused by the infection of the human immunodeficiency virus type-1 (HIV-1). Our laboratory focuses on a conserved region known as the 5′-Leader (5′-L). This region regulates viral functions such as dimerization and translation. The 5′-L of the HIV-1_{MAL} strain has two distinct conformations - a monomer and a dimer. The conformation is due to a mechanism called transcriptional start site heterogeneity that involves the number of guanosines at the 5′-end of the RNA. The dimer sequesters the 5′-cap which inhibits the cap binding protein, eIF4E, from binding and initiating translation. This is not an issue for the monomer because the 5′-cap is exposed. We investigate how structural differences in the monomer affect eIF4E binding. To do this, we use isothermal titration calorimetry (ITC), a quantitative method that provides us with thermodynamic parameters upon the binding of molecules. We purified RNA oligos of the HIV-1 5′-L of different lengths to determine what role different segments play in eIF4E binding. This includes the TAR hairpin and the polyA region of the 5′-L that is believed to be unstructured. ITC allows us to measure the binding affinity of eIF4E to different RNA constructs to compare the relevance of different regions of the 5′-L. Our results indicate that eIF4E binds tighter to a 5′-capped RNA than to the 5′-cap alone. The data also suggest that the top half of the TAR hairpin does not play a significant role in eIF4E binding. We have started to purify additional RNA oligos that include different lengths of the polyA region of the 5′-Leader to assess how this region affects the binding affinity to eIF4E. Once we determine the specific structural elements that are important for eIF4E recruitment to the 5'-Leader, we will better understand how the HIV-1 RNAs are translated to viral proteins.

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COMPREHENSIVE ANALYSIS OF THE *ASPERGILLUS NIDULANS* KINASE DELETION LIBRARY FOR INCREASED SEPTATION UNDER CELL WALL STRESS

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Filamentous fungi are both important human pathogens and are used prevalently in the bioprocess industry to produce valuable products. In both cases, the cell wall plays an important role. For example, in pathogens it can impact virulence and in bioprocessing productivity. To regulate their cell-wall structure, fungi rely on complex signaling pathways, composed of signaling proteins such as kinases. The objective in this study was to investigate the contribution of protein kinases from Aspergillus nidulans in the fungal response to cell-wall stress. By determining which protein kinases (in various signaling pathways) affect cell wall integrity and respond to cell wall stress, we will identify potential targets for new antifungal drugs. Previous research in our

lab has shown (i) that cell-wall stress leads to increased levels of septation and (ii) that genetic mutations which reduce septation lead to more susceptible strains. We hypothesize that other, as yet unknown, kinases are involved in wall-stress-induced septation and survival. To test this hypothesis, we screened the A. nidulans kinase deletion library (98 strains), each lacking a specific kinase. We conducted experiments on each of the library strains under two conditions: one group was treated with micafungin, a cell-wall perturbant, at the 12-hour mark, while the other remained undisturbed. After 16 hours, we captured images of the fungi and measured the quantity of septa formed as well as the overall projected area (to measure growth). By assessing the extent of growth and septation, we are able infer the involvement of each kinase in responding to cell-wall stress.

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Advances in Predicting Ice-Bed Topography Using Machine Learning: A Comprehensive Review and Case Studies

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The purpose of this research project is to investigate current advances in predicting topography in Greenland using ice-penetrating radar data and machine-learning techniques. Accurate representations of bed topography are vital for understanding ice sheet stability and vulnerability to climate change, especially in relation to rising sea levels. To achieve this, we explored three interpolation preprocessing methods (Nearest Neighbor, Bilinear, and Kriging) alongside various machine learning models including Dense Neural Network, LSTM, VAE, XGBoost, Gaussian Process Regression, and Kriging-based Residual Learning. Among the evaluated models, the XGBoost model with nearest neighbor interpolated data exhibited exceptional performance with a Root Mean Square Error (RMSE) of 32.680, Mean Absolute Error (MAE) of 22.273, and coefficient of determination (R^2) of 0.967. We also compared our prediction with a popular Greenland ice bed topography data product called BedMachine using the above metrics and Terrain Ruggedness Index (TRI). The promising results from our research show machine learning models could be used to accurately predict Greenland's ice-bed topography and provide valuable insights into ice sheet stability and climate change impacts on rising sea levels.

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EFFICACY OF PHAGE ENZYME TOOLS WHEN DETERMINING PHAGE CLUSTERS

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Bacteriophages are a type of virus that infects bacteria. Bacteriophage genomes are very diverse. Genetically similar phages are grouped in clusters, with more similar phages grouped into subclusters. Bacteriophage clusters and subclusters are identified through sequencing. But with a restriction enzyme digest the cluster or subcluster can be predicted with a program, Phage Enzyme Tools (PET 2.0). Is PET 2.0 effective with its predictions? We investigated the accuracy of PET 2.0 cluster predictions with data from restriction digests. PET 2.0 is a tool used to aid in the identification of bacteriophage clusters and subclusters, specifically ones we had identification on but wanted to see how PET would identify it. The program works by comparing the results from completed digestion patterns of an unknown phage to simulated digests produced from a database of sequenced phages. We have looked at twelve previously sequenced bacteriophages and ran them through two methods in hopes of finding out how effective one is based on the other. Out of the twelve bacteriophages we chose, none of the sequenced clusters and subclusters matched the predicted clusters and subclusters of PET 2.0. This suggests that PET 2.0 should only be viewed as a prediction and further analysis can be done to verify the cluster or subcluster of the phage.

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Structural Basis and Mechanism of HIV-1 Genome Packaging

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The Human Immunodeficiency Virus type 1 (HIV-1) is a retrovirus that depletes CD4+ cells, weakening the host immune system and resulting in Acquired Immunodeficiency Syndrome (AIDS). Current antiviral therapies target proteins of HIV-1 that are inclined to high rates of mutation. A greater understanding of the structure of HIV-1 is necessary to target a more conserved region. During viral genome packaging, two copies of the genomic viral RNA form a dimer and bind with Gag polyproteins (Gag). Genomic recognition is a highly conserved process and a promising drug target. Mutagenesis studies of selective HIV-1 packaging determined the minimal packaging unit for HIV-1, called the Core Encapsidation Signal (CES) that exhibits native-like dimerization, nucleocapsid (NC) binding, and packaging efficiency. Keane et al. determined the three-dimensional structure of CES. The central finding was that the splice donor (SD) region does not

form a hairpin, instead forming long-range base pair interactions into a tandem-3-way junction and is sequestered. However, this work primarily focused on the monomeric form of the NL4-3 strain of HIV-1, where a GAGA mutation in the Dimer Initiation Site (DIS) prevented dimerization. Our project focuses on the MAL strain of HIV-1 to determine the structure of the native, non-mutated packing signal. Utilizing an enzyme, TGK, which can extend an RNA primer off of a DNA RNA hybrid. This segmental labeling technique allows for unambiguous Nuclear Magnetic Resonance (NMR) signal assignment by selectively eliminating signals from any desired half of the entire CES sequence. Our next goal will be to characterize the RNA and Gag interactions important for nucleocapsid binding, genome selection, and selective packaging. Overall, understanding the conserved region advances HIV antiviral therapies.

Funding for this research is supported by the Howard Hughes Medical Institute (HHMI) and NIAID U54150470. I would like to give special thanks to Dr. Jan Marchant, Dr. Pengfei Ding, and Dr. Nele Hollmann for their invaluable feedback and help. I would like to give thanks to all the members of the Summers lab. Finally, I would like to thank the UMBC Graduate Student Association (GSA) for providing me with a travel award for attending this conference for my professional development.

EXAMINING THE EFFICIENCY AND CAPACITY FOR EFFECTIVE NANOCAPSULE SYNTHESIS

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In drug delivery, one of the main goals is to achieve high efficacy and limit or eliminate undesired side effects. Nanocapsules, a type of nanoparticle consisting of a core that can enclose drugs, may serve to meet these needs with their various properties that allow such control in drug delivery. Acriflavine, a topical antiseptic and antibacterial agent, is one drug that benefits from being encapsulated as it allows for extended release when compared to free acriflavine which is physically too small to act long term within the body. An analysis of drug loading, release, and accumulation was performed with acriflavine. Its uptake into polyurethane nanocapsules was recorded and then characterized to determine the average size of nanocapsules within the batch and its reproducibility. Polyurethane nanocapsules were utilized as it was previously found to be advantageous to poly(lactic-co-glycolic acid) (PLGA) based nanocapsules for its comparative lack of complement activation, better degradability and on-demand delivery potential. Ultimately, the objective is to test nanocapsule synthesis efficiency while ensuring stability and a high yield of the nanocapsules with the encapsulated drug. This serves as a preliminary step to in vivo or in vitro models that intend to utilize encapsulated drugs.

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ANALYSIS OF GENETIC COMPENSATION IN THE *CHLAMYDOMONAS RLS1* MUTANT

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Genetic compensation allows specific genes to compensate for the loss of function of a homologous gene. This mechanism enables organisms to survive despite having mutations that could cause disruption of essential functions. Previous studies have shown that genetic compensation occurs in *Chlamydomonas reinhardtii* triacylglyceride (TAG) biosynthesis genes, but it

has not been detected for any other C. *reinhardtii* genes. In addition, existing data suggest that genes related to another gene, *RLS1*, might be upregulated in a *rls1* knockout mutant. *RLS1* (*RegA-Like-Sequence 1*) encodes a protein that plays a role in regulating gene expression and responding to stress; when deprived of light or nutrients, cells express *RLS1*, leading to suppressed growth and cell division. The goal of this work is to investigate genetic compensation in genes closely related to *RLS1*. Focusing on the closely related *RSL1* genes will determine if there is genetic compensation within this gene family. We are analyzing the expression of *rls2*, *rls8*, and *rls11* mRNA present in the *Chlamydomonas rls1* mutant compared to the CC-4533 wild-type parental strain using RT-qPCR. RT-qPCR provides quantitative data to accurately compare the expression of genes between the *RLS1*mutant and the wild type. We are growing cultures of the parent and *RLS1* mutant, extracting RNA, and using it for cDNA synthesis. In parallel, we are testing *RLS* primers to determine appropriate PCR conditions. Next, we will perform RT-qPCR to analyze and compare the transcript levels. This analysis should help determine whether genetic compensation occurs in *Chlamydomonas* genes other than TAG genes.

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VISUALIZING SINGLET OXYGEN PRODUCTION OF DIFFERENT MOF CATALYSTS

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Chemical warfare agents (CWAs) are extremely toxic weapons of mass destruction and are synthesized to incapacitate their targets. Among CWAs, sulfur mustard is a notorious nerve gas that is designed to burn skin and induce acute respiratory distress. Metal-organic frameworks (MOFs) are porous crystalline materials that have demonstrated promising results within CWA decontamination. NU-1000, a commonly used MOF containing zirconium nodes and functionalized tetra-(benzoic acid) pyrene linkers, has been shown to generate singlet oxygen in the presence of UV and blue light, which successfully oxidized sulfur mustard's stimulant 2-chloroethyl ethyl sulfide (2-CEES). Our research aims to quantify singlet oxygen generation from different NU-1000 MOFs using fluorescent singlet oxygen probes, 1,3-diphenylisobenzofuran (DPBF) and 9,10-anthracenediyl-bis (methylene) dimalonic acid (ABDA). Through absorbance and fluorescence spectroscopies, changes in the singlet oxygen probe's properties could be visualized and used to quantify the production of singlet oxygen that is photosensitized by the NU-1000 MOFs. Our research has identified the limitations of these probes for quantifying the photocatalytic production of singlet oxygen from the NU-1000s. DPBF is not photostable but was capable of detecting singlet oxygen with the inclusion of simultaneous control experiments. In the case of ABDA, the four carboxylate groups adsorbed to the MOF, creating false degradation patterns. As the result of this work, esterified ABDA derivatives are proposed as efficient and selective probes of singlet molecular oxygen produced upon irradiation of MOF materials.

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CORRELATING GENOMIC MINOR TAIL PROTEIN CONTENT ON HOST RANGE EFFICIENCY IN *STREPTOMYCES* PHAGES

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Bacteriophages, or phages, are viruses that infect bacteria, needing a host bacterium to reproduce and grow. Phages are currently studied as potential treatments for bacterial infections. Through genetic engineering, scientists can produce phages with desirable genes that are valuable in therapeutic applications. A bacteriophage's host range is the scope of bacteria a phage can infect; the minor tail protein (MTP) is an integral part of its infection process and is coded in the phage's genome. This study aimed to find a correlation between the amount of genes coding MTPs in a *Streptomyces* phage's genome and its relation to host range efficiency. We hypothesized that the higher the proportion of the genome encoding MTPs, the more hosts it can successfully infect. To determine host range efficiency, phages were exposed to different bacteria to test for successful infections. The number of successful host infections indicated a higher host range efficiency. A genome mapping program was used to observe the MTP content in each phage, and host range data was referenced from data previously collected by UMBC students. No significant correlation was found when comparing the percentage of genes encoding MTPs in a phage's genome and the number of infected hosts; this indicates no significant correlation between a phage's genomic MTP proportion and its ability to infect hosts. Using the insight gained from this study, further research can be done to study the correlation between tape measure proteins and host range efficiency. It would be beneficial to sequence more phages and complete more host range efficiency assays for a larger data set and more confident conclusions in the future.

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U

SITUATION-AWARE ACCESS CONTROL FOR INTELLIGENT TRANSPORTATION SYSTEMS

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Intelligent Transportation Systems (ITS) apply various technologies such as sensing, analysis, control, and communications to ground transportation in order to improve safety, mobility and efficiency. Examples of ITS include Connected Autonomous Vehicles, Traffic Management Systems, Smart Parking Systems etc. These systems are vulnerable to cyber-attacks and privacy violations (e.g., data about an individual's location, trajectory, or other sensitive information may be leaked, especially when such data contains identity information). Sensitive data, such as the license plate number of a car, is frequently exchanged in ITS. Thus, it is necessary to restrict who have access to such sensitive information in ITS. The research proposes a situation-aware access control framework for ITS. The most commonly used access control solution in ITS is role-based access control. However, situation-aware access control is more appropriate for ITS because the access control decisions often depend on dynamically changing situations. For instance, a traffic enforcement officer will only be given access to a vehicle's license plate if it is traveling faster than the speed limit. We implemented a semantic-web based solution to support situation-aware access control in a distributed ITS environment. We first created an ontology for ITS, including major classes such as users, vehicles, sensors, data, and data broker. Our ontology also models some of the popular ITS protocols such as MQTT which uses a publisher/subscriber model. We also proposed a query rewriting method that can modify a query over ITS data to enforce access control rules. Finally, we conducted experiments on a few ITS use cases to show that the overhead of enforcing access control rules is acceptable.

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DETERMINING REGIONS IN USP15 THAT REGULATE ITS STABILITY AND TURNOVER IN OVARIAN CANCER CELLS

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Due to lack of early diagnostic markers and effective therapeutics, human ovarian cancer remains the most lethal gynecologic malignancy. This unfortunate clinical reality highlights the urgent need to identify novel therapeutic targets and more effective treatment strategies. Recent studies show that the deubiquitinase USP15 plays an important role in ovarian cancer progression and therapeutic response. Despite this, mechanisms that govern USP15 stability and turnover in cells have remained unknown. My project aims to address this knowledge-gap by identifying regions in USP15 that regulate its stability in cells. To this aim, we are cloning full-length USP15 and truncation mutants with either N- or C-terminal epitope tags into the mammalian expression vector, pcDNA3.1. Subsequently, cloned plasmids will be transfected into human ovarian cancer cell lines and the half-life of the full length and truncation mutants will be measured using the cycloheximide chase assay. Furthermore, a small-molecule drug called MCB-613 was previously identified to impact USP15 stability. We will also determine how MCB-613 impacts the stability of the full-length USP15 and the truncation mutants. The above structure-function studies will determine regions within USP15 that regulate its stability. The discovery of mechanisms that regulate USP15 stability will allow the development of new therapeutic strategies that target USP15 in ovarian cancer cells.

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V

EVALUATING THE EFFECTS OF EARLY LIFE STRESS ON THE NUCLEUS ACCUMBENS AND HIPPOCAMPUS AND THEIR ASSOCIATED BEHAVIORS IN MICE

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Early life stress (ELS) caused by adverse experiences during developmental periods results in social and cognitive deficits that persist into adulthood and poses a significant risk factor for neuropsychiatric disorders later in life. The hippocampus, a brain region involved in memory, and the nucleus accumbens (NAc), a brain region involved in motivation, largely develop during early life and are stress sensitive, making them particularly vulnerable to the effects of ELS. However, the impacts of ELS on the morphology and function of the NAc and hippocampus are currently unknown. We hypothesize that ELS increases anxiety and depressive-like behaviors and disrupts learning and memory in adulthood due to reduced dendritic branching in the hippocampus and NAc. To induce ELS, mice were exposed to limited bedding and nesting (LBN) during postnatal days (P) 0-10 (LBN-10) or 0-28 (LBN-28). Control mice remained in normal nesting conditions. Maternal behavior was evaluated from P9-P16 to evaluate the differences in maternal care given to the pups. At P45, anxiety and depressive-like behaviors were tested using the open field, social interaction, and sucrose preference tests. Learning and memory was measured with the Y-maze, and blood collection was used to measure corticosterone levels to assess the stress levels. We will repeat these measures at P90 to assess potential differences between adolescence and adulthood. Then, we will use Golgi-staining to analyze the dendritic morphology of hippocampal and NAc neurons. A better understanding of the neurological impacts of early life stress may increase efforts to develop better preventative measures and identify a mechanistic pathway by which these potential alterations occur.

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FORMALIZING PHYSICS EQUATIONS IN THE LEAN THEOREM PROVER

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Scientists and engineers write scientific computing software to solve problems, but sometimes these programs have bugs. Usual programming languages like Python, Java or MATLAB immediately detect syntax errors - errors like missing a semicolon or misspelling a keyword. However, these programming languages don't detect semantic errors - such as using an incorrect form of an equation in a function. To help the scientific community achieve bug free codes, we are exploring a programming language called Lean Theorem Prover, which has been developed by

mathematicians for theorem proving. Lean allows users to state math theorems in code and write proofs about them, automatically checking whether the proofs are correct. By writing scientific equations in Lean, we can use Lean to detect both semantic and syntax errors, ensuring the code is correct. In this way, Lean can ensure the correctness of the codes in a way that other programming languages cannot. To illustrate this new approach to writing code in scientific computing, we consider Kepler's Third Law. Using theorems and tactics from mathlib, Lean's math library, we show how Kepler's Third Law is related to various equations of motion in physics. Formalizing theorems in Lean helps to verify the theorems previously written and also develop new theorems.

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THE EFFECTS OF SUCROSE EXPOSURE ON BEHAVIOR TOWARD DRUGS IN *CAENORHABDITIS ELEGANT*

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Over the years, the rise of sugar in consumer products has continually increased. The average American adult consumes twice the daily sugar content recommendation and this overconsumption of sugar begins during adolescence. Consequently, high sugar consumption increases the risk of health issues such as obesity and cardiovascular diseases. Another risk of a high sugar diet is that sugar causes the release of dopamine and opioids which can result in addictive tendencies. Drug addiction impacts behavioral and neurological function which can result in binging, withdrawal, and substance-seeking which can be seen from high sugar diets. Sucrose, a disaccharide made of glucose and fructose, is a sugar refined from sugar cane known as "table sugar". The purpose of this study was to study how sucrose affects *Caenorhabditis elegans* behavior and if sucrose could be considered a gateway drug for substance abuse. It was hypothesized that an increase in this sugar concentration would increase attraction towards ethanol and nicotine. Wildtype worms were synchronized and lifelong exposed to increasing concentrations of sucrose. A chemotaxis assay was utilized to test C. *elegans* preference towards ethanol and nicotine. Also, a thrashing assay was conducted to measure motility comparing the effect of lifelong sucrose exposure in the acute response to ethanol. The results of the chemotaxis displayed a positive nicotine preference that rose as sugar concentration increased regarding the sucrose exposed C. *elegans*. The thrashing assay index displayed an increase in thrashes as the concentration of sucrose rose. To test if these effects were applicable to other sugars, we conducted the same experiments with glucose and fructose. However, the pattern observed for sucrose was not presented in the other sugars. The data suggests that a high sucrose diet could act as a gateway for substance abuse. Further research on the neurological responses related to sucrose is needed.

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W

INVESTIGATING HYDROGEL DESALINATION OF EGYPTIAN LIMESTONE OBJECTS USING NMR-MOUSE SPECTROSCOPY

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Soluble salts contained within Egyptian limestone objects are a major challenge for the Cultural Heritage field. Fluctuations in humidity during storage can cause these salts to dissolve, migrate, and recrystallize leading to delamination, flaking, and general loss of structural stability of the object. While full submersion into water has been used as a successful treatment approach, especially fragile objects require a gentler method, such as use of a poultice or gel to draw out the salts. This project monitors and evaluates the efficacy of a 3% agarose hydrogel treatment for desalination using a Profiler NMR-MOUSE spectrometer. This portable, non-invasive analytical technique affords in-situ depth profile measurements of the stone and hydrogel throughout treatment to observe the egress of salt water from stone to gel and T_2 (spin-spin) relaxation experiments to track changes in the salinity in the stone over the course of the treatment. Preliminary data shows a decrease in T_2* decay time of water in the stone over 5 days, indicative of a lower concentration of salt after treatment, suggesting the time needed for the agarose hydrogel to desalinate the stone. The use of two different organic polymer consolidants, B-72 and Tetraethyl orthosilicate (TEOS), and their effect on the desalination process were also investigated. In addition, ICP-MS, SEM-EDX, and a series of microchemical tests were employed to analyze the salt composition of powder which had delaminated from three Egyptian limestone objects found in the Walters Art Museum's collection. Quantitative evidence of Na^+, K^+, and Mg^{2+} cations were found in each sample in addition to the likely presence of phosphates, sulfates, and chlorides. This project advanced knowledge of the use of agarose hydrogels in the desalination of fragile objects and shows the utility of interdisciplinary collaboration in the Cultural Heritage field.

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PROTEIN OPTIMIZATION OF HIV-1 MYRISTOYLATED MATRIX FOR FUTURE MEMBRANE BINDING STUDIES

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Human Immunodeficiency Virus (HIV) is a retrovirus. Like all retroviruses, it encodes for a Gag polyprotein that helps direct the assembly of the virus particles in the host cells. The beginning of this Gag polyprotein house the Matrix protein which has an N terminal myristoyl group which is instrumental in anchoring it and the entire Gag complex to the plasma membrane which is the beginning of the assembly process that also directs envelope glycoproteins to these viral assembly sites. We are looking at the protein optimization of the HIV myristoylated Matrix protein to do assembly experiments using a nanodisc model to mimic the plasma membrane. Our vector exists in the pET Duet plasmid which allows expression of both the HIVMA protein and the codon optimized N-myristoyltransferase enzyme (NMT). This is a co- translational process that is mediated by the first six amino acids at the N-terminal of the protein referred to as the myristoyl signal (MGARAS). The myristoyl group attachment consists of a 14 Carbon Fatty acid chain that gets anchored in the hydrophobic layer of the membrane. During transport, this group is sequestered in the protein folded structure. Once in contact with the membrane, this group pops out to anchor it to the plasma membrane. This process is referred to as the myristoyl switch. Some of the challenges faced in purifying the myristoylated matrix are due to the protein being extremely pH dependent. At lower pH's, the myristoyl group is exposed and aggregates to be precipitated out in solution. To optimize protein purification, we use different buffer conditions with a range of pHs. Our findings indicate that the myristoylated Matrix is sequestered at a pH of 7, allowing us to further optimize the expression and purification of this protein.

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AN EXPLORATORY STUDY OF MMWAVE RADAR FOR OBJECT DETECTION AND CLASSIFICATION

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Millimeter wave radar (mmWave radar) operates on the principle that transmits short wavelength electromagnetic waves and estimates the range, velocity, and angle of the objects that obstruct the waves. This project investigates the use of mmWave radar to identify objects that can obstruct UGVs during navigation. The hypothesis is that a system using mmWave Radar can identify and classify the objects (both visible on the surface and hidden beneath the ground) that can potentially obstruct the navigation of UGVs. As mmWave radar is less sensitive to changes in environmental lighting conditions and contains a degree of permeability, it can assist in UGV navigation in situations where a camera would be incapacitated– for example, in low visibility

weather or environments, such as on foggy days or in tall grass (where objects can be obscured). Additionally, mmWave radar does not collect personally identifying information, which is a cause of concern while using RGB cameras. In this work, we perform a literature study on the existing systems that use mmWave radar for object identification and classification. We further explore the various parameters and features of mmWave Radar that can effectively help identify and classify objects on both indoor surfaces, such as tiles, carpets, tables, and outdoor surfaces, such as mulch and grass. In a preliminary study, we collect range doppler and 3D point cloud data of objects pertaining to different materials (plastic, metal, cardboard, and paper). The idea is to find the suitable features of mmWave Radar to identify static objects that are visible/hidden beneath the surfaces. At the end of the study, we present a taxonomy of mmWave Radar features that are suitable for different applications.

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Y

ANALYZING CHITIN COMPOSITION OF *ASPERGILLUS NIDULANS* CELL WALLS IN VARIOUS STRAINS AND DIFFERENT MORPHOLOGIES.

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The vast majority of the world's manufactured materials are nonrenewable and energy-intensive to produce. Viable alternatives must be developed, and "mycelial materials" made from filamentous fungi are an exciting option. A number of different mycelial materials have been reported and, compared to traditional materials, have lower raw-material cost, require less energy to produce, and are eminently biodegradable. These mycelial materials can have a diverse range of mechanical properties, similar to many traditional materials (e.g., leather, foam, wood), due to the complex morphology of filamentous fungi. We hypothesize that genetic means can be used to tune fungal morphological phenotypes, and that these phenotypes can be combined to enable the design of mycelial materials with specific sets of material properties. In regard to phenotype, of particular interest is the fungal cell wall. It is a composite material, composed of several biological polymers, primarily chitin, glucan and protein. Chitin plays an important role as it aggregates to form microfibrils which impart tremendous strength to the wall. We hypothesize that altered wall-chitin content will lead to materials with different mechanical properties. To test this hypothesis, we used the model fungus *Aspergillus nidulans* and sought to measure the chitin content of different strains, under different growth conditions, and different morphologies. The results from our study will eventually help us to understand if there is a correlation between chitin content and mechanical properties of mycelial materials made from these strains or with these morphologies.

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ENHANCING ROBOTIC NAVIGATION: AN EVALUATION OF SINGLE AND MULTI-OBJECTIVE REINFORCEMENT LEARNING STRATEGIES

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This study presents a comparative analysis between single-objective and multi-objective reinforcement learning methods for training a robot to navigate effectively to an end goal while efficiently avoiding obstacles. Traditional reinforcement learning techniques, namely Deep Q-Network (DQN), Deep Deterministic Policy Gradient (DDPG), and Twin Delayed DDPG (TD3), have been evaluated using the Gazebo simulation framework in a variety of environments with parameters such as random goal and robot starting locations. These methods provide a numerical reward to the robot, offering an indication of action quality in relation to the goal. However, their limitations become apparent in complex settings where multiple, potentially conflicting, objectives are present. To address these limitations, we propose an approach employing Multi-Objective Reinforcement Learning (MORL). By modifying the reward function to return a vector of rewards, each pertaining to a distinct objective, the robot learns a policy that effectively balances the different goals, aiming to achieve a Pareto optimal solution. This comparative study highlights the potential for MORL in complex, dynamic robotic navigation tasks, setting the stage for future investigations into more adaptable and robust robotic behaviors. ***Keywords***–Reinforcement Learning, Single-Objective Reinforcement Learning, Multi-Objective Reinforcement Learning (MORL), Robotic Navigation, Dynamic Environments.

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Z

INVESTIGATING THE IMPACT OF SHINY COWBIRDS ON PUERTO RICAN ORIOLES

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Islands harbor a significant portion of the world's biodiversity, but they also face high rates of endemic species extinction, largely due to invasive species. The Puerto Rican Oriole (*Icterus portoricensis*) is an understudied tropical songbird, and understanding the threats it faces is crucial for conservation. The Shiny Cowbird (*Molothrus bonariensis*) is a brood parasite that poses a serious threat to the orioles. We hypothesized that cowbirds follow orioles to locate their nests for parasitism. To investigate this, we conducted 91-point counts to survey bird populations in the Hacienda la Esperanza nature reserve in Puerto Rico. When we detected orioles, 79% of the time we also detected cowbirds in the same count, indicating a significant association (p-value = 0.02). In contrast, cowbirds did now show any significant association with any of the other species in our counts. This suggests that cowbirds are specifically tracking orioles, thus having a disproportionate impact on them. Our findings highlight the need for targeted conservation strategies to protect the Puerto Rican Oriole from the detrimental effects of cowbird parasitism.

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ANALYZING PRIVACY AND UTILITY TRADEOFFS IN SMART HOMES

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The goal of this research is to explore the trade-off that exists between privacy and utility when using smart devices at home. Smart speakers, doorbells, and TVs are becoming pervasive, but raise important privacy concerns. For instance, by collecting audio and video, one could learn private information about us such as our age, emotions, socioeconomic status, and health conditions. To increase trust, there is a need to inform people about potentially sensitive inferences that can be made about them by smart devices and give them a choice to consent to it. We have built a prototype of a framework, using open-source code and AI/ML algorithms, that generates inferences about an individual based on audio (e.g., speech data collected by a smart speaker) and video (e.g., images collected by a smart security camera). The framework also allows the user to select which of these inferences should be "hidden". We have explored different mechanisms to hide those inferences while preserving utility such as: removing specific portions of audio/video that can lead to whether the person might be facing a respiratory disease or modifying the pitch/tone to hide their age and mood.