Summer Undergraduate Research Fest

SURF'S UP!

August 7, 2024

University Center Ballroom and ENG 027
University of Maryland, Baltimore County

Hosted by the College of Natural and Mathematical Sciences

UMBC

Hosted by the

COLLEGE OF NATURAL AND MATHEMATICAL SCIENCES

surf.umbc.edu

Message from the Dean

Welcome to the 2024 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,

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

SURF'S UP!

Participating Programs

The College of Natural and Mathematical Sciences and the Summer Undergraduate Research Fest (SURF) team would like to recognize the support provided by these participating programs that provide research experiences, professional development, and funding for undergraduate researchers during the summer and academic year. These research programs, funded by the federal government, private foundations, and the University, provide career focused research training for undergraduate researchers.

Schedule

8:15 a.m.
Presenter Check-in (University Center Ballroom Lobby)

8:15 – 8:45 p.m.
Poster Set-up (UC Ballroom) & Continental Breakfast (UC Ballroom Lounge)

9 – 9:15 a.m.
SURF Opening Remarks (Engineering Building, Room 027)

9:15 – 9:45 a.m.
Lightning Round Talks (ENG 027)

10 – 10:45 a.m
Poster Session #1 (UC Ballroom)

10:45 – 11:30 a.m.
Poster Session #2 UC Ballroom)

11:45 a.m.
Closing, Special Recognition of Mentors and Presenters (ENG 027)

PRESENTERS:
surf.umbc.edu/2024-presenters

ABSTRACTS:
surf.umbc.edu/2024-abstracts

Lightning Talks!!

The UMBC Beckman Scholars will lead the SURF 2024 Lightning talks. In these condensed presentations, researchers are allotted 5 minutes and may use up to five slides with the intent of sparking conversation and collaborations across disciplines. Six SURF presenters have been selected. Due to time constraints, there will not be an opportunity for Q&A following the individual talks.

Baltimore SCIART
sciart.umbc.edu

Beckman Scholars Program
Arnold and Mabel Beckman Foundation
cnms.umbc.edu/beckman-scholars-program-at-umbc

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

Institute of Marine and Environmental Technology (IMET)
imet.usmd.edu

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

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

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

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

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

NSF-REU in Biochemical, Environmental, and MOlecular Research in Engineering (BEMORE)
bemore.umbc.edu

NSF-REU in Online Interdisciplinary Big Data Analytics in Science and Engineering
bigdatareu.umbc.edu

NSF-REU in Smart Computing and Communications
reu-scc.umbc.edu

Translational Life Science Technology
shadygrove.umbc.edu/program

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

Research Mentors 2024

Jorge Almodovar
UMBC
Chemical, Biochemical and Environmental Engineering

Songon An
UMBC
Biochemistry and Molecular Biology

Bipendra Basnyat
UMBC
Information Systems

Joseph Bennett
UMBC
Chemistry

Charles Bieberic
UMBC
Biological Sciences

Lee Blaney
UMBC
Chemical, Biochemical and Environmental Engineering

Alberto Bosque-Pardos
The George Washington University
Immunology, and Tropical Medicine

Rachel Brewster
UMBC
Biological Sciences

Özgür Çapraz
UMBC
Chemical, Biochemical and Environmental Engineering

Chengpeng Chen
UMBC
Chemistry

Karen Chen
UMBC
Information Systems

Li Cheung
National Cancer Institute, National Institutes of Health
Mathematics & Statistics

Lauren Clay
UMBC
Emergency and Disaster Health Systems

Emon Dey
UMBC
Information Systems

Marylia Duarte Batista
UMBC
Chemical, Biochemical and Environmental Engineering

Ivan Erill
UMBC
Biological Sciences

Indrajeet Ghosh
UMBC
Information Systems

Matthias Gobbert
UMBC
Mathematics & Statistics

Todd Gould
University of Maryland School of Medicine
Psychiatry

Erin Green
UMBC
Biological Sciences

Brian Grossman
UMBC
Biochemistry and Molecular Biology

Justine Anne Guevarra
UMBC
Biological Sciences

Zachary Hartman
Duke University
Pathology and Integrative Immunology

Christopher Hennigan
UMBC
Chemical, Biochemical and Environmental Engineering

Vandana Janeja
UMBC
Information Systems

Tyler Josephson
UMBC
Chemical, Biochemical and Environmental Engineering

Lisa Kelly
UMBC
Chemistry

Usman Ali Khan
UMBC
Mechanical Engineering

Sanjeev Kumar
UMBC
Center for Advanced Sensor Technology

Alicia (Hyun Jin) Lee
Carnegie Mellon University
Human Computer Interaction

Tara LeGates
UMBC
Biological Sciences

Jeff Leips
UMBC
Biological Sciences

Weihong Lin
UMBC
Biological Sciences

Daniel Lobo
UMBC
Biological Sciences

Deepa Madan
UMBC
Mechanical Engineering

Petar Maksimovic
Johns Hopkins University
Physics

Christine Mallinson
UMBC
Center for Social Science Scholarship

Brea Manuel
UMBC
Biochemistry and Molecular Biology

Mark Marten
UMBC
Chemical, Biochemical and Environmental Engineering

Stephen Miller
UMBC
Biological Sciences

Molly Mollica
UMBC
Mechanical Engineering

Camilla Pacifici
Space Telescope Science Institute
Astronomy

Achuth Padmanabhan
UMBC
Biological Sciences

continued...

Bradford Peercy
UMBC
Mathematics & Statistics

Marcin Ptaszek
UMBC
Chemistry

Jessica Queen
The Johns Hopkins School of Medicine
Infectious Diseases

Govind Rao
UMBC
Chemical, Biochemical and Environmental Engineering

Jean-Pierre Raufman
University of Maryland School of Medicine
Biochemistry and Molecular Biology

Anuradha Ravi
UMBC
Information Systems

Dominik Reichert
National Eye Institute
Biochemistry and Molecular Biology

Ryan Robucci
UMBC
Computer Science & Electrical Engineering

Zeev Rosenzweig
UMBC
Chemistry

Katherine Savell
NIDA
Neuroscience

Herana Seneviratne
UMBC
Biochemistry and Molecular Biology

Karndeep Singh
UMBC
Biochemistry and Molecular Biology

Venkatesh Srinivasan
UMBC
Chemical, Biochemical and Environmental Engineering

Michelle Starz-Gaiano
UMBC
Biological Sciences

Jennifer Sullivan
Brown University
Public Health

Michael Summers
UMBC
Biochemistry and Molecular Biology

Ali Tokay
UMBC
Geography and Environmental Systems

Paris Von Lockette
UMBC
Mechanical Engineering

Fernando Vonhoff
UMBC
Biological Sciences

Jianwu Wang
UMBC
Information Systems

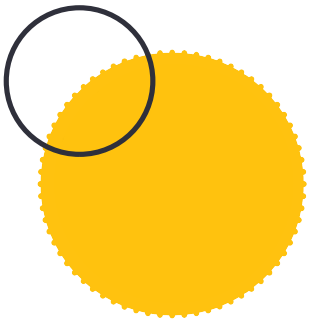
Lin Weihong
UMBC
Biological Sciences

Rebecca Williams
UMBC
Computer Science & Electrical Engineering

TseHuai Wu
UMBC
Mechanical Engineering

Lira Yoon
UMBC
Psychology

Natasha Zachara
Johns Hopkins Medical Institute
Biochemistry and Molecular Biology

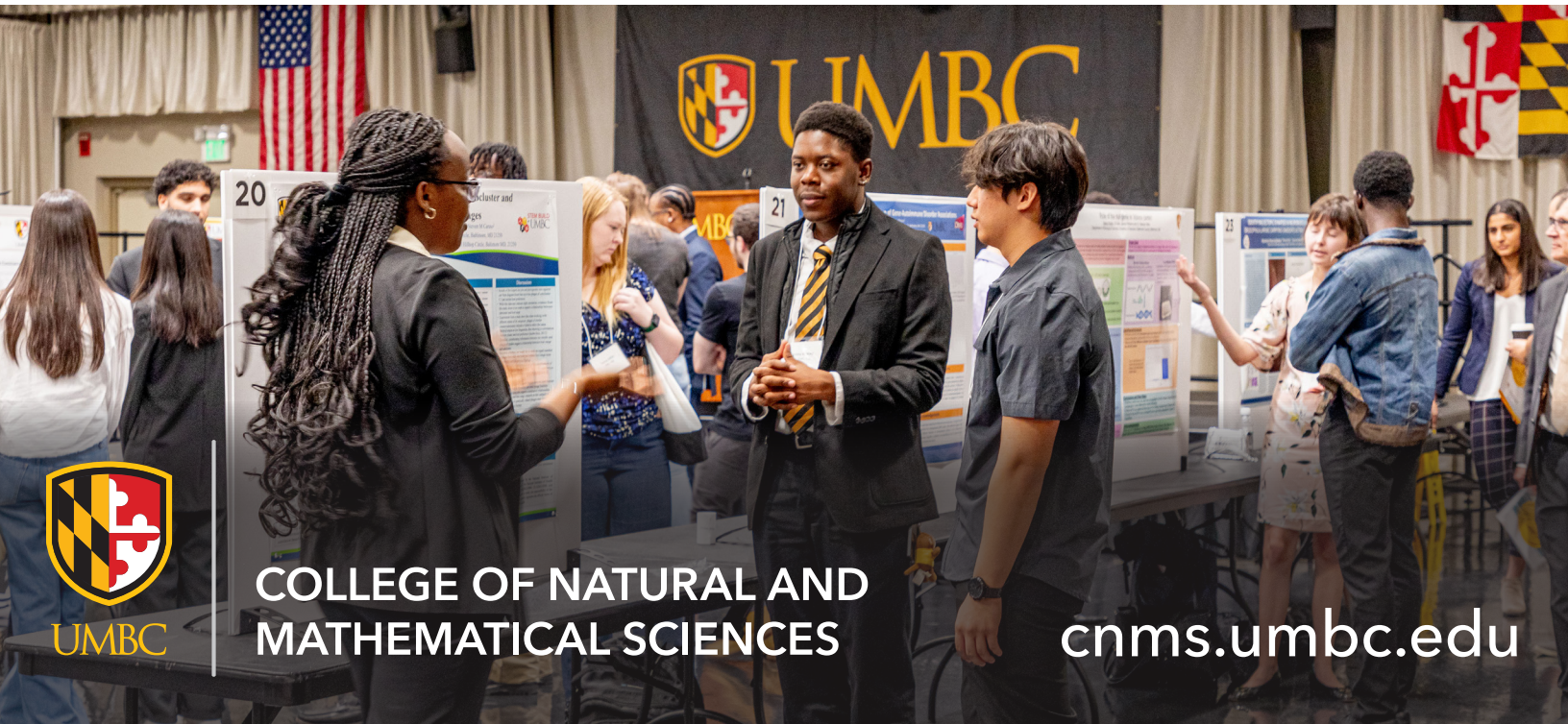


Special Thanks

The Annual Summer Undergraduate Research Fest (SURF) hosted by the College of Natural and Mathematical Sciences (CNMS) highlights the research conducted by undergraduates at UMBC over the summer. SURF enriches the research experience of more than 100 undergraduate researchers each summer, setting them on a path to become researchers and leaders in their chosen fields. SURF also exposes the broader UMBC community to the remarkable scientific contributions of the participating undergraduates.

The college would like to extend a special thank you to the Meyerhoff Scholars Program for their support of SURF 2024. We would also like to extend our appreciation to the federal and state agencies and private institutions and foundations that provide funding to UMBC. Their support creates research opportunities for students matriculating at UMBC and other institutions to conduct research at UMBC and gain valuable experience and mentoring from our outstanding faculty.

UMBC welcomes further philanthropic support for SURF from our alumni and friends. If you or your organization is interested in making a gift to support summer research and SURF, please visit our giving site (umbc.edu/giving) or contact the Office of Institutional Advancement (oia.umbc.edu) to learn more. Thank you!



A

THE EFFECTS OF RETINOIDS IN TREATING TWO CANCER CELL LINES

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In the DC metropolitan Area, cervical cancer and liver cancer are prevalent. Retinoids derived from Vitamin A have been successfully used in the treatment of different cancers. They can regulate cellular proliferation, differentiation, immune function, and apoptosis. In this research, we studied these two prevalent cancers, the CaSki cell line, a model of cervical cancer, and SNU-475 a model of liver hepatocellular carcinoma. The aim of the study was to examine the effects of retinoids in treating both cervical and liver cancers using these two cell lines. We hypothesized that the retinoids would inhibit cell proliferation and enhance Natural Killer (NK) mediated killing. We used three retinoids, Alitretinoin, Tazarotene Acid and AM80. These retinoids target the receptors RAR and RXR, which are expressed in these cell lines. First, we performed a clonogenic assay by plating 500 cells with 1μM of each retinoid and incubated them at 37º for 13 days. We used the stereomicroscope to count the colony growth. To determine if the retinoids enhance NK-mediated killing we used the DELFIA Europium assay. NK cells were co-cultured for 1 hour with BATDA labeled CaSki cells at a 1:1 effector to target ratio in the presence or absence of 1μM of each retinoid with or without IL15. We measured lysis by time-resolved fluorescence of TDA. From the clonogenic assay, we found that retinoids significantly decreased clonal expansion of both CaSki and SNU-475. From the cytotoxic assay we observed enhanced killing of the CaSki cell line with the addition of the retinoids. These results suggest that retinoids are blocking proliferation and enhancing the ability of NK cells to kill CaSki and SNU-475 cells. This research will assist future preclinical and clinical trials in treating different types of cancer malignancies and may be a new avenue to explore future treatment strategies.

This research was supported by GW Summer Program Advancing Research on Cancer (GW-SPARC).

EXPLORING THE FATE OF RNA IN MOLONEY MURINE LEUKEMIA VIRUS

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Moloney Murine Leukemia Virus (MoMuLV) is a gammaretrovirus that causes leukemia and neurological diseases within rodentia. It has been studied since the 1950s as a model to further understand the underlying mechanisms of all retroviruses. Our laboratory mainly focuses on Human Immunodeficiency Virus type-1 (HIV-1), most particularly the segment of the HIV-1 RNA genome necessary 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 (^{Cap}1G) in which the cap is sequestered, and the monomeric conformation adapted by 5'-capped RNAs that begin with two or three guanosines (^{Cap}2G and ^{Cap}3G respectively) where the cap is exposed. We refer to viruses containing these different beginning sites as having transcriptional start site heterogeneity. Inversely, MoMuLV utilizes a promoter with a single transcriptional start site, ^{Cap}1G, from which both packaging and translation occur. We wish to understand what drives RNA packaging versus translation in a retrovirus that contains a single start site. Through our exploration of this process, we hope to gain insight into the machinery that older viruses have conserved for millennia and provide indications of possible characteristics that newer retroviruses may exhibit in the future. Like HIV-1, we suspect that MoMuLV's genome fate is driven by dimerization dependent cap sequestration. We plan to explore the behavior of MoMuLV's genome in vitro by determining the conditions needed for the RNA to function as a monomer or dimer, capping the RNA to get an accurate representation of the virus, and exploring cap sequestration via electrophoretic mobility shift assays. After capping the RNA, to confirm its conformation we will use nuclear magnetic resonance. We will then test the hypothesis that cap sequestration is necessary for packaging in MoMuLV, as previous studies have shown it is essential in HIV-1.

Support for this research was provided by Howard Hughes Medical Institute and NIH/NIAID grant (#5R01AI50498).

THE ROLE OF RWP-RK TRANSCRIPTION FACTORS IN THE EVOLUTION OF CELL DIFFERENTIATION IN VOLVOX CARTERI

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Volvox carteri is a multicellular eukaryotic algal model for investigating cell-differentiation and its evolution. Volvox is ideal for these studies because it has complete division of labor between just two cell types: motile somatic cells and non-motile reproductive gonidia, with differentiation decided in early cell division cycles. Here we are testing the roles of the rwp3 and rwp6 genes (encode members of the RWP-RK transcription factor family) in regulating the gonidial cell type, because previous RNAseq analyses revealed that these genes are highly expressed in gonidia and are repressed by overexpression of a gene (rlsD) that represses cell growth. The RWP-RK transcription factor family has been previously determined to activate embryogenesis in plants, and the involvement of these genes in this role in other green lineages suggests their function may be phylogenetically conserved. We are using CRISPR to knock out rwp3 and rwp6 in V. carteri, and to this end we have ligated annealed oligos into an sgRNA vector to generate two guide RNA expression plasmids for each rwp gene that will be co-transformed with a Cas9-expression plasmid. We are also workshopping a long-PCR method to amplify a full-length version of rwp3 to clone into a Volvox overexpression vector. We will select for successful Volvox transformants using hygromycin resistance genes in our constructs, identify CRISPR mutants by sequencing guide RNA target regions, and characterize the growth and development of mutant and overexpression strains through different stages of the life cycle. These experiments will provide insights into the functions of the rwp-rk genes in Volvox and their potential role in gonidial development. Furthermore, characterizing these genes should lead to a better understanding of origins of cell differentiation in Volvox and possibly other species.

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

THE ROLE OF SUGAR FREE FROSTING (SFF) IN CELL MIGRATION: ESSENTIAL OR NOT?

Boluwatinsola Alawode, Alex George, Michelle Starz-Gaiano

Department of Biological Sciences,University of Maryland: Baltimore County, 1000 Hilltop Cir, Baltimore, MD 21250

Cell migration is essential for proper growth, life, and development in most multicellular organisms. To better understand the mechanisms of cell migration, our lab utilizes fruit flies because they have a well-conserved genome with humans, they are easy to genetically manipulate, and their tissues are transparent so we can observe cells directly. We study border cells and follow their journey as they migrate during oogenesis. We hypothesize that

glycosylation, a type of protein modification where sugar is attached to proteins, might be required for various regulatory steps that govern border cell migration. Sugars could be attached to adhesion proteins, the extracellular signals border cells respond to that guide the migration, and/or the cellular receptors for those signals.This research is focused on a specific gene, sugar free frosting (sff), which is required for some types of protein glycosylation. We are testing whether or not sff is needed for migration in the border cells. We plan to use RNA interference to decrease the function of sff in certain cell types. We used different strains of flies to knock down sff in the border cells or in the surrounding cells that act as the migratory substrate (nurse cells). We also examined homozygous mutants for sff. We are currently in the process of analyzing the data to determine whether or not the Sff protein is needed in border cell migration in the ovaries. The results that we collect could be helpful to understand the potential role of sff in border cell migration along with helping to determine the potential role of sff in cell migration generally.

This research is funded in part by the Meyerhoff program and NSF grants IOS-2303857 to MSG.

ABOVE THE CLOUDS: E-CIGARETTE AND THE OLFACTORY SYSTEM

Kafui Ameko, Leyla Aydin, Agnes Koodaly, Saheedat Odetayo, Sean O'Sullivan, Farhan Augustine, Tatsuya Ogura, Ph.D, Weihong Lin, Ph.D.

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

In the past few decades, electronic cigarette (e-cigarette) usage has increased, affecting millions, particularly youth and adolescent populations. E-cigarettes have chemicals that are toxic, which can damage the olfactory system. Damage to the olfactory system has been proposed as an early marker for neurological and cognitive disorders. It is hypothesized that after continued exposure to toxic chemicals, there is a disruption to the olfactory epithelium, olfactory bulb and connected brain regions such as the limbic system. These are the sites for perception of smell, memory and emotional responses. To understand how e-cigarette exposure may disrupt olfaction, olfactory-guided behaviors are being assessed through various behavioral assays, using mice as a model organism for olfaction. The tests are the T-maze choice preference test, buried food test, and the odor threshold test. These behavioral assays are designed to measure a mouse's attraction to known chemicals, in this case urine and water, a mouse's sense of smell for finding food and investigating new odors. I utilized one control group with e-liquid solvent, and two groups of flavored e-liquid containing nicotine with or without added heavy metals. These various groups will help us ascertain the effects of e-liquid components on olfactory disruptions. At this time, I am in the process of gaining results from its research and experiments. I am working with the

mice and will repeat the experiments at 4 and 8 weeks of the exposure. This ensures that the data is taken from over time and can show the short term effects of exposure on the olfactory system. I expect at both time points a decrease in olfactory sensitivity via reduced attraction to urine of the opposite sex, increased food discovery time, and lowered sensitivity to e-liquid components.

Support for this research was provided by the UMB Accelerated Translational Incubator Pilot (ATIP) Grant, the Department of Biological Sciences and the Meyerhoff Scholars Program.

INVESTIGATING eIF4E RECRUITMENT TO HIV-1 5′-CAPPED RNAs

Efua Amoa, Maxwell K. Amoh-Mayes, Brandon Fonseca, Karndeep Singh, Michael Summers, Ph.D.

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

The human immunodeficiency virus (HIV) is an infectious agent that erodes the body's immune system, impacting more than 39 million individuals worldwide. As of 2021, the most common treatment is antiretroviral therapy (ART) which is used to suppress HIV replication and mitigate viral load. Our laboratory's research focuses on the conserved regions of the HIV-1 RNA genome, particularly the 5′-UTR/5′-Leader (5′-L), which plays a crucial role in regulating viral functions like translation and packaging. The 5′-L can adopt two conformations depending on the heterogeneous transcriptional start site usage: ^{Cap}1G RNAs adopt a dimeric conformation, whereas ^{Cap}3G RNAs adopt a monomeric conformation.

This project aims to: 1) investigate whether and how structural elements of the monomer regulate binding of a cap binding protein, eIF4E, and 2) solve a RNA-protein complex structure of a structured 5′-capped RNA interacting with eIF4E. To achieve these goals, we optimized in vitro transcription and capping to produce 5′-capped RNAs. Next, we used an electrophoretic mobility shift assay (EMSA) and isothermal titration calorimetry (ITC) to study the binding interactions between the 5′-capped RNAs and eIF4E. Additionally, nuclear magnetic resonance (NMR) spectroscopy will be utilized to understand the structural changes of 5′-capped RNAs in the absence and presence of eIF4E.

The anticipated outcomes of this research include insights into the structural regulation of eIF4E binding by the monomeric 5′-L and the first detailed RNA-protein complex structure involving a 5′-capped RNA and eIF4E. This work will enhance our understanding of HIV-1 translation mechanisms and contribute to the development of potential therapeutic strategies targeting HIV-1 RNA-protein interactions.

Funding for this research is supported by the Howard Hughes Medical Institute and the National Institute of Health (NIH, 5R01AI150498).

INVESTIGATING EIF4E RECRUITMENT TO HIV-1 5′-CAPPED RNA'S

Maxwell K. Amoh-Mayes, Efua Amoa, Brandon Fonseca, Karndeep Singh,

Michael Summers, Ph.D.

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The human immunodeficiency virus (HIV) is an infectious agent that erodes the body's immune system, impacting more than 39 million individuals worldwide. As of 2021, the most common treatment is antiretroviral therapy (ART) which is used to suppress HIV replication and mitigate viral load. Our laboratory's research focuses on the conserved regions of the HIV-1 RNA genome, particularly the 5′-UTR/5′-Leader (5′-L), which plays a crucial role in regulating viral functions like translation and packaging. The 5′-L can adopt two conformations depending on the heterogeneous transcriptional start site usage: ^{Cap}1G RNAs adopt a dimeric conformation, whereas ^{Cap}3G RNAs adopt a monomeric conformation.

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Funding for this research is supported by the Howard Hughes Medical Institute and the National Institute of Health (NIH, 5R01AI150498).

UNDERSTANDING GAG: RRE INTERACTIONS IN HIV-1: CHARACTERIZING COMPETITION BETWEEN REV AND GAG FOR RRE STEM 1

Desi Amprey[1], Jake Han[2,3], Trinity Bentsil[1], Arjun Kanjarpane[1], Aarsh Shah[1], Gizaw Melese[1] , Lucia Rodriguez[1] , Jan Marchant[1] , Michael F. Summers[1,2]

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In order for HIV-1 to replicate, it requires unspliced and incompletely spliced RNA transcripts to be exported out of the nucleus. This process is prohibited by cell surveillance systems that prevent unspliced RNA from leaving the nucleus. HIV-1 accounts for these prerequisites by binding the unspliced RNA, the Rev Response Element (RRE) to a nuclear-cytoplasmic transporting protein termed Rev. There are two binding sites associated with high affinity between Rev and RRE, Stem 1A (S1A) and Stem 2B (S2B). Rev transports the RRE into the cytoplasm where Gag, a protein that mediates genome packaging, binds to the RRE at sites close or overlapping with Rev near S1A. This proposes the idea that Gag displaces Rev for binding on the RRE. We theorize that these Rev and Gag interactions demonstrate competition on S1A. The project seeks to characterize and identify these protein-RNA interactions as well as the possibility of competition between Rev and Gag. We utilize a variety of truncated and modified forms of Stem 1 RNA, Rev proteins, as well as a nucleocapsid domain of Gag, NC in EMSA, ITC, SEC, and NMR experiments. We theorize that NC may bind to S1A preferentially over Rev and that the purine-rich bulge is the high affinity site for Gag-RRE binding. The ability to understand and identify these binding events can help characterize which proteins bind when, if there is possible competition, and further allows us to understand HIV-1 replication processes to aid in designing medication that targets HIV-1 replication.

Funding for this research is supported by the Howard Hughes Medical Institute, the NIH/NIAID #5R01AI150498, and the NIH NIH #U54AI170660.

COMPARING COLLAGEN EXTRACTION METHODS AND PREPARATION METHODS FOR USE IN LAYER-BY-LAYER COATINGS

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[1] Ralph E. Martin Department of Chemical Engineering, University of Arkansas

[2] Department of Chemical, Biochemical and Environmental Engineering, University of Maryland Baltimore County

Autografts are the most common treatment option used in peripheral nerve injuries. However, nerve guide conduits (NGCs) require fewer surgeries than autografts[1]. NGCs are only applicable as a treatment option when the injury is less than one centimeter in length. This restriction is caused by the lack of critical resources needed by the extracellular matrix in cellular regeneration[2]. The NGC surface is the main location for regeneration[2]. The NGC surface can be modified with Layer-by-Layer (LbL) coatings, and the characterizations of heparin-collagen (HEP/COL) LbL coatings have been studied extensively by our group [3,4]. We have previously shown that using HEP/COL bilayers can increase the human Schwann cell viability on the surface of NGCs[3]. This work aims to expand our previous research by comparing the viability of human Schwann cells on HEP/COL surfaces constructed using collagen from two different manufacturers, Integra and Biomarix. Biomatrix Collagen pretreated with acetic acid and diluted with pH 4.0 buffer yielded similar results in cell viability experiments to Integra Collagen dissolved in pH 4.0 buffer. The manufacturer protocol for biomatrix collagen in LbL also increased cell viability for hSCs. FTIR testing showed that Biomatrix Collagen and Integra Collagen were almost identical. Overall, our research demonstrates that the HEP/COL coatings are a suitable strategy to increase cell viability using collagen from different manufacturers.

References

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This project was supported by the National Science Foundation (#2050728).

FORMALIZING PROOFS REGARDING CHEMICAL EQUILIBRIUM USING LEAN THEOREM PROVER

Shashane Anderson, Oscar Matemb, Tyler Josephson

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A surplus of metal toxins is being emitted into our water due to our use of chemicals, in industries ranging from fuels to cosmetics. Ingestion or contact with these metals risks anemia and cancer, as well as damage to the liver, kidneys, and intestines. Metal toxins released into water form many species. Among the reactions that occur are precipitation, acid-base, and oxidation-reduction reactions. The freeware chemical equilibrium model, Visual MINTEQ, can simulate these water reactions and more closely observe the behavior of various species in water.

How can we verify the credibility of chemical equilibrium software like Visual MINTEQ? We are developing a novel approach to software development using the Lean Theorem Prover to create programs accompanied by proofs of their correctness. In this work, we aim to bring that approach to chemical equilibrium calculations. While the Lean Theorem Prover is mostly used for mathematical proofs, it is not just limited to purely mathematical theories. In this situation, it was used to confirm the math behind the theory of chemical equilibrium calculations.

To compare our LeanChemEQ software with Visual MINTEQ, we also used Visual MINTEQ to generate predictions of chemical speciation for mixtures of varying complexities, by collecting data including output species, log K, and change in enthalpy values. After this the types and structure of the substances and chemical equations are defined, followed by verification of chemical equilibria using Lean.

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INVESTIGATING THE MECHANISMS UNDERLYING CONVERGENCE OF THE NEURAL FOLDS

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Failure of the neural tube (the precursor of the brain and spinal cord) to close during neurulation often results in neural tube defects. During neurulation, a flat sheet of epithelial cells, known as the neural plate, undergoes a series of cell shape changes in order to form a tube-like structure. The neural folds lie at the edges of the neural plate, and their elevation and fusion at the dorsal midline is crucial for neural tube formation. Recent work from our lab has revealed that cellular mechanisms that shape the neural tube in the anterior region are very similar to those of other vertebrates, with the formation of neural hingepoints and neural folds. My project aims to uncover molecular mechanisms that mediate neural fold convergence. Laminin, an extracellular matrix glycoprotein involved in cell signaling, is restricted to the border of the neural plate where the neural folds lie. I hypothesize that Laminin provides a spatial cue for the neural fold cells to meet at the dorsal midline. I found that the process of neural fold fusion in Laminin-depleted early somitogenesis embryos are not affected using the emx3 neural plate marker, suggesting that neural fold elevation may still occur properly after the depletion of this gene. Strikingly, I observed that the dorsal midline of the neural tube is disrupted in Laminin knock down 24 hour old embryos using the wnt1a gene marker, suggesting that Laminin is required for neural fold fusion. I am currently examining the younger stage of 10 somites after the neural folds fuse and the older stage of 24 hours to perform an analysis at the cellular level. My data so far supports my hypothesis that the late stage of neural fold fusion is disrupted in Laminin-depleted embryos.

Support for this research was provided by the HHMI grant (52008090) and funding from the URISE NIH grant (PAR-21-146).

B

USING CONDITIONED PLACE PREFERENCE TO EXAMINE CONTEXTUAL LEARNING WITH FOOD AND SOCIAL REWARDS

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Our ability to establish learned associations between rewarding stimuli and contextual information is important for survival. For instance, determining and remembering the location of

a food source is critical for successfully obtaining food. In our research, we aim to better understand the neuronal circuits in the brain that allow for these associations to occur.

We developed a behavioral paradigm where mice would be conditioned to learn these associations. We used conditioned place preference (CPP) to determine whether mice could learn to associate contextual cues in the arena with rewards, in this case food and social interaction. Over time, the mouse associates the specific compartment with the pleasurable or aversive effects of the stimulus.

We followed a 5 day conditioning protocol. On the habituation day, the mouse explores the apparatus with two distinctly textured compartments, one dotted, one striped, and a neutral corridor to measure any initial preferences. On the conditioning days (days 2-4), the mouse is repeatedly paired with a specific compartment and the reward or no reward in the other compartment. On the final day of the experiment, the mouse is once again given free access to explore the apparatus. Behavior is monitored by a camera mounted above the arena and AnyMaze is used to measure the time spent in each chamber of the arena. Increased time spent in the compartment associated with the reward after conditioning indicates CPP. Our preliminary results suggest that mice show CPP in response to food rewards. This work will lay a foundation for investigating the neuronal mechanisms in the brain associated with learning, memory, and behavior modulation.

We would like to thank the LeGates lab for their input and support. This work was funded by startup funds from UMBC.

INVESTIGATING THE INTERACTIONS OF STAUFEN1 WITH THE HIV-1 GENOME AND GAG POLYPROTEIN

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HIV-1 is a retrovirus that creates new infectious virions by packaging its genomic RNA and exporting it from the host cell. HIV-1 can progress into the chronic immune disease AIDS, and treatments for HIV-1 are necessary to terminate virion reproduction, but are changing due to the

rapidly mutating nature of the virus. One aspect of the viral lifecycle that is missing any therapeutic approaches is the selective genome packaging. Therefore, it is important to understand this process to be able to develop novel treatments. The HIV-1 Gag polyprotein contains a Nucleocapsid (NC) domain that binds to a region on the genome called the Core Encapsidation Signal (CES). It is the smallest region that is required to get packaged. The Gag protein is mediated to the cell membrane of the host cell where complex formation, budding, and fission occur. Studies have shown that the host cell factor Staufen1, a double stranded RNA binding protein, is hijacked by HIV-1 to facilitate in packaging as Staufen1 interacts with both the viral RNA and the Gag protein.

To understand better how HIV-1 utilizes host cellular factors to increase its infectivity, we are studying the binding interactions between Gag, CES, and Staufen1. Using gel studies, we were able to show that full-length Staufen1 forms a trimeric complex with NC and CES. We are currently testing the four double stranded RNA binding domains of Staufen1, which we already expressed and purified, on their ability to individually interact with the NC-CES complex. The ultimate goal of this project will be to structurally unravel the molecular mechanism of this trimeric interaction and thereby elucidating the role of Staufen1 in the HIV-1 viral assembly. This structure may show us specific target sites that can get used to develop novel therapeutics that will help us fight against this ongoing pandemic.

Funding for this research is supported by the Howard Hughes Medical Institute, NIH 5R01AI150498, NIH AI170660, NIH (NIAID) 1K99AI186598-01.

MECHANISTIC REGULATION OF PLANARIAN SHAPE DURING REGENERATION

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Planarians are flatworms that can regenerate a full organism from almost any amputated piece. Furthermore, their adult body size is extremely plastic, as they can grow and degrow (shrink in size) depending on the amount of food available. Our previous studies have shown that the dynamics of growth and degrowth in planarians follow the same linear rate in terms of length and width over time. Here we demonstrate that the regeneration of transversally amputated pieces, however, follows a different behavior from growth and degrowth as the worm increases its length while reducing its width. Utilizing this data, we were able to perform simulations modeling the regeneration of the worms. Progress is still ongoing to calibrate the simulation to match the observed data. Towards this, we have improved the computational simulation of whole-body planarian dynamics. Crucially, these improvements include the optimization of a

flux slope limiting function, which is critical in determining the motion of the cells according to the governing differential equations modeling cell adhesion. The simulation was then run on a high-performance computer cluster both with and without the optimizations in the flux slope limiting function. This optimization resulted in an improvement in the run time of a simulation by 60%. Future work will calibrate the model to the experimental data, and possibly identify unknown factors necessary for the regulation of regeneration in planarians.

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DESIGNING STRUCTURAL MEMBERS USING BIO-INSPIRED DESIGN PRIMITIVES

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Bio-inspired design is the process in which innovation aims to emulate nature's patterns, processes, and/or materials to develop efficient solutions to design challenges. Although there exists countless examples of engineering advancements that have taken influence from nature, the constraints and contextual factors inherent to bio-inspired design remain insufficiently examined. Therefore, this project investigates nature's innate ability to optimize for a set of structural elements when designing fibrous structures. Multiphysics modeling software, COMSOL, is used to generate finite element models (FEMs) to analyze the response of downward force applied to ends of various simulated fibrous branch structures. Trends in these responses are analyzed using a theoretical model to compare maximum (σmax) and minimum stresses (σmin), displacements (Δy), and strain energies (U) across different reinforcement geometries. The validity of these trends will soon be tested by applying the same loading conditions to the real models of tree branch structures in bending.

Continuing with this research would allow researchers and designers to explore the advantages, limitations, and conditions underlying bio-inspired designs. This investigation postulates that

nature's ability to produce optimal designs for fibrous structures adheres to a set of "design rules", creating a strong potential to integrate these principles into design-based software to enhance the design processes of its users.

This research was partially funded by the Meyerhoff Scholarship Program alongside the USM LSAMP program, supported by NSF LSAMP Award # 2207374.

TESTING THE HETEROGENEITY OF PROSTATE INFLAMMATION USING GFP AS AN EX-VIVO MARKER USING DIFFERENT LINEAGES OF A CHRONIC INFLAMMATORY MOUSE MODEL

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Chronic inflammation is thought to be a risk factor in the initiation of malignancy for approximately 25% of all human cancers. Emerging evidence suggests that long term chronic inflammation can be a precursor for prostate cancer, however due to lack of definitive data, this has not yet been verified. In order to determine the role of long-term chronic inflammation in prostate cancer initiation, we have developed an inducible mouse model of chronic inflammation localized to the mouse prostate gland, termed RIG, that recapitulates key features observed in human cases. The RIG model is characterized by the expression of a pro-inflammatory cytokine Interleukin-1 Beta (IL-1ß) and, Green Fluorescent Protein (GFP), as a marker, using the Tet-On system in which the reverse Tetracycline transactivator (rTta) under the control of Hoxb13 promoter in an inducible fashion selectively in the mouse prostate gland. To study the aforementioned effects of long-term chronic inflammation developed multiple lineages of RIG mice to determine the impact of inflammation expressivity and its impact on pre-neoplastic lesions. We hypothesized the heterogeneity of expressivity of pro-inflammatory cytokines will result in differences of pre-neoplastic lesions. To test this hypothesis, we performed in vivo imaging followed by necroscopy of the prostates and quantifying GFP expression using multiple imaging and histopathological analyses to identify lineage-dependent effects on severity of prostate cancer initiation using GFP as a marker. Our preliminary data demonstrates that prostate inflammation is strongly correlated with GFP, however, there is no conclusive data to determine which lineage is the most robust for expressivity of chronic inflammation. In future studies, we plan to understand the molecular basis for premalignant lesions, where we will also aim to quantify the expression of immune cell markers to identify the specific type of immune cells that contribute to prostate inflammation.

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

INVESTIGATING THE INTERACTIONS OF STAUFEN1 WITH THE HIV-1 GENOME AND GAG POLYPROTEIN

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HIV-1 is a retrovirus that creates new infectious virions by packaging its genomic RNA and exporting it from the host cell. HIV-1 can progress into the chronic immune disease AIDS, and treatments for HIV-1 are necessary to terminate virion reproduction, but are changing due to the rapidly mutating nature of the virus. One aspect of the viral lifecycle that is missing any therapeutic approaches is the selective genome packaging. Therefore, it is important to understand this process to be able to develop novel treatments. The HIV-1 Gag polyprotein contains a Nucleocapsid (NC) domain that binds to a region on the genome called the Core Encapsidation Signal (CES). It is the smallest region that is required to get packaged. The Gag protein is mediated to the cell membrane of the host cell where complex formation, budding, and fission occur. Studies have shown that the host cell factor Staufen1, a double stranded RNA binding protein, is hijacked by HIV-1 to facilitate in packaging as Staufen1 interacts with both the viral RNA and the Gag protein.

To understand better how HIV-1 utilizes host cellular factors to increase its infectivity, we are studying the binding interactions between Gag, CES, and Staufen1. Using gel studies, we were able to show that full-length Staufen1 forms a trimeric complex with NC and CES. We are currently testing the four double stranded RNA binding domains of Staufen1, which we already expressed and purified, on their ability to individually interact with the NC-CES complex. The ultimate goal of this project will be to structurally unravel the molecular mechanism of this trimeric interaction and thereby elucidating the role of Staufen1 in the HIV-1 viral assembly. This structure may show us specific target sites that can get used to develop novel therapeutics that will help us fight against this ongoing pandemic.

Funding for this research is supported by the Howard Hughes Medical Institute, NIH 5R01AI150498, NIH AI170660, NIH (NIAID) 1K99AI186598-01.

UNDERSTANDING GAG: RRE INTERACTIONS IN HIV-1: CHARACTERIZING COMPETITION BETWEEN REV AND GAG FOR RRE STEM 1

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In order for HIV-1 to replicate, it requires unspliced and incompletely spliced RNA transcripts to be exported out of the nucleus. This process is prohibited by cell surveillance systems that prevent unspliced RNA from leaving the nucleus. HIV-1 accounts for these prerequisites by binding the unspliced RNA, the Rev Response Element (RRE) to a nuclear-cytoplasmic transporting protein termed Rev. There are two binding sites associated with high affinity between Rev and RRE, Stem 1A (S1A) and Stem 2B (S2B). Rev transports the RRE into the cytoplasm where Gag, a protein that mediates genome packaging, binds to the RRE at sites close or overlapping with Rev near S1A. This proposes the idea that Gag displaces Rev for binding on the RRE. We theorize that these Rev and Gag interactions demonstrate competition on S1A. The project seeks to characterize and identify these protein-RNA interactions as well as the possibility of competition between Rev and Gag. We utilize a variety of truncated and modified forms of Stem 1 RNA, Rev proteins, as well as a nucleocapsid domain of Gag, NC in EMSA, ITC, SEC, and NMR experiments. We theorize that NC may bind to S1A preferentially over Rev and that the purine-rich bulge is the high affinity site for Gag-RRE binding. The ability to understand and identify these binding events can help characterize which proteins bind when, if there is possible competition, and further allows us to understand HIV-1 replication processes to aid in designing medication that targets HIV-1 replication.

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OPTIMIZING CAPPING METHODS FOR THE MOLONEY MURINE LEUKEMIA VIRUS

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The Moloney Murine Leukemia Virus (MoMuLV) is a distant relative of the Human Immunodeficiency Virus (HIV). Both MoMuLV and HIV are retroviruses and thus possess a dimeric RNA genome headed by a 5'UTR that regulates many processes, such as dimerization, packaging, and translation. HIV-1 has been discovered to possess a heterogeneous transcriptional start site. This allows the virus to transcribe single-stranded RNA with either 1, 2, or 3 guanosines following the 5'cap. The difference in guanosines plays a strong deterministic factor in the fate of RNA to be packaged or translated. However, MoMuLV contains a unique transcription start site, meaning the virus consists of only one start site, indicated by ^{Cap}1G. To understand what drives RNA packaging versus translation in a retrovirus that contains unique start sites, we must cap our RNA, which has been proven difficult. The RNA forms secondary structures as our full 5' leader is significant in size. Therefore, we aim to optimize capping methods for RNAs where capping may be difficult. The capping enzyme, the Faustovirus Capping Enzyme (FCE), has recently been discovered. It possesses unique properties compared to the currently utilized capping enzyme, Vaccinia Virus Capping Enzyme (VVCE), such as greater thermostability and single polypeptide structure, allowing for greater purification through size exclusion chromatography. While we optimize our synthesis and application of the enzyme, we are also interested in exploring co-transcriptional capping. In vivo, capping of all RNA occurs co-transcriptionally. We are working with different methods, such as position-selective labeling of RNA (PLOR), to cap our RNA. PLOR is a method of stopping transcription prematurely to allow for modification or labeling of RNA. In our case, we aim to halt transcription to allow for capping and proceed with transcription. Our work will provide more efficient and affordable capping methods within the scientific field.

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INVESTIGATING THE INTERACTION BETWEEN CHROMATIN REGULATOR SET4 AND TRANSCRIPTION FACTOR UPC2

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Set4 is a Saccharomyces cerevisiae (baker's yeast) protein part of the Set3 SET subdomain family. The mammalian proteins in this family, MLL5 and SETD5, are implicated in cancer and neurodevelopmental disorders such as autism spectrum disorder and attention-deficit/hyperactivity disorder. In researching how this protein works in yeast, we hope that these results can help those who study mammalian proteins. We hypothesize that Set4 acts as a scaffolding protein, interacting with chromatin-interacting proteins to change gene expression during stress. Using yeast cells grown in hypoxia to induce Set4 expression, we first did a co-immunoprecipitation assay of Set4 and Upc2. Upc2 is a protein previously shown to possibly interact with Set4 by mass spectrometry. Doing a pulldown of the FLAG-tagged Set4 protein, we observed whether Upc2 and Set4 interact with each other by Western blot analysis. The first Western blot of the co-immunoprecipitation assay found a direct interaction between Upc2 and Set4. However, upon repeating this experiment subsequently to confirm the results, we couldn't see an interaction again in Western blot analysis. There is possibly an interaction between Upc2 and Set4 and further optimization of the co-immunoprecipitation technique needs to be done to confirm this.

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INVESTIGATING BINDING INTERACTIONS BETWEEN THE MONOMERIC HIV-1 RNA GENOME AND CAP-DEPENDENT TRANSLATIONAL MACHINERY, EIF4E

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The human immunodeficiency virus type-1 (HIV-1) affects over 39 million people worldwide. Current treatments include a drug cocktail consisting of inhibitors that target multiple steps of the viral replication cycle. However, many patients experience disruptive side effects due to the copious amount of drugs needed to combat the high viral mutation rates. Thus, our laboratory investigates a highly conserved segment of the HIV-1 RNA genome, the 5′-Leader (5′-L), as it is less susceptible to mutations. This region controls 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. Our group focuses on the monomeric conformation's exposed 5′-cap. This exposed 5′-cap recognizes cellular cap-dependent translation machinery, such as the protein eIF4E, in order to produce HIV viral proteins. However, it is unknown how structural elements of the HIV-1 RNA genome impact binding of eIF4E. We designed and purified 5′-capped RNA oligos with varying lengths of the TAR hairpin and the unstructured poly-A to determine if these regions of the RNAs affect eIF4E binding. We investigated the binding interactions between eIF4E and these truncated RNAs both qualitatively and quantitatively; electrophoretic mobility shift assays (EMSAs) confirmed binding and isothermal titration calorimetry (ITC) measured binding affinities. Our ITC data revealed that the HIV-1 5′-capped RNA bound >2 folds tighter to eIF4E than to the 5′-cap alone, supporting our hypothesis that electrostatic interactions between structural elements of the RNA and the eIF4E protein affect recruitment and binding. This research can be utilized to pinpoint a potential drug target within the highly conserved across HIV-1 RNA genome.

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C

EFFECT OF COPPER INTAKE ON SURVIVAL RATES OF WT AND APPLd D. MELANOGASTER FLIES

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In humans, the Amyloid Precursor Protein (APP) is a highly conserved transmembrane protein encoded by the APP gene and expressed ubiquitously. It is mainly found in neuronal cell bodies and is involved in various cellular processes that regulate the nervous system. APP is also

associated with Alzheimer's Disease (AD). In the Drosophila melanogaster fly model, the APP homolog is called Amyloid Precursor Protein-Like (APPL), which shares similar roles and characteristics with APP, including extracellular binding domains for copper (Cu) and zinc (Zn). It has been hypothesized that because these domains regulate cellular copper and zinc levels, APP/APPL may be protective against metal-induced toxicity. In our broader study, we focus on the effect of metal-induced toxicity on flight performance and survival by feeding copper at increasing concentrations to WT and APPLd (loss-of-function mutant) flies. We run either a flight assay or a survival assay for each group of flies. Preliminary data shows that in the two cohorts for the flight assay, most WT flies in the food vials with the highest concentration of copper die by day 10. This project particularly focuses on the survival assay, wherein we will examine how many flies are still alive on days 2, 4, 6, 8, 10, 12, 15, 20, and 30 after transferring them to vials with copper-embedded food. By day 6, data shows that at least two WT flies from each copper concentration died while the APPLd flies were unaffected, suggesting WT flies are more susceptible to metal-induced toxicity. Overall, this study will contribute to our understanding of the protein APPL in the context of metal exposure in flies, and eventually, apply this knowledge in studying APP in humans.

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IMAGE EXPLORATION WITH JDAVIZ, THE JAMES WEBB SPACE TELESCOPE DATA ANALYSIS AND VISUALIZATION TOOL

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The James Webb Space Telescope (JWST) was designed to look further back into the Universe than ever before. The amount and quality of data received, with both imaging and spectroscopy, is unprecedented. This is why, at the Space Telescope Science Institute (STScI), engineers worked on developing modern and efficient data analysis and visualization tools tailored to work with JWST data.

This summer, I worked along with these engineers to add functionality to the Imviz configuration of the open-source software Jdaviz (JWST Data Analysis and Visualization tool). Imviz is an image viewer that can be used to load images and perform quick-look analysis. The

initial workflow allowed users to upload an image along with a corresponding catalog, after which Imviz would flag all the sources (galaxies and stars) within the image. However, the scientific and astronomy community requested the additional functionality to highlight on the image the position of user-selected sources in the catalog, and zoom in on those sources. Using python, javascript, and html scripts I addressed these requests. Specifically, I included the possibility to visualize the catalog within the tool in the form of a table and I incorporated the ability to select various rows from this table and then zoom into the viewer at the appropriate location. These features make searching through long catalogs of data and locating interesting sources more accessible.

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2D MXENES AS CHEMICAL SENSORS IN THE ART MUSEUM ENVIRONMENT

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It is necessary to monitor for contaminants in museum environments which could be harmful to the longevity of the artwork, whether on display or in storage. These contaminants may originate from the atmosphere as cleaning agents or as pollutants, or be introduced from incompatible storage materials. The interaction between the contaminants and works of art can affect rates of discoloration, tearing, and cause irreversible damage to structural integrity. Using a class of 2D materials called MXenes, we can take advantage of their nanoscale dimensions and large surface area to develop thin film sensors for deployment in museums to detect pollutants and increase the longevity of works of art. The research we performed develops computational models, based on density functional theory, to look at stable MXene surface structures, their energies, and interactions with adsorbates. The MXene we analyzed was titanium carbide (Ti3C2), where we analyzed the effects of fluorine, oxygen, and hydroxide surface terminations with common small molecule adsorbates. Here we compare changes in adsorption energies, bond lengths, and surface chemistry, where our preliminary results can be used to inform synthesis by developing interfacial surface chemistry structure-property relationships of MXenes.

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.

DIVERSITY AND ROLE OF FUSOBACTERIUM NUCLEATUM AND CLOSTRIDIOIDES DIFFICILE IN COLORECTAL CANCER: INSIGHTS FROM A MALAYSIAN COHORT

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Fusobacterium nucleatum and Clostridioides difficile have been epidemiologically and experimentally linked to colorectal cancer (CRC). F. nucleatum, a member of the human oropharyngeal microbiota, is a heterogeneous species consisting of four subspecies: animalis, nucleatum, polymorphum, and vincentii. C. difficile can be asymptomatically carried in the colon or cause diarrheal disease through its key virulence protein, Toxin B (TcdB). Recent animal studies have demonstrated that chronic C. difficile colonization can promote colon tumorigenesis. This study aims to quantify, isolate, and characterize F. nucleatum and C. difficile within a CRC cohort. We hypothesized that these bacteria would exhibit distinct prevalence patterns in tumors compared to paired normal tissue, providing insights into their potential roles in CRC pathogenesis. Tumor and normal tissue samples from 110 Malaysian CRC patients underwent analysis using 16S rRNA amplicon sequencing, PCR, and culturing on selective media. In parallel, fixed tissues were screened for biofilms using FISH with the EUB338 oligonucleotide probe. F. nucleatum was significantly enriched in the tumor microbiome compared to paired normal tissue ($p<0.0001$), predominantly subspecies animalis, and only in biofilm-positive tumors. Although C. difficile abundance did not differ between tumors and normal tissues, it was more frequently detected in tumors that displayed biofilms. 29 tumors were positive for C. difficile by sequencing and 8 strains have been successfully isolated with 7 of the isolates having the tcdB gene. In parallel, 13 Fusobacterium strains have been isolated, with subspecies animalis most frequently isolated. C. difficile and F. nucleatum subsp. animalis are both associated with colon tumor biofilms. These findings underscore the complex microbial dynamics in CRC, implicating both Fusobacterium nucleatum and Clostridioides difficile in disease pathogenesis. Future directions include whole genome sequencing of isolated strains, and measurement of TcdB toxin activity of C. difficile isolates using an in vitro cytotoxicity assay.

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INVESTIGATING THE INDUCTION OF EPITHELIAL MESENCHYMAL TRANSITION THROUGH HYPOXIA TOLERANT ZEBRAFISH EMBRYOS

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Hypoxia (reduced oxygen concentration) can negatively impact the ability of an organism to maintain homeostasis. Hypoxia has been linked to a number of human diseases, such as obstructive pulmonary disease, diabetes, and sickle cell anemia. Furthermore, recent studies have shown that hypoxia promotes cancer metastasis via the induction of Epithelial-Mesenchymal Transition (EMT). EMT is characterized by the loss of Epithelial polarity and the gain of Mesenchymal characteristics, such as the ability to migrate. Hypoxia promotes EMT in cancer cells via the stabilization of the transcription factor called Hypoxia inducible factor 1-Alpha (HIF1a), and the activation of downstream targets such as SNAIL, SLUG, AND TWIST. Interestingly, these EMT-inducing transcription factors were also identified in an RNA Sequencing screen for genes that mediate hypoxia tolerance in a Zebrafish embryo, conducted by Timothy Hufford (a former member of Brewster Lab).

The goal of my research project is to investigate the hypothesis that EMT can also be induced in normal cells of a developing organism in response to anoxia. More specifically, I aim to determine which cell populations express EMT genes Slug(Snai2), ZEB1, ADAM12 and HEY1 and to examine whether these cells have an altered morphology or physiology that would enhance their survival in hypoxia. Towards this goal, I have focused my efforts this summer on analyzing RNA expression of my candidates using wholemount in situ hybridization and analyzing protein expression using immunolabeling of Zebrafish embryos exposed to anoxia (zero oxygen) and normoxic (normal oxygen) controls. Overall, this project is meant to uncover where and why EMT responses are induced in normal cells in response to low oxygen.

I would like to acknowledge my mentor Dr. Rachel Brewster, and the rest of the Brewster Lab for their support and contributions. Also, thank you to the Meyerhoff Scholars program and the Howard Hughes Medical Institute Undergraduate Scholars Program. I was supported by the HHMI grant (52008090); the Brewster lab was funded by NIH/NIGMS (1R01GM154212-01).

HARNESSING ANION EXCHANGE TO DETECT AND REMOVE PFAS OF VARYING CHAIN LENGTHS

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Per- and polyfluoroalkyl substances (PFAS) are emerging contaminants of concern facing increasing regulations from the Environmental Protection Agency. Growing reports of their carcinogenic and teratogenic effects demand their improved detection and removal. Anion exchange is one widely used method that is currently being developed to accomplish these two goals. By refining uptake mechanisms of anion exchangers, limitations such as removal of ultrashort- and short-chain PFAS can be addressed in water treatment. On the other hand, constructing monitoring devices such as passive samplers requires identification of membrane selectivity to choose a membrane that detects PFAS of interest. However, depending on chemical properties such as carbon chain length and other parameters, these materials' selectivity for PFAS can vary. To identify the processes governing membrane selectivity, the PFAS selectivity of membranes of differing exchange capacities were compared. Using liquid chromatography mass spectrometry, selectivity coefficients of the membranes were then determined for PFAS of varying chain lengths. These results corroborated our hypothesis that selectivity by chain length depends on the ability of active sites to interfere with hydrophobic interactions. Further exploring the applications of this principle mechanism, resins were experimentally loaded with hydrated ferric (oxy)hydroxide nanoparticles (HFO) to increase selectivity for short-chain PFAS. Selectivity coefficients of the parent resins for the ultrashort-chain PFAS trifluoroacetic acetate were determined by conducting isotherm experiments. Resins thereafter were modified through the deposition of HFO nanoparticles. Isotherm results of modified resins were fit to a Langmuir model and the maximum adsorption capacity between altered and parent resins were compared. The HFO-loaded resin's maximum adsorption capacity for the ultrashort-chain PFAS was strengthened over the parent resins, suggesting selectivity of current commercial anion exchange materials can be enhanced for ultrashort-chain PFAS.

This project was supported by the National Science Foundation (#2050728) and the Strategic Environmental Research and Development Program (ER20-1073, ER24-4224).

MARKOV MODELING FOR ORAL PRE-CANCER NATURAL HISTORY

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Oral cancers, frequently arising from precancerous conditions, rank among the most prevalent cancers globally, especially in Southeast Asia. Commonly attributed to smoking, drinking, and chewing habits, these cancers demand robust screening strategies. This study employs Markov modeling to estimate the transition probabilities between various health states(healthy, precancerous, and cancerous)in high-risk individuals. Utilizing data from a Taiwanese cohort with 2874 lesions, including 785 cancer patients and 1711 controls, the model follows transitions over a five-year period. The analysis aims to provide evidence-based recommendations for oral cancer screening practices, particularly in regions with high incidences of high-risk individuals. The model's structure assumes transitions are state-dependent and does not consider previous states, adhering to the Markov assumption.

We anticipate that this Markov model will accurately estimate the probabilities of transitioning from a healthy state to precancerous and cancerous states in high-risk populations. Moreover, the study is expected to provide actionable insights for health policymakers in regions with high oral cancer prevalence, guiding the development of targeted screening and prevention programs. The model's outcomes may also contribute to refining current screening guidelines, leading to more efficient resource allocation and better health outcomes for at-risk populations.

This project has been funded in whole or part with the federal fund from the National Cancer Institute, National Institutes of Health, under contract HHSN261200800001E.

EXPLORATION OF MODELING & SIMULATION FOR VEHICLE DYNAMICS

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VxSIM™ is a new and innovative modeling and simulation software by Dynamic Dimension Technologies LLC (DDT), with many configurable objects and vehicles, and complex terrains. VxSIM™ can display physics-based movement from their vehicles and simulate a variety of data from the models using different sensors, like a GPS sensor, proximity sensors, a Light Detection and Ranging (LIDAR) sensor, and more. The goal of this project is to explore the software for non-military research projects as currently the major customer of VxSIM™ is US Navy. Exploring the software allows users to get familiar with the user interface and makes it easier to find new and testable aspects of the software. A basic but important function explored throughout the more than 5 weeks of testing was how to make the vehicles move. There are 3 main configurations for movement: kinematics, dynamics, and path-follower. All the 3 configurations are explored using various vehicle models. Various examples and video demonstrations were recorded. Those examples will be used as instructional material for future classes teaching VxSIM™.

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

THE ORIGINS OF CELL DIFFERENTIATION: KNOCK OUT OF VOLVOX CARTERI RLSD GENE

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Volvox carteri serves as an excellent model organism for studying the origins of multicellular cell differentiation, as it contains two distinct cell types (germ and soma) that evolved relatively recently (~200 MYA) compared to other differentiated organisms. The rlsD gene is a paralog of regA, the gene responsible for determining somatic cell fate in V. carteri, and both genes were generated by duplication of a proto-rlsD gene in an undifferentiated Volvox ancestor. Overexpression of rlsD represses genes required for light and sulfur acquisition, and represses growth, suggesting that rlsD regulates growth based on nutrient/resource availability. The goal of this work is to use CRISPR to knock out the rlsD gene to test this idea and gain further insight

into the role of rlsD. Determining the function of rlsD will provide insights into the shared role of the progenitor rlsD/regA gene and gain an understanding of how the co-option of regA led to the ability to create differentiated cells. Thus far we have generated two guide RNA gene constructs by ligating annealed oligonucleotides into a guide RNA expression vector, and we are in the process of transforming them into V. carteri through gold particle bombardment, along with a plasmid containing the Cas9 gene. We will screen transformants by sequencing the region targeted by the guide RNAs to identify mutants. Once we have obtained mutants, we will grow them under various stress-inducing conditions including light and sulfur deprivation to determine survivability compared to wild-type. Understanding the regulatory roles of rlsD should provide important insights into the evolution of cell differentiation in Volvox.

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

D

INVESTIGATING THE INTERACTIONS OF STAUFEN1 WITH THE HIV-1 GENOME AND GAG POLYPROTEIN

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HIV-1 is a retrovirus that creates new infectious virions by packaging its genomic RNA and exporting it from the host cell. HIV-1 can progress into the chronic immune disease AIDS, and treatments for HIV-1 are necessary to terminate virion reproduction, but are changing due to the rapidly mutating nature of the virus. One aspect of the viral lifecycle that is missing any therapeutic approaches is the selective genome packaging. Therefore, it is important to understand this process to be able to develop novel treatments. The HIV-1 Gag polyprotein contains a Nucleocapsid (NC) domain that binds to a region on the genome called the Core Encapsidation Signal (CES). It is the smallest region that is required to get packaged. The Gag protein is mediated to the cell membrane of the host cell where complex formation, budding, and

fission occur. Studies have shown that the host cell factor Staufen1, a double stranded RNA binding protein, is hijacked by HIV-1 to facilitate in packaging as Staufen1 interacts with both the viral RNA and the Gag protein.

To understand better how HIV-1 utilizes host cellular factors to increase its infectivity, we are studying the binding interactions between Gag, CES, and Staufen1. Using gel studies, we were able to show that full-length Staufen1 forms a trimeric complex with NC and CES. We are currently testing the four double stranded RNA binding domains of Staufen1, which we already expressed and purified, on their ability to individually interact with the NC-CES complex. The ultimate goal of this project will be to structurally unravel the molecular mechanism of this trimeric interaction and thereby elucidating the role of Staufen1 in the HIV-1 viral assembly. This structure may show us specific target sites that can get used to develop novel therapeutics that will help us fight against this ongoing pandemic.

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UNDERSTANDING THE DEGRADATION OF VERDIGRIS & DEVELOPING STRATEGIES FOR ITS CONSERVATION IN ARTWORK

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Conservation science focuses on the preservation and protection of artwork. One of the most difficult challenges faced by conservation scientists is understanding how the components of an artwork interact with the environment. For paintings in particular, pigment degradation poses a considerable threat due to altering the color profile of the artworks. The focus of this project was verdigris, an organometallic pigment used in ancient and modern artwork. Its history dates back to ancient times when it was the brightest green pigment available, making it widely used in artwork. Verdigris is known to irreversibly degrade over time. In this project, we studied the degradation profile of verdigris through various thermal and photodegradation experiments. Comparisons between verdigris in solution and as a paint with lipidic binders were studied. Analysis of the degradation was conducted using UV/Vis spectroscopy, FTIR, and NMR. Our results demonstrate that verdigris is both thermally and photosensitive. The next step in our research is employing the use of a member of a new class of transition metal carbide nanomaterials, MXenes, to determine their effects on the degradation profiles of verdigris.

MXenes have demonstrated the capacity to absorb UV light which may prevent direct exposure of verdigris to harmful radiation.

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CHARACTERIZATION OF AROMATASE EXPRESSION IN THE PREFRONTAL CORTEX OF AGED MALE MICE

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The prefrontal cortical area of the brain plays a critical role in executive functioning. Unfortunately, executive functioning declines with aging due to several factors, including inflammation. In other inflammatory disease states, including traumatic brain injury and stroke, the enzyme that synthesizes estrogens, aromatase, is upregulated and has shown anti-inflammatory properties. Aromatase has not been characterized in the aging prefrontal cortex, but I hypothesize there will be upregulation of aromatase in the prefrontal cortex of aged male mice.

Three- and twenty-three-month-old male mice underwent orchiectomy or sham surgery and were given nine weeks to recover before euthanasia and tissue extraction. Brains were cryosectioned at 20 micron increments and processed with florescent in-situ hybridization, RNAscope, probing for aromatase (Cyp19a), neuronal marker (RbFox3), and astrocyte marker (GFAP). Four channel fluorescent images were taken from the prefrontal cortex and processed using Imaris bitplane workstation for cell quantification and colocalization of RNAscope probes. In Imaris, regions of interest were drawn around the infralimbic and prelimbic cortex to determine the expression in these two distinct subregions.

Our laboratory has preliminary evidence to suggest that aromatase is upregulated in the hippocampus, medial amygdala, and basolateral amygdala of aged male mice. Similarly, I predict an upregulation of aromatase in the prefrontal cortex and each of its subregions. Orchiectomized young mice will have significantly more aromatase expression than young intact mice indicating that a decline in peripheral hormone availability may be driving aromatase upregulation in the prefrontal cortex.

We plan to characterize aromatase expression in other brain regions including the nucleus accumbens and claustrum. This work will then relate to the other data collected by Gould lab using the same technique, to create a more complete understanding of the changes in aromatase in the aged male mouse brain.

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EFFECT OF SLBO-DEPENDENT APT DEGRADATION IN A BISTABLE JAK/STAT SYSTEM

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Cell migration is important for many biological functions such as development, wound healing, and cancer metastases. Externally triggered signaling within a cell will determine whether that cell will be motile or idle. Such a signal within epithelial cells is the JAK/STAT receptor-transcription factor combination followed by a cross-repression system between APT and SLBO which determines the paused or active cell fate.

We previously explored the model described by Ge and Stonko's seven variables for gene states, mRNA, and protein for APT and SLBO. These seven differential equations were then simulated

within MATLAB to give a visual outcome for these biochemical processes over time. We also explored the bistability between the two cell fate states in time by showing hysteresis in APT/SLBO as it depends on the STAT level as well as tracking bifurcations in the system. Achieving either of the two steady states depends on initial state variables and a parameter for the STAT level. Now we alter the rate of SLBO-dependent degradation of APT to mimic the effect of micro RNA interference and show a change in the bifurcation. Modeling mathematically the properties of JAK/STAT interactions could help us expand our knowledge of the initiation of cell migration.

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IDENTIFYING AND CHARACTERIZING CLINICALLY RELEVANT BREAST CANCER MODELS OF TUMOR DORMANCY

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Although outcomes have improved for breast cancer (BC) survivors, approximately 30% will eventually succumb to the disease upon locoregional or metastatic recurrence. For estrogen receptor (ER) positive patients, this can occur as many as 30 years post diagnosis with the likelihood of metastatic relapse remaining consistent each year. We previously demonstrated that certain dormant tumor cells maintain both epithelial and mesenchymal features, and can evade the adaptive immune system via induction of Tregs within the microenvironment. Thus, the aim of this study is to determine the universality of these findings and develop reliable models to further study dormant tumor-immune interactions. Syngeneic mouse breast cancer cell lines (D2.OR, TSAE1) were sorted to enrich for epithelial (CD104+) or mesenchymal (CD44+) phenotypes, confirmed via qRT-PCR and RNAseq. A dormancy reporter with non-functional p27 fused to mVenus was added by lentiviral transduction and 3D culture assays were performed by seeding tumor cells on a basement membrane extract. ER activity was assessed in 2D culture by qRT-PCR for ER response gene Greb1 after treatment with 4-hydroxytamoxifen (4-OHT); 3D culture cells were plated with increasing doses of 4-OHT or Fulvestrant. For in vivo studies, 500k cells were implanted into the mammary fat pad of female syngeneic Balb/c mice. In vitro 3D cultures and in vivo implantation demonstrated that the hybrid epithelial/mesenchymal tumor

population was less proliferative than more mesenchymal cells from the same tumor. Treatment with 4-OHT reduced Greb1 mRNA expression, and 3D culture assays revealed that ER antagonism could inhibit colony growth. Finally, immunohistochemistry of tumors confirmed ER protein expression in vivo. Our studies suggest that dormancy-competent tumor cells indeed exist as an independent population with classical epithelial and mesenchymal expression patterns. Importantly, these cells respond to ER antagonism, which supports their usefulness as clinically-relevant models of tumor dormancy and delayed relapse.

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INVESTIGATING THE ROLE OF HYPOXIA IN INDUCING EPITHELIAL TO MESENCHYMAL TRANSITION

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Hypoxia is manifested in many human diseases and, in its most severe form, is detrimental to cell survival. However, hypoxia can also have beneficial outcomes for different cell populations. For example, it induces a transition in cellular architecture, from epithelial to mesenchymal, a process known as EMT. In cancer cells, EMT promotes metastasis (which is beneficial to cancer cells) while in normal development it is essential for gastrulation, neural crest emigration and more. In cancer cells, the molecular pathway inducing EMT involves the stabilization of the transcription factor HIF1a, which activates several key downstream genes, including snail, slug and twist. Interestingly, an RNA seq screen — carried out by a former member of the Brewster lab — aiming to identify genes that mediate hypoxia tolerance in the zebrafish embryo, uncovered multiple genes previously implicated in EMT. Given that major EMT events that occur during development are completed by the embryonic stage at which the screen was carried out, where is EMT activated in the hypoxic zebrafish embryo and what purpose does it serve? My project aims to address these questions by carrying out wholemount in situ hybridization and immunolabeling for candidate genes/proteins. I hypothesize that EMT or partial EMT may be induced in specific embryonic cell populations, maintaining their stemness or promoting their

migration and that such responses are beneficial for hypoxia survival. This study is expected to increase our understanding of organism-level responses to hypoxia and reveal new contexts in which EMT is activated.

Support for this research was provided by the HHMI grant (52008090) and funding from the National Institute of Health/NIGMS (1R01GM154212-01).

AI-CARING: AGENT, CARE COORDINATION, TRUST AND AFFILIATION

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Our research focuses on the coordination and communication between informal caregivers and older adults who face cognitive decline, such as mild cognitive impairment (MCI).

Our method included semi-structured interviews with the older adult and one informal caregiver. The first interview was held at their home because it helped them recall activities, allowed researchers to see the placement of physical materials that they used, and allowed researchers to capture and observe body language. We had two follow-up interviews that allowed researchers to have discussions by pre-analyzing their data to have more insights into each pair's characteristics, communication breakdowns, and care networks. During the interviews, we used our observation field notes to write observations about their body language. After the interview, we transcribed recordings of each session using an automated audio-to-text service which has a disclosure agreement with CMU.

Through ongoing sessions, the research team analyzed the data using affinity diagrams [1]. This method, affinity diagramming, is effective at unpacking relationships within the data and identifying patterns and themes. It is particularly effective when developing and designing new tech. Overall, our goal is to help create technology that allows older adults to live independently for as long as they want at their desired place of residence.

Support for this research was provided by the NSF (2112633), Amazon, and Google.

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2D MXenes AS CHEMICAL SENSORS IN THE ART MUSEUM ENVIRONMENT

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It is necessary to monitor for contaminants in museum environments which could be harmful to the longevity of the artwork, whether on display or in storage. These contaminants may originate from the atmosphere as cleaning agents or as pollutants, or be introduced from incompatible storage materials. The interaction between the contaminants and works of art can affect rates of discoloration, tearing, and cause irreversible damage to structural integrity. Using a class of 2D materials called MXenes, we can take advantage of their nanoscale dimensions and large surface area to develop thin film sensors for deployment in museums to detect pollutants and increase the longevity of works of art. The research we performed develops computational models, based on density functional theory, to look at stable MXene surface structures, their energies, and interactions with adsorbates. The MXene we analyzed was titanium carbide (Ti_3C_2), where we analyzed the effects of fluorine, oxygen, and hydroxide surface terminations with common small molecule adsorbates. Here we compare changes in adsorption energies, bond lengths, and surface chemistry, where our preliminary results can be used to inform synthesis by developing interfacial surface chemistry structure-property relationships of MXenes.

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.

E

EXAMINING GENDER DIFFERENCES IN INTERPRETATION BIAS

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The ability to interpret facial expressions is crucial when navigating everyday life and fostering relationships. Oftentimes, however, facial expressions are ambiguous, making them difficult to interpret and increasing the likelihood that they will be misconstrued. The tendency to misread facial expressions in a negative manner (i.e., a negative interpretation bias), which maintains negative emotions, increases an individual's likelihood of developing emotional disorders. Importantly, women are almost twice as likely as men to be diagnosed with depression or anxiety disorders, but no study has examined gender differences in interpretation bias. This study aimed to examine if men and women differ in their perception of facial expressions with different intensities, ranging from neutral to full-blown emotions, such as anxiety, fear, or happiness.

Participants (N = 146) were recruited from a private university in the midwestern United States and its surrounding communities. Facial pictures were taken from the Karolinska Directed Emotional Faces (KDEF) set, and the software FantaMorph was used to blend a neutral face with an emotional face (angry, fearful, happy). MATLAB and the Psychophysics Toolbox were utilized to show each face appearing for 500 milliseconds, to depict the progression of emotional facial expressions. The participants were told to watch the face develop and click the spacebar once they identified an emotion.

Consistent with the hypothesis, there was a significant gender x emotion interaction, $F(2, 284) = 7.32$, $p = .001$, which was qualified by a significant gender x emotion x behavioral inhibition interaction, $F(2, 284) = 7.04$, $p = .001$. Women identified anger and fear at a significantly lower intensity than men, which was more pronounced in women with higher (vs. lower) levels of behavior inhibition. The study suggests gender and behavior inhibition impact the perception of subtle negative emotions, warranting further investigation into their roles in emotional disorders.

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ASSESSING FOOD INSECURITY DISPARITIES ACROSS VARIOUS RACIAL, ETHNIC, AND SOCIOECONOMIC COUNTIES IN MARYLAND

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Food insecurity is a significant issue in Maryland, with notable differences between regions. In Baltimore City, one of the worst-affected areas, residents frequently face challenges in accessing sufficient and nutritious food due to high poverty rates and limited availability of healthy food options. In contrast, Montgomery County, one of the wealthiest regions, experiences lower levels of food insecurity, but still has pockets of the population dealing with food access issues. Food insecurity leads to poor health outcomes, increased healthcare costs, and hampers educational and economic opportunities. There are disparities in food access and quality based on socioeconomic and demographic factors. This research project investigates food insecurity across different racial and ethnic communities in Maryland counties. Using a comprehensive survey, we assess the frequency of food insecurity, access to food, and the quality and affordability of available food. The survey includes questions on household concerns about food availability, frequency of running out of food, transportation modes used to access food, and the regularity of consuming fresh fruits and vegetables. It also examines the use of food assistance programs and the main barriers to obtaining sufficient and preferred food types. This study aims to provide a nuanced understanding of these disparities and offer data-driven recommendations to address food insecurity in Maryland. The findings will contribute to developing targeted interventions to ensure equitable access to nutritious food for all communities.

This experience was funded in part by the EDUCATE Program at the University of Maryland, Baltimore County (UMBC), which is supported by the National Institute on Drug Abuse (NIDA/NIH) under award R25DA051338.

HARNESSING ANION EXCHANGE TO DETECT AND REMOVE PFAS OF VARYING CHAIN LENGTHS

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Per- and polyfluoroalkyl substances (PFAS) are emerging contaminants of concern facing increasing regulations from the Environmental Protection Agency. Growing reports of their carcinogenic and teratogenic effects demand their improved detection and removal. Anion exchange is one widely used method that is currently being developed to accomplish these two goals. By refining uptake mechanisms of anion exchangers, limitations such as removal of ultrashort- and short-chain PFAS can be addressed in water treatment. On the other hand, constructing monitoring devices such as passive samplers requires identification of membrane selectivity to choose a membrane that detects PFAS of interest. However, depending on chemical properties such as carbon chain length and other parameters, these materials' selectivity for PFAS can vary. To identify the processes governing membrane selectivity, the PFAS selectivity of membranes of differing exchange capacities were compared. Using liquid chromatography mass spectrometry, selectivity coefficients of the membranes were then determined for PFAS of varying chain lengths. These results corroborated our hypothesis that selectivity by chain length depends on the ability of active sites to interfere with hydrophobic interactions. Further exploring the applications of this principle mechanism, resins were experimentally loaded with hydrated ferric (oxy)hydroxide nanoparticles (HFO) to increase selectivity for short-chain PFAS. Selectivity coefficients of the parent resins for the ultrashort-chain PFAS trifluoroacetic acetate were determined by conducting isotherm experiments. Resins thereafter were modified through the deposition of HFO nanoparticles. Isotherm results of modified resins were fit to a Langmuir model and the maximum adsorption capacity between altered and parent resins were compared. The HFO-loaded resin's maximum adsorption capacity for the ultrashort-chain PFAS was strengthened over the parent resins, suggesting selectivity of current commercial anion exchange materials can be enhanced for ultrashort-chain PFAS.

This project was supported by the National Science Foundation (#2050728) and the Strategic Environmental Research and Development Program (ER20-1073, ER24-4224).

F

TOWARDS LINGUISTIC INCLUSIVITY: EXPANDING DEEPFAKE DETECTION TO MULTILINGUAL AND SIGNED LANGUAGES

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There are over 7,000 languages in the world, yet Standard American English (SAE) predominates as the language used in research on audio deepfakes– natural-sounding speech generated using artificial intelligence (AI) methods that have notoriously been used as tools for fraud and deception. Deepfakes, in multiple languages, have also been identified as a tool in the propagation of misinformation around the world. Research regarding audio deepfake detection in languages other than Standard American English is scarce, however, leaving researchers to face a lack of tools to address this global challenge. This presentation reviews key gaps in existing literature on audio deepfakes, in two main areas. First is a review of main languages that are included in audio deepfake research and an exploration of the many language families and geographic regions that are overlooked as a result. Second is a review of an even greater dearth of research on deepfakes in non-spoken, e.g., signed languages. With approximately 40 to 45 million blind individuals across the world, a lack of attention to signed languages in deepfake research is another dimension that underscores a lack of linguistic diversity in AI research. This presentation identifies important areas for future research, such as the compilation of additional datasets, resources, and techniques about deepfakes across languages and how they can be applied for more linguistically inclusive spoofed audio detection.

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EVALUATING DIRECTIONAL CUES THAT AFFECT MIGRATORY PREFERENCE IN BORDER CELL MIGRATION

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Collective cell migration is vitally important to development, immune response, wound healing, and cancer metastasis. Characterizing the signaling pathways and regulation of this process is crucial to the advancement of current therapies. Model systems are used to understand conserved signaling pathways and regulation related to collective cell migration. Border cell migration is observed during Drosophila melanogaster oogenesis, within the tissue that gives rise to the egg, the egg chamber. The border cell cluster (BCC) detaches from the anterior epithelium and migrates posteriorly toward the oocyte, extending membrane protrusions in the direction of migration. This migration is guided by chemoattractants and interactions with egg chamber architecture. How these directional cues interact to regulate border cell migration is still unclear. Using genetic tools, we induced mosaic expression of an oncogenic pathway to produce ectopic BCCs and analyzed directional preferences of BCCs within novel migration paths. We predict that quantifying directional selection of protrusions from ectopic BCCs will show they

consistently protrude toward features that aid in migration and prefer specific tissue structures along the migration path. Additionally, chemoattractant concentrations alter both direction and length of BCC protrusions. Heparan sulfate proteoglycans (HSPG) have been shown to modify distribution of extracellular signaling molecules, including chemoattractants, and we hypothesize they have the same function in regulating border cell migration. The tout velu (ttv) gene involved in the biosynthesis of HSPG interacts with multiple signaling pathways, but its role in border cell migration has not been characterized. We are currently using RNA interference to reduce ttv expression in the BCC and to test the prediction that it has an effect on regulation of border cell migration. This project provides insight into mechanisms that alter collective cell migration in diseases like cancer metastasis, which can occur in novel tissue environments.

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G

IMPROVING SCALE-UP EFFICIENCY FOR CELL-FREE PROTEIN SYNTHESIS WITH INTERMEDIATE-SCALE BIOREACTORS

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In vivo protein production is crucial for the pharmaceutical industry and a growing host of other sectors. However, the process is constrained by the host cell's tolerance to the product and its inefficient energy utilization. A promising solution to these challenges is cell-free protein synthesis (CFPS), which employs cellular components not confined within a cell wall. CFPS has the potential to optimize energy usage when compared to in vivo production because energy can be focused on specific objectives rather than the multifunctional goals of living cells. Furthermore, CFPS enables the production of biologics that are too complex or toxic for in vivo production. Nevertheless, scaling CFPS for commercial operations remains a significant obstacle.

Currently CFPS experimentation and optimization are performed at small volumes of 15 μL in microcentrifuge tubes with large head volume or at intermediate volumes of 1-30 mL in petri dishes. Sensing in these configurations is difficult and does not serve as a good model for large CFPS reactions performed in traditional stirred-tank reactors. Furthermore, experimentation and optimization in large stirred-tank reactors are extremely expensive due to the large volume of

reagents consumed for each reaction. To address this challenge, we aimed to design intermediate scale stirred-tank reactors that better model large stirred-tank reactors and allow for sensing of process parameters and reagent consumption.

While this research is ongoing, we have successfully developed a reactor that can accommodate 2.5 mL reactions in which we can make real time measurements of dissolved oxygen and green fluorescent protein yield. Additionally, we can directly sample from the reactor to measure adenosine triphosphate, 1,4-dihydronicotinamide adenine dinucleotide, and other reaction components, all while surpassing protein yields commonly reported in large stirred-tank reactors.

This investigation was sponsored by the DARPA Biological Technologies Offices under the Reimagining Protein Manufacturing grant [HR001121S0038].

H

INTEGRATING BLACK DOT AND LAYER-BY-LAYER TECHNIQUES FOR SINGLE-CELL TRACTION FORCES ON ECM MIMETIC SURFACES

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Mechanical traction forces exerted by biological cells are responsible for key organic processes and are important indicators of biological function and health. Traditional methods of measuring cell forces at the single-cell level have resulted in limited throughput and incompatibility with cellular structure measurements. The recently developed “Black Dots” (BD) works by microcontact printing a fluorescent pattern onto a flexible polydimethylsiloxane substrate. This enables high-resolution and high-yield assessment of cellular stresses based on cell deformations. Additionally, the Layer-by-layer (LbL) assembly is a method to create extracellular matrix (ECM) mimetic surfaces by sequentially exposing surfaces to polyelectrolyte solutions of opposite charges. This results in surfaces that better mimic layers of proteins. Using ECM components such as collagen, these LbL coatings precisely modulate animal cell functions. Examples of such cell functions include adhesion, migration, protein expression, cytokine interaction, and differentiation. The coatings are versatile, stable, and can act as reservoirs for cytokines and growth factors without affecting the underlying surface’s mechanical properties. This research sought to determine the optimal parameters of combining the LbL and Black Dot technologies. This was performed by coating collagen onto Black Dot patterns via LbL

assembly. Non-ECM component-coated or conventional BD substrate samples were analyzed against coated BD samples by visualizing their fluorescence microscope images for their pixel resolution as well as dot spacing, size, and singularity. The analysis testing provided an insufficient basis for identifying the ideal technique between conventional and ECM component-coated Black Dot method. Despite this ambiguous result, this study highlights the existing potential of combining LbL and Black Dot technologies for improved cell force measurements.

The support for this research was provided by the COEIT Interdisciplinary Proposals grant.

UNDERSTANDING GAG: RRE INTERACTIONS IN HIV-1: CHARACTERIZING COMPETITION BETWEEN REV AND GAG FOR RRE STEM 1

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In order for HIV-1 to replicate, it requires unspliced and incompletely spliced RNA transcripts to be exported out of the nucleus. This process is prohibited by cell surveillance systems that prevent unspliced RNA from leaving the nucleus. HIV-1 accounts for these prerequisites by binding the unspliced RNA, the Rev Response Element (RRE) to a nuclear-cytoplasmic transporting protein termed Rev. There are two binding sites associated with high affinity between Rev and RRE, Stem 1A (S1A) and Stem 2B (S2B). Rev transports the RRE into the cytoplasm where Gag, a protein that mediates genome packaging, binds to the RRE at sites close or overlapping with Rev near S1A. This proposes the idea that Gag displaces Rev for binding on the RRE. We theorize that these Rev and Gag interactions demonstrate competition on S1A. The project seeks to characterize and identify these protein-RNA interactions as well as the possibility of competition between Rev and Gag. We utilize a variety of truncated and modified forms of Stem 1 RNA, Rev proteins, as well as a nucleocapsid domain of Gag, NC in EMSA, ITC, SEC, and NMR experiments. We theorize that NC may bind to S1A preferentially over Rev and that the purine-rich bulge is the high affinity site for Gag-RRE binding. The ability to understand and identify these binding events can help characterize which proteins bind when, if there is possible competition, and further allows us to understand HIV-1 replication processes to aid in designing medication that targets HIV-1 replication.

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OPTIMIZING BLACK DOTS TECHNIQUE BY CHANGING BSA-ALEXA FLUOR-594 CONCENTRATION

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Platelets generate forces as they contract to adhere and form a plug during hemostasis. Black Dots involve printing fluorescent grid patterns using bovine serum albumin (BSA) onto a flexible polydimethylsiloxane (PDMS) substrate. To measure platelet size and forces, we look at the displacement and deformity of the dots after cells are applied. The BSA-Alexa Fluor-594 used is a type of fluorescent protein used to stain the grid. To effectively analyze platelets using Black Dots, it is crucial to produce the best possible dots without any imperfections. Several factors likely contribute to producing clear, bright, and uniform Black Dots; however due to the BSA's important role in the process, this experiment hypothesizes that variations in BSA concentration can affect the intensity and uniformity of the fluorescent grid. Increasing BSA concentration will result in enhanced fluorescence, making the Black Dots more visible under the microscope.

The concentrations used are the standard concentration (1 μg/mL), double concentration (2 μg/mL), and quadruple concentration (4 μg/mL). After visualizing the Black Dots on a fluorescence microscope, a positive correlation was observed between concentration and image saturation. From these results, we conclude that using the standard concentration is effective, but doubling the concentration allows for a brighter image without oversaturation. Although the image's brightness was good, some sections of the Black Dots were still damaged. This suggests other factors are limiting the dots from being produced perfectly. Improving our technique makes for consistent, high-quality results. It's essential to also refine and optimize related factors ensuring the dots are suitable for accurate analysis in future experiments. Achieving this level of precision will greatly enhance the reliability and validity of our research outcomes.

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ACCURATE AND INTERPRETABLE RADAR QUANTITATIVE PRECIPITATION ESTIMATION WITH SYMBOLIC REGRESSION

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Accurate quantitative precipitation estimation (QPE) is essential for creating hydrological models, managing water resources, addressing flood risk, and more. Traditional methods of obtaining precipitation data from rain gauges and radar have limitations such as sparse coverage and inaccurate estimates for different precipitation types and intensities. Symbolic regression, a machine learning method that generates mathematical equations fitting the data, presents a unique approach to estimating precipitation that is both interpretable and functional. We tested symbolic regression methods, based on genetic programming, deep learning, and combined approaches, to estimate precipitation from WSR-88D dual-polarimetric radar data for three case studies across Oklahoma and Florida. We found that symbolic regression was both accurate in estimating rainfall and interpretable through learned equations. Our research provides insights into improving the accuracy of quantitative precipitation estimation through interpretable and efficient symbolic regression methods.

This work is supported by an NSF grant “REU Site: Online Interdisciplinary Big Data Analytics in Science and Engineering” (grant no. OAC-2348755).

OPTIMIZING CAPPING METHODS FOR THE MOLONEY MURINE LEUKEMIA VIRUS

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The Moloney Murine Leukemia Virus (MoMuLV) is a distant relative of the Human Immunodeficiency Virus (HIV). Both MoMuLV and HIV are retroviruses and thus possess a dimeric RNA genome headed by a 5'UTR that regulates many processes, such as dimerization, packaging, and translation. HIV-1 has been discovered to possess a heterogeneous transcriptional start site. This allows the virus to transcribe single-stranded RNA with either 1, 2, or 3 guanosines following the 5'cap. The difference in guanosines plays a strong deterministic factor in the fate of RNA to be packaged or translated. However, MoMuLV contains a unique transcription start site, meaning the virus consists of only one start site, indicated by ^{Cap}1G. To understand what drives RNA packaging versus translation in a retrovirus that contains unique start sites, we must cap our RNA, which has been proven difficult. The RNA forms secondary structures as our full 5' leader is significant in size. Therefore, we aim to optimize capping methods for RNAs where capping may be difficult. The capping enzyme, the Faustovirus Capping Enzyme (FCE), has recently been discovered. It possesses unique properties compared to the currently utilized capping enzyme, Vaccinia Virus Capping Enzyme (VVCE), such as greater thermostability and single polypeptide structure, allowing for greater purification through size exclusion chromatography. While we optimize our synthesis and application of the enzyme, we are also interested in exploring co-transcriptional capping. In vivo, capping of all RNA occurs co-transcriptionally. We are working with different methods, such as position-selective labeling of RNA (PLOR), to cap our RNA. PLOR is a method of stopping transcription early to allow for modification or labeling of RNA. In our case, we want to stop transcription early to allow for capping and proceed with transcription. Our work will provide more efficient and affordable capping methods within the scientific field.

Support for this research was provided by the Howard Hughes Medical Institute and NIH/NIAID grant #5R01AI50498.

MODELING VAPOR LIQUID EQUILIBRIUM BEHAVIOR OF CHLORINATED WATER CONTAMINANTS USING MONTE CARLO SIMULATIONS

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Chlorinated contaminants such as trichloroethylene (TCE), 1,1-dichloroethylene (1,1-DCE), and trichloroethane (TCA) are prevalent in both industrial effluents and groundwater sources. These compounds, often detected in concentrations ranging from parts per million (ppm) to parts per billion (ppb), pose significant health risks. Consequently, understanding their behavior in environmental systems is crucial for developing effective remediation strategies.

This research uses Monte Carlo simulations to model these chlorinated contaminants and validate the models against their vapor-liquid equilibrium (VLE) properties from the literature. VLE gives a precise benchmark for thermodynamic properties in multiple phases over a wide range of temperature and pressure. We employed NVT-Gibbs Ensemble Monte Carlo (GEMC) method to simulate the phase behavior of TCE, 1,1-DCE, and TCA. OPLS-AA force field was used for TCA while models for TCE and 1,1-DCE were taken from a transferable force-field validation work in literature. Our experiments focused on reproducing the VLE properties of the contaminants at different temperatures. Future work will involve extending these simulations to study and validate their binary behaviors with water, and predict their competitive adsorption in hydrophobic all-silica zeolites. Since the concentration ranges are from ppm to ppb, we will use the thermodynamic extrapolation approach developed in our previous work to model these systems.

This project was supported by the National Science Foundation (#2050728).

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USING NEURAL NETWORKS TO SANITIZE COMPTON CAMERA SIMULATED DATA THROUGH THE BRIDE PIPELINE FOR IMPROVING GAMMA IMAGING IN PROTON THERAPY ON THE ADA CLUSTER

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Precision medicine in cancer treatment increasingly relies on advanced radiotherapies, such as proton beam radiotherapy, to enhance treatment efficacy. When the proton beam interacts with molecules in the patient, the excited nuclei may emit prompt gamma photons, whose interactions a Compton camera captures. The image reconstruction from this captured data faces the issue of mis-characterizing the incoming scattering event sequences and may cause excessive background

noise. To address this problem, several multi-layer machine learning models were developed in PyTorch to properly characterize the scattering sequences using supervised learning on simulated datasets, which were generated through a pipeline of the GEANT4 and Monte-Carlo Detector Effects (MCDE) software.

These models were implemented by using the novel 'Big-data REU Integrated Development and Experimentation' (BRIDE) Platform, a modular pipeline that streamlines preprocessing, novel feature engineering, model development, evaluation, and tuning. Taking advantage of the GPU cluster ada in the UMBC High Performance Computing Facility, Distributed Data Parallelism (DDP) can be used to rapidly develop, implement, evaluate, and tune the models. The present studies utilize various models, including both Feed-forward Neural Networks (FNNs) and Recurrent Neural Networks (RNNs). These machine learning models may offer suitable improvements to the real time image reconstruction of the Compton camera to aid in cancer treatment. A long short term memory (LSTM) model achieved over 90% validation accuracy.

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THE DNA BINDING ABILITY OF ZINC FINGER PROTEIN 217 IS CRITICAL FOR MEDIATING ITS ONCOGENIC FUNCTION IN OVARIAN CANCER CELLS

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Due to vague symptoms and lack of early biomarkers, many ovarian cancer patients are diagnosed with metastatic disease. There is urgent clinical need to identify factors that drives ovarian cancer metastasis and develop novel strategies to target them. Our data suggests that the transcription factor Zinc Finger Protein 217 (ZNF217) functions as a potent oncogene in ovarian cancer cells. ZNF217 mRNA is overexpressed in ovarian cancer, and elevated ZNF217 expression promotes ovarian cancer cell proliferation and metastasis in both in vitro and in vivo models. I hypothesize that ZNF217's ability to bind DNA and function as a transcription factor is critical in mediating its oncogenic effects in ovarian cancer cells. ZNF217 H489A mutant was previously shown to be defective in DNA binding. I performed site-directed mutagenesis to introduce a Histidine to Alanine mutation at amino acid position 489 in ZNF217 (H489A) into the lentiviral plasmid pLVX-Hygro. I transfected this plasmid (pLVX_ZNF217-H489A) along

with lentiviral packaging plasmids in human embryonic kidney cells to generate ZNF217-H489A lentivirus particles. These lentivirus particles were used to transduce the pLVX_ZNF217-H489A vector into ovarian cancer cells in which endogenous ZNF217 was depleted previously using stable expression of a shRNA targeting the 3'UTR. Using hygromycin, I selected stable cells expressing ZNF217-H489A. I then collected stable cell lines I generated, lysed them to isolate the mRNA, and performed reverse transcription-quantitative polymerase chain reaction (RT-qPCR) to measure the expression of direct ZNF217 target genes such as SNAIL1. I successfully confirmed that the ZNF217-H489A mutant is defective in DNA binding. I performed in vitro assays to determine the ability of the ZNF217 H489A mutant to rescue the effect of ZNF217 depletion on cell proliferation, migration, and invasion. The results suggest that the DNA binding ability of ZNF217 is critical in mediating its oncogenic effects in ovarian cancer cells.

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FUNCTIONALIZATION OF ANION-EXCHANGE RESINS FOR ENHANCED SELECTIVITY OF ULTRASHORT- AND SHORT-CHAIN PFAS

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Per- and poly-fluoroalkyl substances (PFAS), also known as "forever chemicals", are a class of toxic man-made compounds found in food, packaging, household products, personal care products, and more. Classified as contaminants of emerging concern, PFAS are very difficult to degrade in the environment due to their strong carbon-fluorine bonds. The effects of PFAS on human health are numerous, impacting the immune and reproductive systems, natural hormones, and fetal development. As such, there is a recent rule from the Environmental Protection Agency that enforces the monitoring and removal of PFAS from drinking water. Water treatment facilities will need to adapt their treatment processes to abide by this rule. Commercially available anion-exchange resins are an effective technology for removing long-chain PFAS from water, but not for ultrashort- and short-chain PFAS due to their lower hydrophobicity. We

hypothesized that hydrated ferric oxyhydroxide (HFO) functionalization of anion-exchange resins would enhance their ability to take in ultrashort- and short-chain PFAS from water. Two types of anion-exchange resins with quaternary ammonium functional groups were modified: a gel- and a macroporous-type resin. HFO nanoparticles were deposited onto the resins and uptake performance was evaluated for one ultrashort- and one short-chain PFAS. We conducted batch experiments to find selectivity coefficients of PFAS over chloride for unmodified resins and used the Langmuir adsorption isotherm model for comparing performance across modified and unmodified resins. We found that functionalization via HFO increased the uptake capacity of the resins for ultrashort- and short-chain PFAS, making this a promising material for the treatment of drinking water in light of current regulations.

This investigation was sponsored by the National Science Foundation (#2050728), the Strategic Environmental Research and Development Program (ER20-1073, ER24-4224), and the U-RISE Program at the University of Maryland, Baltimore County (UMBC), which is supported by the National Institute Of General Medical Sciences of the National Institutes of Health under Award Number T34GM136497.

I

IMPACT OF COPPER EXPOSURE ON APPL GENE-INDUCED DEGENERATION: INSIGHTS FROM DROSOPHILA MELANOGASTER

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Amyloid precursor protein (APP) is an integral membrane protein expressed in several tissues and particularly found in the synapses of neurons. In humans, it is encoded by the APP gene, located on chromosome 21, and associated with Alzheimer's Disease (AD). APP is a highly conserved protein with amyloid precursor protein-like (APPL) being the homolog in Drosophila melanogaster (or also known as fruit flies). APP/APPL contains binding domains that have an affinity for copper (Cu) and zinc (Zn). The interaction with these metals can lead to structural changes that play a significant role in the regulation of APP. In this study, we aim to understand this process by observing the effects of metal-induced toxicity on flight performance in flies. For this model, a flight assay was performed with wild-type flies (WT) and APPL loss-of-function mutant flies (APPL-d), which were subjected to various copper concentrations. Preliminary results showed that flies who were treated with medium and high copper concentrations had a lower flight recovery height than those treated with deionized water or low copper concentration. The WT and APPL-d flies did not have much of a difference in their overall flight recovery height. However, statistical analysis is yet to be conducted to compare groups and additional

trials are needed to increase the sample size. Overall, this research will help us better understand aging-related motor degeneration and metal exposure in relation to APPL, suggesting more studies are needed to explore the detailed processes involved.

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LARGE LANGUAGE MODELS FOR THEOREM PROVING IN LEAN 4

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Theorem proving is an important subfield of computer science and mathematics that verifies proofs of mathematical statements. Writing formal proofs requires significant domain knowledge in programming, mathematics, and advanced logic. Even experts can find this time-consuming and complex. These factors have limited widespread adoption. On the other hand, Large Language Models (LLMs) have demonstrated capabilities in natural language processing (NLP), reasoning, code generation, and completion.

In this work, we explored the use of LLMs to facilitate theorem proving in Lean 4. We approach this by applying different LLM model architectures to different steps of the theorem proving process. Encoder-decoder models, optimized for tactic generation, are integrated with GPT-style models proficient in natural language processing. This hybrid approach aims to overcome the limitations of individual model types and enhance the overall theorem proving process. Indeed, ChatGPT alone does poorly when asked directly to formalize proofs.

The methodology uses GPT-4 as an NLP interface to process natural language inputs and generate Lean 4 code structures. The structured data is then fed into specialized tactic generation models like Pythia (2.8B parameters) and LeanDojo ByT5 (300M parameters) to produce tactics for finishing the proofs. This process is iterative, with GPT-4 refining, debugging, and completing the proofs based on the generated tactics.

Preliminary results show promising performance on simple math theorems which validates the problem thesis. Further testing is required for more complex, multi-step problems.

This project contributes to making formal proofs easier and more accessible for scientists and engineers unfamiliar with theorem proving. It also provides a potential to address the challenges of limited datasets and increasing formal proof libraries in different fields of math and science.

This work was supported by NSF CAREER Grant # 2236769 and a UMBC Undergraduate Research Award.

UTILIZING BEHAVIORAL ASSAYS TO STUDY GENES ASSOCIATED WITH AUTISM SPECTRUM DISORDER IN DROSOPHILA MELANOGASTER

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Autism Spectrum Disorder (ASD) is a complex neurological and developmental disorder that is characterized by atypical social behaviors. One of the most obvious characteristics of ASD is low sociability levels with other individuals. Individuals with ASD often avoid socializing with other individuals and have trouble understanding nonverbal forms of communication. While there has been no direct cause of this disorder, there are numerous genetic mutations predicted to be associated with the disorder. We use the fruit fly, Drosophila melanogaster, as a model organism to study genes associated with ASD at the molecular, anatomical, and behavioral levels. We used a previously established behavioral social assay to assess the effects of genetic knockdown on genes hypothesized to be associated with sociability. We will compare the socialization patterns of our control wild type line of flies, DGRP-774, to our experimental line of flies, for example, elav-GAL4; UAS-Dicer/ UAS-nrx-RNAi, with the Nrx-1 gene, a presynaptic cellular adhesion protein that plays a role in connecting neurons at the synapse, knocked down. Further research will help us understand the molecular mechanisms of these genes following cellular and anatomical techniques. Establishing suitable animal models and behavioral tests will help better understand potential causes for this disorder and may help with better diagnosing ASD.

Support for this research was provided by Dr. Vonhoff's start-up funds.

J

IN VITRO ASSEMBLY OF LARGE DNA FRAGMENTS USING ROLLING CIRCLE AMPLIFICATION AND CYCLIC HETERODUPLEX THERMOSTABLE LIGASE ASSEMBLY

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Genome engineering is a powerful tool that can be applied to a diverse range of problems, from vaccine development to environmental remediation. However, efficient in vitro assembly of DNA fragments >20 kb remains a challenge in the generation of large synthetic genomes. Current methods for assembling DNA fragments >20 kb require time-consuming and laborious procedures including stepwise bacterial transformations, followed by selection. To address this challenge, we developed Cyclic Heteroduplex Thermostable Ligase Assembly (CHTLA), an innovative in vitro method that generates user-designed, ligation-ready, single-stranded overhangs to create sticky end blocks capable of efficiently assembling DNA fragments >20 kb. In this project, our strategy utilizes rolling circle amplification (RCA), a circular DNA amplification technique that generates CHTLA precursors in high yields. Here we demonstrate the success of using RCA in generating two 6.7 kb bacmid and two 3 kb bacmid-Kanamycin CHTLA precursors and their assembly via CHTLA. By addressing the challenge associated with efficient in vitro assembly of DNA fragments >20 kb, our integrated approach using RCA and CHTLA holds promise for advancing synthetic genome construction.

This research was funded by the Arnold and Mabel Beckman Foundation and award R41GM145048 from NIH NIGMS to CJB.

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RECHARGEABLE ORGANIC GEL ELECTROLYTE FOR ZN-MNO2 BATTERIES

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Rechargeable batteries are a necessary component of everyday life as society becomes more dependent on electronics. Notably lithium-ion batteries have been a primary use in everyday electronics. Unfortunately, they can easily become unstable and very dangerous to handle in

those same applications. This is why there needs to be an alternative, like zinc manganese dioxide batteries that present a safer composition and high energy capabilities. Nevertheless, there are some challenges that acidic zinc manganese dioxide (Zn-MnO_2) batteries present that need to be addressed, such as low ionic conductivity. To cater to such challenges, an alkaline and flexible electrolyte is introduced that is based on a bio-compatible polymer, i.e., chitosan, coupled with a synthetic polymer polyvinyl alcohol (PVA). When soaked in 5M KOH, this bio-degradable Chitosan-PVA film displays high ionic conductivity (IC), i.e., ~>100 mS/cm, without compromising the flexibility and mechanical strength of the electrolyte. The high IC values obtained for the Chitson-PVA electrolyte show that it can be used as an efficient, safe, and flexible electrolyte for Zn-MnO_2 batteries for various applications like wearable electronics.

Support for this research was provided by FlexMESHED lab UMBC. This research was partially funded by the USM LSAMP program, supported by NSF LSAMP Award # 2207374

TOWARDS SUSTAINABLE COEXISTENCE: SOUND-BASED ANIMAL DETERRENCE FOR WILDLIFE AND HUMANS

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We propose a sustainable and ethical wildlife management, this study explores the development and implementation of selective sound-based animal deterrence systems using ultrasonic audiograms. This innovative approach aims to promote harmonious coexistence between wildlife and human environments, such as gardens and residential areas. The system dynamically adjusts its operation, activating only when necessary to deter animals from specific zones, and remaining inactive to minimize disruption to natural behaviors and habitats. By integrating advanced sound-based technologies, this research proposes a non-invasive, eco-friendly solution that aligns with ethical wildlife practices. The ultimate goal is to create a ubiquitous deterrence system that respects the natural ecosystem while protecting human spaces, fostering a balanced coexistence between humans and wildlife.

Support for this research was provided by the University of Maryland Baltimore County Faculty Entrepreneurship Accelerator Fund (FEAT2405) and NSF REU Site Grant (#2050999).

N-MYC DOWNSTREAM REGULATED GENE 1A (NDRG1A), A CANDIDATE GENERALIST STRESS PROTEIN THAT RESPONDS TO BOTH HYPOXIA AND SALINITY CHANGES

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Climate change poses significant threats to ecosystems and biodiversity, making it crucial to understand how organisms adapt to shifting environmental conditions. Zebrafish are an ideal organism for such research because of their high level of tolerance to a range of environmental stressors such as oxygen and salinity levels. Previous research in the Brewster lab established that zebrafish embryos can adapt to severe hypoxia by entering an energy- conserving, hypometabolic state. The adapter protein N-myc downstream regulated gene 1a (Ndrg1a) is elevated in response to hypoxia and plays a key role in metabolic suppression by downregulating the energy-demanding Na+K+ATPase pump (NKA) in the kidney and ionocytes; organs that mediate ion homeostasis. Interestingly, a study on salinity adaptation in tilapia fish also established a negative correlation between ndrg1 levels and several ion channels, raising the question of whether ndrg1a may play a broader role in organismal adaptation to environmental changes. The goal of my research project is to determine whether Ndrg1a functions as a generalist responder to environmental stress by testing whether it also regulates NKA levels or distribution in changing salinity. I have tested this by exposing 24 hours post-fertilization (hpf) Wild-type zebrafish and Ndrg1a knockdown embryos to different salinity conditions between 0 ppt to 10 ppt and performing whole mount double immunolabeling using antibodies targeting both proteins. My preliminary data indicate that the levels and distribution of both proteins change distinctly with different salinity levels, indicative of an ion homeostasis response. However, there appears to be a positive rather than a negative correlation between these proteins, possibly indicating that Ndrg1a promotes NKA expression/ distribution. Our findings so far support the hypothesis that Ndrg1a is a generalist stress responder, but it does not react the same as when under hypoxia.

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CHARACTERIZING OF LAYER-BY-LAYER HEPARIN COLLOGEN COATING AND ELECTROSPUN SCAFFOLDS

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Electrospinning is a technique to create a fibrous scaffold out of polymers. It is done by creating an electric field and slowly pumping the polymer in solution through it, which evaporates the solvent and manipulates the polymer. Then, the fibers are caught on a collector; an iron block covered in aluminum foil, in our case. Electrospinning is a versatile technique as there are many small adjusts that can give different results with the same polymer, such as changing the distance to the collector or the strength of the electric field. Additionally, a layer-by-layer coating of heparin and collogen has been developed with a goal of adding it to a nerve guide conduit for improved treatment of peripheral nerve injuries. Characterization of a biomaterial is necessary to effectively choose how to utilize it and to give new directions to modify it in the future; in this work, two imaging techniques were applied. Using a confocal microscope, we quantified the thickness of the layer-by-layer coating of $(Hep/Col)_6$. Imaging with a scanning electron microscope allowed us to examine the morphology of the electrospun scaffolds, including the pore size and diameter of the fibers. Both of these materials have the potential to be used as scaffolds in tissue engineering applications.

This project was supported by the National Science Foundation (#2050728).

TEACHING AUDIO DEEPFAKE DETECTION WITH DATA SCIENCE CASELETS & REPOSITORIES

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Audio deepfakes are synthetic recordings generated using artificial intelligence methods to mimic human voices. Audio deepfakes have been used for malicious purposes such as spreading

misinformation and committing financial fraud. Advancements in research have produced innovative and effective methods to detect audio deepfakes, although much more work is needed to make this work widely available for research and educational applications. In this presentation, we address a significant gap in the availability of educational resources that teach data science students about audio deepfakes and current detection methods through two approaches. First, we are developing data science caselets for use in data science classrooms to provide students with learning and analysis opportunities. Two data science caselets were created, with interactive counterparts in Jupyter Notebook in development as well. Second, we are creating a data repository with compiled resources for publicly accessible research and training. The repository includes 11 papers thus far with 18 different datasets. Future research will study the efficacy of implementing caselets in classroom contexts.

Support for this research was provided by the National Science Foundation through Awards #2118285 and #2346473.

THE ROLE OF RWP-RK TRANSCRIPTION FACTORS IN THE EVOLUTION OF CELL DIFFERENTIATION IN VOLVOX CARTERI

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Volvox carteri is a multicellular eukaryotic algal model for investigating cell-differentiation and its evolution. Volvox is ideal for these studies because it has complete division of labor between just two cell types: motile somatic cells and non-motile reproductive gonidia, with differentiation decided in early cell division cycles. Here we are testing the roles of the rwp3 and rwp6 genes (encode members of the RWP-RK transcription factor family) in regulating the gonidial cell type, because previous RNAseq analyses revealed that these genes are highly expressed in gonidia and are repressed by overexpression of a gene (rlsD) that represses cell growth. The RWP-RK transcription factor family has been previously determined to activate embryogenesis in plants, and the involvement of these genes in this role in other green lineages suggests their function may be phylogenetically conserved. We are using CRISPR to knock out rwp3 and rwp6 in V. carteri, and to this end we have ligated annealed oligos into an sgRNA vector to generate two guide RNA expression plasmids for each rwp gene that will be co-transformed with a Cas9-expression plasmid. We are also workshopping a long-PCR method to amplify a full-length version of rwp3 to clone into a Volvox overexpression vector. We will select for successful Volvox transformants using hygromycin resistance genes in our constructs,

identify CRISPR mutants by sequencing guide RNA target regions, and characterize the growth and development of mutant and overexpression strains through different stages of the life cycle. These experiments will provide insights into the functions of the rwp-rk genes in Volvox and their potential role in gonidial development. Furthermore, characterizing these genes should lead to a better understanding of origins of cell differentiation in Volvox and possibly other species.

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

OPTIMIZING CAPPING METHODS FOR THE MOLONEY MURINE LEUKEMIA VIRUS

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The Moloney Murine Leukemia Virus (MoMuLV) is a distant relative of the Human Immunodeficiency Virus (HIV). Both MoMuLV and HIV are retroviruses and thus possess a dimeric RNA genome headed by a 5'UTR that regulates many processes, such as dimerization, packaging, and translation. HIV-1 has been discovered to possess a heterogeneous transcriptional start site. This allows the virus to transcribe single-stranded RNA with either 1, 2, or 3 guanosines following the 5'cap. The difference in guanosines plays a strong deterministic factor in the fate of RNA to be packaged or translated. However, MoMuLV contains a unique transcription start site, meaning the virus consists of only one start site, indicated by ^{Cap}1G. To understand what drives RNA packaging versus translation in a retrovirus that contains unique start sites, we must cap our RNA, which has been proven difficult. The RNA forms secondary structures as our full 5' leader is significant in size. Therefore, we aim to optimize capping methods for RNAs where capping may be difficult. The capping enzyme, the Faustovirus Capping Enzyme (FCE), has recently been discovered. It possesses unique properties compared to the currently utilized capping enzyme, Vaccinia Virus Capping Enzyme (VVCE), such as greater thermostability and single polypeptide structure, allowing for greater purification through

size exclusion chromatography. While we optimize our synthesis and application of the enzyme, we are also interested in exploring co-transcriptional capping. In vivo, capping of all RNA occurs co-transcriptionally. We are working with different methods, such as position-selective labeling of RNA (PLOR), to cap our RNA. PLOR is a method of stopping transcription prematurely to allow for modification or labeling of RNA. In our case, we aim to halt transcription to allow for capping and proceed with transcription. Our work will provide more efficient and affordable capping methods within the scientific field.

Support for this research was provided by the Howard Hughes Medical Institute and NIH/NIAID grant #5R01AI50498.

IDENTIFYING CONTEXTUAL FACTORS AFFECTING LONG-TERM SERVICES AND SUPPORTS PROGRAM IMPLEMENTATION IN THE U.S. DEPARTMENT OF VETERANS AFFAIRS: A RAPID SCOPING REVIEW

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Implementing evidence-based practices within Long-Term Services and Supports (LTSS) programs in the Veterans Health Adm inistration (VHA) is complex and influenced by various contextual determinants. This scoping review aims to systematically identify and categorize these factors to understand their influence on program implementation within LTSS programs.

We conducted a scoping review using four databases, including studies from their inception to July 31, 2024. We screened for 146 abstracts after the removal of duplicates using Covidence software. Two reviewers independently applied inclusion/exclusion criteria, with discrepancies resolved by a third reviewer. We reviewed the full texts of the included articles, and extracted data on the LTSS setting type, intervention type, study design, theoretical frameworks, and contextual determinants. In total, we reviewed 37 full-text articles.

Preliminary findings from the 29 included articles span publication years from 1993 to 2024. Key determinants were most often found for the Community Living Center (34%), Home-based Primary Care (28%), and Geriatric Patient-Aligned Care Team (13%) settings. We identified 108 instances of determinants being documented within the studies. The contextual determinants were categorized using the five domains of the Consolidated Framework for Implementation

Research framework. The Inner Setting domain had the highest percentage of identified determinants (51%), followed by Innovation (21%), Individuals (19%), Process (5%), and Outer Setting (4%). The most often identified determinants within these domains were: available resources (15%), networks and communication (15%), structural characteristics (7%) (Inner Setting); and staff access to knowledge or need training (11%) (Individuals).

This scoping review highlights the contextual determinants that affect evidence-based program implementation in VHA LTSS settings. This review found several commonly identified determinants that could target strategy identification prior to the implementation phase. Understanding these factors is crucial for developing strategies to improve the implementation and effectiveness of LTSS programs, ultimately enhancing care for older veterans.

This work was supported through the Leadership Alliance Summer Research Early Identification Program and funded by the Department of Veterans Affairs, Office of Research and Development, Summer Research Program (DEI SRP-009-22S, PI: Mills) and HSR&D (CIN-13-419).

INVESTIGATING THE ENZYMATIC ROLE OF NUCLEOTIDASES IN THE DEPHOSPHORYLATION OF FLUDARABINE METABOLITES

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Fludarabine (FAMP) is a chemotherapy drug widely used in the first and second-line treatment of B-cell chronic lymphocytic leukemia. FAMP is administered as a prodrug and its triphosphate form is pharmacologically active. Nucleotidases are enzymes that catalyze the dephosphorylation of nucleotides into nucleoside and inorganic phosphate. There are two major types of nucleotidases: 5'-nucleotidases (5'-NTs) and nucleoside triphosphate diphosphohydrolases (NTPDases). Of these, 5'-NTs are known to catalyze the dephosphorylation of nucleoside monophosphates. On the other hand, NTPDases catalyze the dephosphorylation of nucleoside triphosphates by sequentially removing phosphate groups. Due to the structural similarities of pharmacologically active metabolites of nucleoside analog drugs and endogenous nucleotides, we hypothesize that these nucleotidases potentially play a role in the dephosphorylation of metabolites of nucleoside analog drugs. To test this hypothesis, in vitro incubations were performed using a range of nucleotidases, including cytosolic 5'-nucleotidase 1A (NT5C1A), NT5C2, NT5C3, NT5C, and mitochondrial 5' (3')-deoxyribonucleotidase (NT5M) to assess nucleotidase enzymatic activities toward FAMP. Additionally, nucleotidase activity toward their natural substrate, adenosine monophosphate (AMP) was investigated. In this work, a Malachite

Green Phosphate Assay was used for the quantification of inorganic phosphate released during dephosphorylation reactions. From these experiments, we observed the dephosphorylation of FAMP in the presence of NT5C3 only. In addition to NT5C3, NT5C1A also showed enzymatic activity towards AMP. We plan to investigate the enzymatic activity of NTPDases towards their triphosphate metabolite and the endogenous substrate ATP. These findings highlight the specific roles of different 5'-NTs in the metabolism of FAMP, suggesting that these enzymes could influence the efficacy of FAMP in treating chronic lymphocytic leukemia. Further research into the regulation and inhibition of these nucleotidases may provide insights into optimizing FAMP therapy and improving patient outcomes.

This research was funded by a startup grant from University of Maryland, Baltimore County (H.K.S.), START (H.K.S.), and SURFF (H.K.S.).

EVALUATING THE FUNCTION OF SET6 IN PROTEOSTASIS

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In Saccharomyces cerevisiae, Set6 is a member of a family of twelve proteins that each of which have the SET domain. By catalyzing the methylation of lysine residues on their targets, several members of this protein family change the function of histones and nonhistone proteins. Although relatively little is known about Set6, it has been found to methylate various proteins in previous in vitro investigations, and our team has preliminary results indicating additional candidates crucial for controlling protein homeostasis, or proteome quality control. To define Set6's role, our lab evaluates TDP-43, a frequently misfolded protein involved in transcriptional repression and pre-mRNA splicing. Disorders such as ALS, Alzheimer's, and other neurodegenerative diseases are characterized by the presence of this protein and its misfolding in cellular nuclei. TDP-43 is inherently prone to aggregation, rendering it significantly more probable to follow deleterious misfolding pathways and result in cell death. We aim to find the biological function of Set6 in the proteostasis network and determine if it has a role in TDP-43 folding regulation and aggregation in cells. We have used fluorescence microscopy to evaluate the role of Set6 in TDP-43 aggregation. Additionally, we have been performing sedimentation assays which showed increases in insoluble TDP-43 in the absence of Set6. My future experiments will continue to investigate the role of Set6 in regulating TDP-43 aggregation under different conditions to better understand functions for Set6 in proteostasis.

This investigation was sponsored by the U-RISE Program at the University of Maryland, Baltimore County (UMBC), which is supported by the National Institute Of General Medical Sciences of the National Institutes of Health under Award Number T34GM136497.

EXPLORING THE FATE OF RNA IN MOLONEY MURINE LEUKEMIA VIRUS

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Moloney Murine Leukemia Virus (MoMuLV) is a gammaretrovirus that causes leukemia and neurological diseases within rodentia. It has been studied since the 1950s as a model to further understand the underlying mechanisms of all retroviruses. Our laboratory mainly focuses on Human Immunodeficiency Virus type-1 (HIV-1), most particularly the segment of the HIV-1 RNA genome necessary 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 (^{Cap}1G) in which the cap is sequestered, and the monomeric conformation adapted by 5'-capped RNAs that begin with two or three guanosines (^{Cap}2G and ^{Cap}3G respectively) where the cap is exposed. We refer to viruses containing these different beginning sites as having transcriptional start site heterogeneity. Inversely, MoMuLV utilizes a promoter with a single transcriptional start site, ^{Cap}1G, from which both packaging and translation occur. We wish to understand what drives RNA packaging versus translation in a retrovirus that contains a single start site. Through our exploration of this process, we hope to gain insight into the machinery that older viruses have conserved for millennia and provide indications of possible characteristics that newer retroviruses may exhibit in the future. Like HIV-1, we suspect that MoMuLV's genome fate is driven by dimerization dependent cap sequestration. We plan to explore the behavior of MoMuLV's genome in vitro by determining the conditions needed for the RNA to function as a monomer or dimer, capping the RNA to get an accurate representation of the virus, and exploring cap sequestration via electrophoretic mobility shift assays. After capping the RNA, to confirm its conformation we will use nuclear magnetic resonance. We will then test the hypothesis that cap sequestration is necessary for packaging in MoMuLV, as previous studies have shown it is essential in HIV-1.

Support for this research was provided by Howard Hughes Medical Institute and NIH/NIAID grant (#5R01AI50498).

SELF-SUSTAINING LOW-COST AND WIDELY AVAILABLE ENERGY HARVESTING AND SENSING DEVICES FOR USE IN MUSEUM ENVIRONMENTS

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In art preservation, low-cost and widely available ambient environment (temperature, vibrational, and humidity) sensors are critical to ensuring a safe environment that helps to monitor art stability. Current battery technology cannot meet the needs of these sensors due to frequent recharging or replacement. This work investigates optimal methods of incorporating MXene 2D nanosheets into thermoelectrics for use as supplemental power sources for ambient environment sensors such as triboelectric vibrational sensors. Thermoelectrics allow for the conversion of waste heat energy present in environments such as art storage warehouses for the charging of batteries utilized in art preservation sensors. To further reduce the dependence of batteries in art preservation sensors, this work manufactured triboelectric vibrational sensors that passively sense disturbances to art pieces by spikes in voltage outputs. These triboelectric sensors produce voltage spikes upon lateral rubbing or vertical movement to or from two materials on the triboelectric series. Triboelectric materials are low-cost, widely available materials used as waste products in thermoelectric manufacturing contributing to overall sustainability and scalability. This work presents thermoelectric devices potential to act as a supplemental power supply for charging capacitors and batteries used in art sensors upon a heat difference. Additionally, this work presents a triboelectric vibrational sensor that detects disturbances and movements in art pieces. These devices were connected to a computer program which can notify art conservators to events such as earthquakes, robberies, or any rough physical contact that may be of interest.

The project is supported by the SCIART program with funds from Mellon Foundation grant G-2109-11420 and the U-RISE Program at the University of Maryland, Baltimore County (UMBC), which is supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number T34GM136497. The authors thank Dr. Swapnil Ambade from the Department of Chemistry at the John's Hopkins University for providing the MXene 2D nanosheets. The authors thank Leopoldo Posada Escobar and Dr. Zeev Rosenzweig from the Department of Chemistry at the University of Maryland, Baltimore County for their guidance.

INVESTIGATING SINGLET OXYGEN PRODUCTION FROM NU-1000 MOFS USING eABDA

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Chemical warfare agents (CWAs) are of concern for environmental contamination. Sulfur mustard, commonly known as mustard gas, is a CWA that can linger within soil after deployment leading to severe skin and lung irritation if ingested or inhaled. The use of metal-organic frameworks (MOFs) was studied to investigate their ability to facilitate neutralization of CWAs without formation of toxic byproducts. The NU-1000 MOFs used in this study contain zirconium centers and pyrene-based organic linkers. The proposed mechanism for the oxidation of a sulfur mustard simulant, 2-chrloroethyl ethyl sulfide (2-CEES), is through the production of singlet oxygen ($^1O_2$) using the photochemical properties of MOFs. This method of oxidation requires milder conditions, and no toxic byproducts are formed. The goal of this study is to develop a chemical probe that can quantify the amount of $^1O_2$ produced from blue-light irradiated MOFs. The rates of $^1O_2$ production of NU-1000 MOF derivatives were determined by the degradation of 2-(10-(bis-ethoxycarbonyl-et)-anthracen-9-ylmethyl)-malonic acid diethyl ester (eABDA) through absorption and fluorescence spectroscopies after each blue-light irradiation. Independent suspensions of the MOF and eABDA in acetonitrile irradiated for an hour showed that eABDA degradation in the presence of the MOF is caused by MOF interactions. Furthering investigation of eABDA as a $^1O_2$ probe, a known photosensitizer, Rose Bengal, and eABDA were irradiated with green light by the same method. This resulted in eABDA being fully bleached after 20 minutes of green light irradiation with Rose Bengal using absorbance and fluorescence spectroscopy. eABDA itself was found to be stable after 20 minutes of green light irradiation. The preliminary findings indicate that eABDA can be used as a photochemical probe for $^1O_2$ production of blue light irradiated MOFs. Observations showed MOFs with different organic linkers differed in $^1O_2$ production rates.

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L

CONCENTRATION-DEPENDENT EFFECTS OF FORMALDEHYDE ON INTRACELLULAR CALCIUM STORES IN MOUSE OLFACTORY SENSORY NEURONS

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Formaldehyde is a toxic compound formed by chemicals present in electronic cigarette liquid via thermal degradation. Upon e-cigarette usage, the main olfactory epithelium (MOE), the first neuronal tissue exposed to vapor, is prone to this harmful compound. In this study, we aimed to investigate the impact of formaldehyde on intracellular calcium stores within olfactory sensory neurons (OSNs) of the MOE by using e-cigarette equivalent concentrations of formaldehyde. To achieve this, we used Fura-FF, a fluorescent calcium indicator that localizes in intracellular compartments, such as the mitochondria and endoplasmic reticulum, to examine calcium mobilization under conditions that mimic daily e-cigarette usage. Our findings reveal a concentration-dependent effect of formaldehyde on intracellular compartments, suggesting potential disruption of calcium homeostasis in OSNs. Additionally, we explored whether the presence of extracellular calcium influences OSN calcium responses by comparing normal and non-normal extracellular calcium conditions. Ultimately, our results suggest that formaldehyde alters calcium signaling in OSNs, potentially disrupting sensory integrity, function, and long-term olfactory health. The disruption in calcium signaling induced by formaldehyde opens up new perspectives of research to investigate the adverse effects of e-cigarette usage on the olfactory system, and may also serve as a potential therapeutic target for future interventions along with medical findings.

This project was funded in part by a UMB-ATIP pilot grant to Dr. Weihong Lin and the 2024 Undergraduate Research Award.

UNDERSTANDING THE DEGRADATION OF VERDIGRIS & DEVELOPING STRATEGIES FOR ITS CONSERVATION IN ARTWORK

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Conservation science focuses on the preservation and protection of artwork. One of the most difficult challenges faced by conservation scientists is understanding how the components of an artwork interact with the environment. For paintings in particular, pigment degradation poses a considerable threat due to altering the color profile of the artworks. The focus of this project was verdigris, an organometallic pigment used in ancient and modern artwork. It's history dates back to ancient times when it was the brightest green pigment available, making it widely used in artwork. Verdigris is known to irreversibly degrade over time. In this project, we studied the degradation profile of verdigris through various thermal and photodegradation experiments. Comparisons between verdigris in solution and as a paint with lipidic binders were studied. Analysis of the degradation was conducted using UV/Vis spectroscopy, FTIR, and NMR. Our results demonstrate that verdigris is both thermally and photosensitive. The next step in our research is employing the use of a member of a new class of transition metal carbide nanomaterials, MXenes, to determine their effects on the degradation profiles of verdigris. MXenes have demonstrated the capacity to absorb UV light which may prevent direct exposure of verdigris to harmful radiation.

This project was supported by the Baltimore SCIART research program funded by the Andrew W. Mellon Foundation under Award G-2109-11420. The students of the program would like to extend our gratitude to Dr. Joseph Bennett, Dr. Deepa Madan, Dr. Shreyasi Sengupta, Kushani Mendes. MCAC staff Josh Valencia and Cynthia Niedermeier.

SELF-SUSTAINING LOW-COST AND WIDELY AVAILABLE ENERGY HARVESTING AND SENSING DEVICES FOR USE IN MUSEUM ENVIRONMENTS

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In art preservation, low-cost and widely available ambient environment (temperature, vibrational, and humidity) sensors are critical to ensuring a safe environment that helps to monitor art stability. Current battery technology cannot meet the needs of these sensors due to frequent recharging or replacement. This work investigates optimal methods of incorporating MXene 2D nanosheets into thermoelectrics for use as supplemental power sources for ambient environment sensors such as triboelectric vibrational sensors. Thermoelectrics allow for the

conversion of waste heat energy present in environments such as art storage warehouses for the charging of batteries utilized in art preservation sensors. To further reduce the dependence of batteries in art preservation sensors, this work manufactured triboelectric vibrational sensors that passively sense disturbances to art pieces by spikes in voltage outputs. These triboelectric sensors produce voltage spikes upon lateral rubbing or vertical movement to or from two materials on the triboelectric series. Triboelectric materials are low-cost, widely available materials used as waste products in thermoelectric manufacturing contributing to overall sustainability and scalability. This work presents thermoelectric devices potential to act as a supplemental power supply for charging capacitors and batteries used in art sensors upon a heat difference. Additionally, this work presents a triboelectric vibrational sensor that detects disturbances and movements in art pieces. These devices were connected to a computer program which can notify art conservators to events such as earthquakes, robberies, or any rough physical contact that may be of interest.

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M

ELECTROCHEMICAL PERFORMANCE OF AQUEOUS ZINC-ION BATTERY CATHODES AT DIVERSE TEMPERATURES

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In order to complete the transition to renewable energy sources like wind and solar, grid-level energy storage must be installed to compensate for out of sync energy generation and demand profiles. Battery installations offer a potential option, but current lithium-ion chemistries are expensive, contain flammable electrolytes, suffer capacity degradation at low temperatures, and are not environmentally friendly. Aqueous zinc-ion batteries offer a safer and more sustainable

alternative to lithium-ion batteries. The zinc metal anode has a high theoretical capacity and is both cheaper and more abundant than lithium, while the aqueous electrolyte eliminates many safety concerns; however, current cathode materials are a limiting factor preventing their commercialization. Vanadium pentoxide (V_2O_5) cathodes promise high theoretical capacities, but these have yet to be realized in practice. A better understanding of the charge storage and degradation mechanisms could allow V_2O_5 cathodes to reach closer to their theoretical capacity. Our study aims to provide these insights by analyzing them over a range of temperatures.

Cyclic voltammetry (CV) analysis was chosen for the depth of insight it offers into the redox processes beyond the standard galvanostatic measurements performed in literature studies of zinc-ion battery temperature performance. We conducted a series of experiments using CV on Swagelok-type cells to analyze the electrochemical performance of V2O5 cathodes at temperatures from 0°C to 50°C. The cells were held at temperature in an environmental chamber, and comparisons between voltammograms from cells cycled at different temperatures allowed us to compare rates of reactions, contributions of different redox processes, and to analyze degradation mechanisms. Preliminary results show temperature-dependent redox behavior in V2O5 cathodes. Further analysis aims to enable a better understanding the mechanisms affected by temperature and their impact on the electrochemical performance of V2O5 as a cathode material.

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EVALUATION OF PRECIPITATION PHASE ALGORITHMS IN SOUTHERN NEW ENGLAND

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Precipitation's global distribution, anomaly, and extremes are fundamental in nature. There are three sequential questions to determine the precipitation climatology: Is it precipitating? What is the phase of the precipitation? What is the amount of precipitation? The response to these three questions comes with uncertainty. The oceans covers over 70% of Earth's surface, therefore satellite-based precipitation products are the sole source of global precipitation mapping. NASA's gauge-adjusted multi-satellite product, IMERG, has been operated and funded by the Global Precipitation Measurement (GPM) mission and is the most used precipitation product globally. The poor coverage of ground-based precipitation measurements across the land surface is one of the key reasons for the high demand for external precipitation resources. NOAA's

Multi-Radar Multi-Sensor (MRMS) with high spatial and temporal resolution precipitation mapping using national weather radar and multiple gauge platforms, was adopted by the GPM program as a validation product for satellite-based precipitation estimates from IMERG.

Both IMERG and MRMS have their own precipitation phase algorithms. MRMS's deterministic algorithm relies on High-Resolution Rapid Refresh (HRRR) air and wet-bulb temperature forecast, while IMERG's probabilistic algorithm uses European Reanalysis (ERA5) wet-bulb estimates. This study aims to evaluate these two algorithms utilizing data from a three-winter-long field campaign in Connecticut. The campaign included an All-In-One (AIO) weather station, laser-optical PARSIVEL disdrometer, Precipitation Imaging Package (PIP), and Micro-Rain-Radar (MRR) among other instruments. MRMS and IMERG algorithms utilizing the AIO temperatures are used as references. MRMS and IMERG algorithms utilizing HRRR, ERA5, and NASA's global modeling and assimilation office (MERRA-2) reanalysis have been evaluated. The phase algorithms of particle size and fall velocity-based PARSIVEL, PIP-derived and MRR-measured Doppler fall speed, and PIP-based bulk and equivalent density provided independent resources for the evaluation of MRMS and IMERG algorithms. The study focused on phase transition events but also included snow events.

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TEACHING AUDIO DEEPFAKE DETECTION WITH DATA SCIENCE CASELETS & REPOSITORIES

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Audio deepfakes are synthetic recordings generated using artificial intelligence methods to mimic human voices. Audio deepfakes have been used for malicious purposes such as spreading misinformation and committing financial fraud. Advancements in research have produced innovative and effective methods to detect audio deepfakes, although much more work is needed to make this work widely available for research and educational applications. In this presentation, we address a significant gap in the availability of educational resources that teach data science students about audio deepfakes and current detection methods through two approaches. First, we are developing data science caselets for use in data science classrooms to provide students with learning and analysis opportunities. Two data science caselets were created, with interactive counterparts in Jupyter Notebook in development as well. Second, we

are creating a data repository with compiled resources for publicly accessible research and training. The repository includes 11 papers thus far with 18 different datasets. Future research will study the efficacy of implementing caselets in classroom contexts.

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INHIBITING HEXOSAMINE BIOSYNTHETIC PATHWAY FLUX TO STUDY THE IMPACT OF O-GLCNAC ON PHYSIOLOGY

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Thousands of intracellular proteins are modified by monosaccharides of O-linked ß-N-acetylglucosamine (O-GlcNAc). The O-GlcNAc-modification, is an essential post-translational modification that regulates protein function in response to environmental and physiological stimuli. The dysregulation of O-GlcNAc-cycling has been linked to a multitude of diseases including neurodegeneration, cancer, hypertension, heart failure, diabetic cardiomyopathy, and ischemic heart disease. The addition of O-GlcNAc is catalyzed by the enzyme O-GlcNAc transferase (OGT). UDP-GlcNAc is the substrate of OGT and is generated by the Hexosamine Biosynthetic Pathway (HBP). The removal of O-GlcNAc is catalyzed by the enzyme, O-GlcNAcase (OGA). To study the impact of metabolism on UDP-GlcNAc abundance, as well as O-GlcNAc, we developed a mouse model in which UDP-N-Acetylglucosamine Pyrophosphorylase (UAP) can be deleted using cre-lox technology. UAP catalyzes the last step in the HBP by converting N-Acetylglucosamine-1-phosphate into UDP-GlcNAc through the addition of UTP. Using AAV8-TBG-Cre, which drives the expression of cre recombinase in the liver, we confirmed UAP deletion. To probe the impact of metabolism on UDP-GlcNAc levels and O-GlcNAc, UAP wild-type and knockout animals were fed or fasted. Immunoblotting was used to assess the abundance of UAP, O-GlcNAc, OGT, and OGA. UAP abundance was reduced and this was associated with a suppression in UDP-GlcNAc levels. OGT abundance was increased in UAP knockout livers, whereas OGA abundance decreased. O-GlcNAc was assessed using two different antibodies: CTD 110.6 detected little differences in O-GlcNAc, which may be consistent with enhanced OGT abundance. Counterintuitively, enhanced RL2 signal was detected and this may represent an alteration in OGT substrate selectivity. Unlike deletion of UAP, OGT abundance was decreased. Collectively, these data do not suggest that extracellular

glucose levels impact O-GlcNAcylation by controlling HBP flux. Rather, they imply that other signaling events control the abundance of UAP, OGT, and OGA, to impact O-GlcNAc and downstream cellular pathways.

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BUILDING A FORMALLY-CORRECT MANCALA GAME IN LEAN

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Lean 4 pairs an interactive theorem prover with a functional programming language, enabling us to write provably-correct code. We demonstrate this by developing a version of the ancient board game Mancala in Lean 4. This approach facilitates the understanding and proficiency in functional programming, which is less common as an entry point compared to imperative programming languages like Python or C# are prone to bugs.

The choice of Mancala is strategic due to its interesting parameters, which test various programming concepts such as input handling, user recognition, string interpolation, structured switching, and recursion. While imperative languages like Python and C# utilize loops (for, while) to manage complex functions and scripts, Lean 4 simplifies error identification due to its unique interactivity, not commonly seen in other high-level programming languages. Lean 4 can pinpoint and correct syntax or logical errors in the code, paving the way for “Provably-Correct Programming.”

The vision of this study is to make functional programming more accessible to individuals from both technical and non-technical backgrounds, such as scientists, engineers, and novices in coding. It aims to reduce the hassle of handling redundant errors in code, especially when dealing with multiple lines of code. Our “Provably-Correct Programming” approach through the Lean 4 Functional Programming Language highlights the benefits of a less common aspect of high-level coding. This approach enables a learning cycle complemented by a fully capable “hands-free” debugger, showcasing Lean 4’s potential in education and practical applications.

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SELF-SUSTAINING LOW-COST AND WIDELY AVAILABLE ENERGY HARVESTING AND SENSING DEVICES FOR USE IN MUSEUM ENVIRONMENTS

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In art preservation, low-cost and widely available ambient environment (temperature, vibrational, and humidity) sensors are critical to ensuring a safe environment that helps to monitor art stability. Current battery technology cannot meet the needs of these sensors due to frequent recharging or replacement. This work investigates optimal methods of incorporating MXene 2D nanosheets into thermoelectrics for use as supplemental power sources for ambient environment sensors such as triboelectric vibrational sensors. Thermoelectrics allow for the conversion of waste heat energy present in environments such as art storage warehouses for the charging of batteries utilized in art preservation sensors. To further reduce the dependence of batteries in art preservation sensors, this work manufactured triboelectric vibrational sensors that passively sense disturbances to art pieces by spikes in voltage outputs. These triboelectric sensors produce voltage spikes upon lateral rubbing or vertical movement to or from two materials on the triboelectric series. Triboelectric materials are low-cost, widely available materials used as waste products in thermoelectric manufacturing contributing to overall sustainability and scalability. This work presents thermoelectric devices potential to act as a supplemental power supply for charging capacitors and batteries used in art sensors upon a heat difference. Additionally, this work presents a triboelectric vibrational sensor that detects disturbances and movements in art pieces. These devices were connected to a computer program which can notify art conservators to events such as earthquakes, robberies, or any rough physical contact that may be of interest.

The project is supported by the SCIART program with funds from Mellon Foundation grant G-2109-11420 and the U-RISE Program at the University of Maryland, Baltimore County (UMBC), which is supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number T34GM136497. The authors thank Dr. Swapnil Ambade from the Department of Chemistry at the John's Hopkins University for providing the MXene 2D nanosheets. The authors thank Leopoldo Posada Escobar and Dr. Zeev Rosenzweig from the Department of Chemistry at the University of Maryland, Baltimore County for their guidance.

EXPLORING MUTATIONAL RESILIENCE OF TRANSCRIPTION FACTOR BINDING SITE SPECIFICITY MECHANISMS

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Transcription factors are proteins that regulate the expression of genes by binding onto specific DNA sequence patterns called motifs. A motif must contain enough information for the transcription factor to distinguish its binding sites from the rest of the genome. This information could be encoded in two ways: conservation of letters at specific positions across binding sites or correlation between binding site positions, known as Mutual Information (MI). Analyses of real motifs have shown that MI-encoded information is rare, but the evolutionary rationale for this absence has not been elucidated. Given the centrality of motifs in genomics analyses, understanding how they evolve to regulate gene expression is of critical importance. Here, we computationally simulate the evolution of transcription factor-binding motifs based on different information-encoding strategies. We find that motifs that primarily use MI are less resilient to mutational events and lose their information faster than conservation-based motifs. Our findings suggest that the use of conservation as a primary means of encoding motif information evolved as an evolutionary strategy to maximize the mutational resilience of regulatory networks.

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DEVELOPMENT OF A MOUNTING SYSTEM FOR FMCW RADAR ON UGVs AND DRONES FOR DETECTING OBSCURED OBJECTS WITHIN THE GROUND USING MMWAVE RADAR SIGNALS

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In the pursuit of advanced subsurface detection, this study presents the design and implementation of a robust mounting system for Frequency-Modulated Continuous-Wave (FMCW) Radar on Unmanned Ground Vehicles (UGVs) and Drones. The objective is to harness mmWave Radar signals to identify and map obscured objects (partially visible on the surface) within the ground, enhancing situational awareness and operational efficiency in diverse environments. Real-time detection of obscured objects improves the maneuverability of UGVs, assisted by drones that can better capture the surface of the objects. The research details the engineering challenges and solutions in integrating FMCW Radar with UGVs and drones, ensuring stability, accuracy, and optimal signal acquisition during movement.

Despite their advanced capabilities, FMCW radars often encounter artifacts such as noise, motion disturbances, and environmental interferences, which can degrade data quality and obscure true signals. To overcome these challenges, we developed a mounting system that extracts point cloud data of objects from different angles and views using mmWave Radar. The mount is equipped with an interlocking arm extended from the top of the robot to remove the possibility of obstruction during data collection. The end of the mount consists of a gear system that connects the radar to programmatically driven servos allowing the radar to actuate and collect data from various angles. The point clouds extracted from these angles serve as input to machine learning models, coupled with RGB image data to create Synthetic Aperture Radar (SAR) images of the objects.

We tested the mount's integrity and 3D printed a mount to attach to both the RosMaster2 UGV vehicle and the Modal AI drone. The 3D-printed mount was tested in real-time to collect data on obscured objects from different angles, demonstrating its effectiveness in subsurface detection and object identification. This work is a testament to the collaboration between Mechanical Engineering and Information Systems.

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SEX-DIFFERENCES IN STRESS SUSCEPTIBILITY AND SYNAPTIC PROTEIN EXPRESSION

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Females have a higher susceptibility to developing stress-related psychiatric disorders such as depression. However, there is limited knowledge regarding the sex-specific mechanisms that arbitrate behaviors relating to these disorders. This further complicates our understanding and treatment mechanisms for these debilitating conditions. Stress has many deleterious effects on brain function, particularly in the nucleus accumbens (NAc). The NAc, a crucial area in the brain, mediates motivated behaviors and is involved in psychiatric disorders.Recently, we discovered a female-specific role for GABAb receptors. Especially, modulating the strength of connections in the NAc is essential for supporting motivated behaviors. This poses the question regarding the role of GABAb receptors in sex-differences in behavior and stress susceptibility. Utilizing a commonly used stress paradigm shown to elicit sex-differences in susceptibility helped determine whether the expression of GABAb receptors differs in a sex-dependent manner. Males and female mice were then exposed to identical variable stress paradigms involving alternating days between foot-shocks, tail hang, and restraint. Unstressed littermates served as controls. To evaluate stress susceptibility, we measured several physiological and behavioral outcomes including sucrose preference testing and novelty suppressed feeding. The NAc was then extracted and used for Western blot analysis.

Our findings have shown the experimental mice had a lower sucrose preference and a higher latency during novelty suppressed feeding which indicates the stress paradigm was successful. Currently using Western blotting, we aim to find a relationship between the GAPDH and Br2 subunit.This is important because research focusing on GABABr2 can help pharmaceutical developers create new medicine for those with depression. Moreover, this helps us understand the effect of stress on females and aids in understanding if sex plays a role in differing protein expressions. This will give another perspective on how stress plays a role in mental health, especially for females.

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A SEARCH FOR TWO MASSIVE SCALAR RESONANCES IN THE BB+TT FINAL STATE

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Since the discovery of the Higgs boson, observing decays that produce this boson can lead to potentially new hypothetical resonances that decay into particles previously unseen in our current understanding of the Standard Model, furthering our current understanding of particle physics. This study aims to show the decay of a heavy resonance that creates a Higgs boson and another resonance that further decays into a top quark and an anti-top quark. Using signals generated by the Large Hadron Collider (LHC), signal samples are analyzed to detect resonances that then break down into a Higgs boson and another resonance that then decays into a top quark and an anti-top quark, with these quarks decaying further, either hadronically or leptonically, to find new particles unknown to our current Standard Model.

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FEATURE EXTRACTION ANALYSIS AND BASELINE MODELING OF COGNITIVE LOAD IN WORKING MEMORY USING EEG, GSR, AND PPG DATA

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Working memory, a subset of our short-term memory, facilitates the temporary storing and processing of information. Its uses extend to several cognitive functions, aiding us in daily tasks such as reading, driving, and recalling where we last placed our keys. In a previously conducted study, the project leader collected multimodal sensor data to extract significant cognitive state

changes during navigation tasks, aiming to intelligently cue and improve the recall of those activities. Currently, we propose an evaluation of the working memory dataset alongside several cognitive load assessment datasets to assess and classify cognitive load levels. Our proposed method begins with extracting features from physiological data, specifically electroencephalography (EEG), galvanic skin response (GSR), and photoplethysmography (PPG). We then train various shallow classification algorithms, such as random forest (RF), decision tree (DT), and support vector machine (SVM), to predict the induced cognitive load levels. Furthermore, we conduct an analysis of the feature extraction module to determine the most informative features among those extracted for each modality.

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IMPROVING THE CARBON-CONCENTRATING MECHANISM IN THE GREEN ALGA CHLAMYDOMONAS

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Photosynthesis is a process that is able to take place due to the abundance of CO_2 in the atmosphere. However, for organisms like green algae that live in aquatic environments, where the CO_2 levels are low, it becomes a challenge. The Carbon-Concentrating Mechanism (CCM) is these organisms' adaptation to their environment. This mechanism involves the uptake of inorganic carbon in the form of bicarbonate (HCO_3^-) and transforming it into CO_2 in the pyrenoid where the enzyme rubisco fixes it into sugars. This project focuses on two specific carbonic anhydrases, CAH1 and CAH3, that interconvert bicarbonate and CO_2. Our hypothesis is that these enzymes play critical roles in the CCM by increasing the concentration of CO_2 near rubisco, and we predict that overexpressing them in the green alga *Chlamydomonas* will lead to increased algal growth. This project aims to test this hypothesis and prediction. We previously transformed overexpression plasmids for these genes into *Chlamydomonas* and now are testing recipient cells to determine whether they have the plasmids, express the CAH proteins, and have improved photosynthetic and growth rates. So far we have used PCR to test for presence of the genes, and preliminary results indicate that the transformants have them. Next we will do western blots to measure the protein abundance, and we will measure growth and photosynthetic rates. Ultimately this work should provide a strategy for improving biomass production so that green algae can be an effective platform for biofuel production.

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MUSCARINIC RECEPTOR REGULATION OF HUMAN COLON CANCER CELL MICROTENTACLE FORMATION

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Metastatic colon cancer remains the second leading cause of cancer-related death in the United States, resulting in approximately 50,000 deaths yearly. Recent findings suggest that tentacle-like extensions, designated as microtentacles, facilitate cancer cell attachment and spread. Previous work elucidated several mechanisms whereby muscarinic receptor activation modulates colon cancer cell biology. M3 muscarinic receptor (M_3R) activation stimulates colon cancer cell proliferation, migration, and invasion. In contrast, M1 muscarinic receptor (M_1R) activation inhibits colon cancer cell proliferation. In the present investigation, we will use a human colon cancer cell line that overexpresses M_3R (HT29 cells) and a cell line that overexpresses M_1R (HCT116 cells) to see if muscarinic receptor activation alters colon cancer cell microtentacle formation. In initial experiments, HT29 human colon cancer cells were cultured in McCoy's medium with 10% FBS, loaded onto tether chips (30,000-50,000 cells/well), and treated with vehicle (phosphate buffered saline, PBS), or 100 and 300 μM acetylcholine for 45 min. After each treatment, we fixed cells with 3.7% formaldehyde, stained with Wheat Germ Agglutinin

(WGA) and Hoechst (nuclear stain), and washed cells twice with PBS. Fixed cells were mounted with Fluoromount-G and imaged at 40x and 60x magnification using a fluorescence microscope; we measured the number and length of microtentacles. Initial observations confirmed the formation of microtentacles by some but not all HT29 cells. Ongoing investigations will determine the percentage of HT29 and HCT116 cells forming microtentacles at baseline and after stimulation with non-selective and M1R and M3R selective muscarinic receptors agonists. We will then elucidate the post-muscarinic receptor signaling pathway mediating these changes. Modulation of microtentacle formation by selective activation or inhibition of M_1R and/or M_3R may provide a novel approach to prevent or retard colon cancer metastasis.

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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 estimated 1 in every 36 children is diagnosed with autism in the United States, which raises a need for 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 they compare 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.

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DISCOVERING FUNCTIONAL DEFECTS IN CILIOPATHY-DERIVED IPSC-RPE

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The primary cilium, a microtubule-based cellular protrusion present in all cell types, is associated with a spectrum of heterogeneous developmental disorders called ciliopathies. Retinal degeneration is one of the most common outcomes, leading to gradual vision loss. Primary cilia play a vital role in the structure and function of the retinal pigment epithelium (RPE), a monolayer of highly polarized cells adjacent to the photoreceptors and important for retinal health. Previous studies suggest that primary cilia might regulate metabolism in various cell types. However, whether these affect RPE health is not yet known.

This study aims to identify the different ways the RPE phenotype is affected by ciliopathy-associated mutations, specifically in regards to mitochondrial health and autophagy. Therefore, we generated induced pluripotent stem cell (iPSC)-derived RPE (iRPE) from patients that had mutations in various ciliary proteins causing different ciliopathies (BBS1, BBS10, CEP290, LCA5, MYO7A, or PRPF31), all of which are associated with different degrees of retinal degeneration. To identify the effect of these ciliary mutations on mitochondria and autophagy in the RPE, we tested for known markers using methods such as Western Blotting (p62, TOMM20, COX4, LC3B, HMGCS2, GLUT1) and immunohistochemistry (TOMM20, COX4, p62, DLP1).

Patient iRPE revealed differential effects of ciliary mutations on mitochondrial morphology seen in hyperfused or apoptotic mitochondria and increased mitochondrial mass compared to controls. Preliminary results point towards defects in autophagy seen in dysregulated levels of p62 and LC3B. Using transmission electron microscopy, measurements of mitochondrial DNA, and live-cell imaging, we will further investigate the mitochondrial defects in patient iRPE.

These results indicate a potential involvement of defective mitochondria and dysregulated autophagy in the RPE of ciliopathy patients and will help to further understand the underlying cellular defects arising from ciliary mutations as well as the role of the primary cilium in regulating metabolic processes.

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AUTO ANNOTATION OF EXPERT DEFINED LINGUISTIC FEATURES (EDLFS) TO IMPROVE AUDIO DEEPFAKE DETECTION

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The rise of deep fakes, including AI-generated audio, poses significant challenges in terms of fraud, deception, and impersonation. Current detection methods for audio deep fakes, such as utilizing deep neural networks, often prove brittle against adversarial models. (Mai et al. 2023). To address these challenges, we introduced a methodology that encompasses annotating discords (anomalies) and motifs (repetitive patterns) with the aim of annotating for and cross validating a set of five Expert Defined Linguistic Features (EDLFs)–pitch, pause, word-initial or word-final consonant burst, breath, and overall sound quality–that had previously been labeled by linguistics experts and found to improve audio deepfake detection. Fifty English audio samples were annotated as subsequences in a time series for four discords and motifs respectively across lengths ranging from 0.1 to 1.5 seconds. These discords and motifs were then carefully checked for overlap with annotations for EDLFs provided by linguistic experts. We found that discords and motifs performed similarly overall in capturing EDLFs. However, each method excelled in different specific metrics, showcasing their combined potential to enhance audio deepfake detection.

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PH DEPENDENCE OF BROWN-CARBON OPTICAL PROPERTIES IN CHINESE FOG WATER

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Light absorbing organic molecules known as brown carbon (BrC), are abundant through the atmosphere, though the extent of their influence on radiative forcing effects within the climate is uncertain. The presence of clouds, in spite of their large variations in pH, likely serve as an element for BrC production and bleaching reactions. The acidity and other chemical properties of these atmospheric compounds have been shown to influence the extent to which they absorb or reflect light. Due to the wide variety of acidities found within different compounds in the atmosphere, a large range of pH's optical properties of atmospheric samples need to be classified to accurately characterize their effect on the climate. In order to do this, the samples are tested at different pH's, cycling down from 9 to 1.5 using acids and bases. Optical properties of BrC, specifically light absorption at 365 nanometers (Abs_{365}), the mass absorption coefficient (MAC_{365}), and the Absorption Ångström exponent (AAE), were measured from fog water sampling collected at the Shanghuang Site in China following agricultural burning in the surrounding area. Results of the collected data indicate an exponential decrease in absorption and increasing wavelength, suggesting a linear, positive relationship with pH and absorbance at 365 nm. However, due to differences in cloud water composition for each sample, the increasing slope between pH and absorption at 365 nm is expected to vary. Future plans will involve continuing to classify pH's optical properties within the fog water samples across a wide range of acidities, as well as executing reverse pH cycles, cycling up from 1.5 to 9 by increments of 1 unit, to test pH dependence reversibility. In addition to this, a secondary system will be created and validated to increase the tempo at which samples are tested.

Support for this research was funded by the National Science Foundation REU Grant (Award #2050728) and the U.S. Department of Energy.

DECODING GLUCOSOME: REVEALING THE FUNCTION-DEPENDENT COMPOSITION OF GLUCOSOMES

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Glucosome is a multi-enzyme assembly that regulates glucose flux between glycolysis and building block biosynthesis (i.e., the pentose phosphate pathway and serine biosynthesis) in human cells. Initially, glucosome was discovered to be composed of at least four rate-determining enzymes from glucose metabolism, including phosphofructokinase (PFK), fructose bisphosphatase, pyruvate kinase, and phosphoenolpyruvate carboxykinase. Subsequent high-content imaging assays and mathematical modeling approaches have revealed 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 glucosomes. We hypothesize that other enzymes in glucose metabolism may also play an important role as glucosome components in guiding glucose flux in human cells. In this work, we first generated fusions proteins of phosphoglucose isomerase (PGI), aldolase, triose phosphate isomerase, glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase, phosphoglycerate mutase, and enolase with a monomeric enhanced green fluorescent protein. Fluorescent live-cell imaging has been then used to determine if these enzymes present any spatial relationship with the rate-determining enzymes in glucosomes. Preliminary results have suggested that aldolase and PGI may colocalize with PFK in Hs578T cells, and we aim to evaluate all the enzymes in the pathway. Collectively, we envision that this study would advance our understanding of how glucose metabolism is regulated inside living human cells, thereby leading therapeutic intervention toward the treatment of human metabolic diseases.

This research was supported by the National Institute of Health (to S.A). and by the Undergraduate Research Award at UMBC (to A.O).

ASSESSING ANXIETY-LIKE BEHAVIORS IN MICE FOLLOWING SUBCHRONIC E-CIGARETTE EXPOSURE

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Electronic cigarette (e-cigarette) use has surged in popularity, prompting concerns about potential health risks. Emerging evidence suggests links between e-cigarette use and negative mental health outcomes, including anxiety and depression. This study aims to investigate the hypothesis that e-cigarette exposure increases anxiety and depression-like behaviors in mice.

To establish baseline behavior before e-cigarette exposure, we conducted a pre-testing phase using three established tests: the elevated plus maze, light/dark box, and tail suspension test. These tests are designed to assess anxiety-like behaviors in mice through various parameters, including decreased movement, latency to enter the bright side of the light/dark box, and positive thigmotaxis in the elevated plus maze. While the complete analysis of this pre-testing data is ongoing, we expect it to reveal similar levels of anxiety-like behavior across all test groups. Following this pre-testing phase, mice will be exposed to e-cigarettes for a designated period of 8 weeks exposure and re-testing behavior at the midpoint and the endpoint. We hypothesize that chronic e-cigarette exposure will lead to a significant decrease in time spent in the open arms of the elevated plus maze and the light compartment of the light/dark box, as well as increased immobility time during the tail suspension test. These behavioral changes would be indicative of heightened anxiety and depression-like behaviors in the mice. By repeating these behavioral tests at the designated time points after e-cigarette exposure, we aim to establish a causal link between e-cigarette use and the development of anxiety and depression-like behaviors. This research, if supported by the post-exposure data, could contribute valuable insights into the potential mental health risks associated with e-cigarette use in humans.

We gratefully acknowledge the financial support provided by the UMBC Louis Stokes Alliance for Minority Participation (LSAMP) (2207374). We extend our sincere thanks to the undergraduate and graduate students whose invaluable contributions were essential to this project. Special appreciation goes to Dr. Lin Weihong for their expert guidance and mentorship throughout this endeavor.

DEVELOPING A MOUSE MODEL OF CHRONIC PROSTATITIS/CHRONIC PELVIC SYNDROME

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Chronic Prostatitis/Chronic Pelvic Syndrome (CP/CPPS) is one of the most common reasons that men visit a urologist. This disorder is characterized by diffuse pelvic pain and altered voiding patterns. While the cause of CP/CPPS remains unknown, a potential contributing factor is chronic prostatic inflammation. To determine if chronic prostate inflammation is sufficient to cause symptoms consistent with CP/CPPS, we employed a genetically engineered mouse model of prostate inflammation. In this model, exposure of the mice to Doxycycline results in expression of the proinflammatory cytokine IL-ß in the prostate gland. To determine if mice with prostate inflammation experience pelvic inflammatory discomfort, we performed the Von Frey assay to quantify pelvic discomfort. The Von frey assay protocol is a method we used to test prostate specific pain sensitivity in male mice. In the Von Frey assay, a set of filaments ranging in size and thickness that exert different forces of 0.02 g, 0.04 g, 0.16 g, 0.4 g, and 1.0 g were applied repeatedly to the pelvic area of mice with and without prostate inflammation. The response of each mouse to the filament application was recorded. Positive responses included scratching the area and sudden jumping movements. Our preliminary results indicate that the lineage B when compared to the lineage A is more sensitive to Von Frey tests, this could be attributed to the expressivity of proinflammatory cytokine IL-Beta. More data still needs to be gathered to determine to make more conclusive results of lineage differences and their inflammatory phenotypes.

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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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A ROLE OF HEPARAN SULFATE PROTEOGLYCAN PROCESSING ENZYMES IN MEDIATING CELL MIGRATION IN DROSOPHILA MELANOGASTER EGG CHAMBERS

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Cell migration is essential to understanding cancer metastasis, immune responses, embryogenesis, and wound repair. Our model system for cell migration is the border cell cluster, which arises during Drosophila melanogaster oogenesis and has well-conserved regulatory mechanisms with those in human motile cells. This cluster detaches from the anterior epithelia of the egg chamber (the tissue that houses the egg) and migrates between the surrounding germline toward the oocyte. Cytokines induce cell motility, and chemoattractants guide border cell

migration. Current models suggest that a chemotactic gradient forms across the egg chamber to guide migration toward the oocyte, but the precise chemoattractant distribution and how the border cells sense it remains unclear.

We hypothesize that extracellular heparan sulfate proteoglycans (HSPGs) regulate border cell migration by facilitating the diffusion and proper spatial distribution of chemoattractants and cytokines. We downregulated the expression of glycosylation enzymes that produce HSPGs using the Gal4/UAS system and RNA interference in border cell migration-relevant cell types. We downregulated the HSPG sulfotransferase, Heparan sulfate 6-O-sulfotransferase, and dehydrogenase, sugarless, and observed significant migratory delays, supporting our hypothesis. Interestingly, we also observed extra migrating cells outside of the cluster, potentially indicating changes in the motility-inducing cytokines. Clues into the spatial importance of HSPGs can help narrow down potential protein targets to aid in migration. We are currently conducting experiments to replicate our results and will validate the effectiveness of the RNAi using qRT-PCR. In the future, we will also perform genetic screens to discern which specific proteins are affected by glycosylation. By understanding where HSPGs are necessary for development, we can determine their role in migration for the context of human development and disease.

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NDRG1B, A NOVEL REGULATOR OF N-CADHERIN DURING TISSUE MORPHOGENESIS AND HYPOXIA

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Cadherin-based cell adhesion is essential for many aspects of morphogenesis, and has been extensively studied owing to its essential role in epithelial integrity and development. The Brewster lab has a longstanding interest in the role of N-cadherins(N-cad) in tissue morphogenesis, and identified an essential role for this adhesion molecule in shaping the neural tube, the precursor of the brain and spinal cord. In this study we report on the role of N-myc Downstream regulated gene 1b (ndrg1b) as a novel regulator of N-cad trafficking during myogenesis of the zebrafish embryo and under hypoxia, low oxygen conditions. Ndrg1b is a member of the NDRG subfamily of adapter proteins, several members of which have been

shown to be hypoxia responsive and mediate the recycling of transmembrane proteins, including the glucose transporter and E-cadherin members. We show here that ndrg1b is ubiquitously expressed during gastrula and segmentation stages, with higher expression in the developing nervous system and somites. Ndrg1b knockdown using morpholinos results in developmental defects that are remarkably similar to those observed in N-cad mutants, especially with regards to impaired myogenesis. In zebrafish, slow muscle precursor cells originate from the adaxial cells next to the notochord that express N-cad. These precursor cells undergo lateral migration to reach their final destination in the flank of the embryo, where they differentiate into slow muscle fibers. In ndrg1b-depleted embryos and under hypoxa, slow muscle precursors do not complete their migration and N-cad appears misclocalized intracellularly. Based on these observations, we hypothesize that N-cad turnover is essential for slow muscle precursor migration and that Ndrg1b mediates N-cad trafficking in this cell population under normoxic and hypoxic conditions. Data supporting this model will be presented.

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P

DETERMINING A ROLE FOR THE MICRORNA, BEREFT, DURING BORDER CELL MIGRATION

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Cellular migration contributes to numerous biological events, such as developmental feats, wound healing, and adversely during cancer metastasis. Therefore, researching cellular migration can give nuance to our understanding of developmental progression and relevant diseases. To better understand cellular migration regulation, our lab studies border cells, invasive follicle cells that migrate posteriorly as a cluster through the egg chamber toward the oocyte during Drosophila oogenesis. The Drosophila fly is a valuable model system because they have fast generation times and easily manipulated genes that are conserved with humans. While many experiments have focused on the regulation of border cell movement – and cells in general – less is known about the role of microRNAs (miRNAs) within this context. MiRNAs are short, non-coding RNAs that post-transcriptionally regulate gene expression. This study aims to identify how the knockdown of a certain miRNA called bereft impacts border cell migration. Previous work in our lab has shown that the bereft miRNA may post-transcriptionally target the border cell specification gene, unpaired. Thus, we hypothesize that inhibiting bereft function will cause incorrect specification and a change of migration behavior within border cells. To test this hypothesis, we knocked down bereft function in border cells and evaluated their migration

phenotype. While migration occurred normally in a control genotype, when bereft was knocked down, there were no observable egg chambers that developed into a relevant stage, so further experiments are necessary. Future goals involve using different lines to observe how various cellular pathways impact border cell differentiation and migration. In a broader sense, this study could uncover how a miRNA regulator pathway can orchestrate cellular migration and the physiologies it evokes.

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EXPLORING ICEBERG LIFE CYCLES THROUGH VISUALIZATION AND GAMIFICATION

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Understanding the dynamics of ice mass loss, including glacier calving and subsequent iceberg drift, fracturing, temporospatial distribution, and melting, is crucial for climate research in polar regions. Satellite remote sensing systems, including electro-optical (EO) and Synthetic Aperture Radar (SAR), can be used to track and visualize the spatial and temporal distribution of icebergs, including their density and trajectories, allowing for a comprehensive study of their life cycle—from calving to drifting, fracturing, and melting. This information is useful to climate scientists because melting icebergs release freshwater and nutrients into the ocean, and contribute to the formation of sea ice and ocean currents, all of which are important contributors to scientific models of sea level rise. How can visualizing and characterizing these processes aid scientists in the development and understanding of more accurate climate change models? In addition to scientific visualization for model development, the visual narration of compelling stories about specific calving events can help scientists engage the public and policy-makers, and highlight the significance of these processes in the broader context of climate change. Can the gamification of these visualizations create a more interactive and engaging experience? A gamified visualization will serve as the experimental aspect of the project to explore the iceberg lifecycle and provide an interactive visual narrative. This visual narrative approach not only informs, but also motivates action towards addressing climate challenges, involving the viewers in the tension and outcome of a visual story that will inevitably change life on Earth.

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PH DEPENDENCE OF BROWN-CARBON OPTICAL PROPERTIES IN CHINESE FOG WATER

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Light absorbing organic molecules known as brown carbon (BrC), are abundant through the atmosphere, though the extent of their influence on radiative forcing effects within the climate is uncertain. The presence of clouds, in spite of their large variations in pH, likely serve as an element for BrC production and bleaching reactions. The acidity and other chemical properties of these atmospheric compounds have been shown to influence the extent to which they absorb or reflect light. Due to the wide variety of acidities found within different compounds in the atmosphere, a large range of pH's optical properties of atmospheric samples need to be classified to accurately characterize their effect on the climate. In order to do this, the samples are tested at different pH's, cycling down from 9 to 1.5 using acids and bases. Optical properties of BrC, specifically light absorption at 365 nanometers (Abs_{365}), the mass absorption coefficient (MAC_{365}), and the Absorption Ångström exponent (AAE), were measured from fog water sampling collected at the Shanghuang Site in China following agricultural burning in the surrounding area. Results of the collected data indicate an exponential decrease in absorption and increasing wavelength, suggesting a linear, positive relationship with pH and absorbance at 365 nm. However, due to differences in cloud water composition for each sample, the increasing slope between pH and absorption at 365 nm is expected to vary. Future plans will involve continuing to classify pH's optical properties within the fog water samples across a wide range of acidities, as well as executing reverse pH cycles, cycling up from 1.5 to 9 by increments of 1 unit, to test pH dependence reversibility. In addition to this, a secondary system will be created and validated to increase the tempo at which samples are tested.

Support for the research was funded by the National Science Foundation REU Grant (Award #2050728) and the U.S. Department of Energy.

COMPARING COLLAGEN EXTRACTION METHODS AND PREPARATION METHODS FOR USE IN LAYER-BY-LAYER COATINGS

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Autografts are the most common treatment option used in peripheral nerve injuries. However, nerve guide conduits (NGCs) require fewer surgeries than autografts[1]. NGCs are only applicable as a treatment option when the injury is less than one centimeter in length. This restriction is caused by the lack of critical resources needed by the extracellular matrix in cellular regeneration[2]. The NGC surface is the main location for regeneration[2]. The NGC surface can be modified with Layer-by-Layer (LbL) coatings, and the characterizations of heparin-collagen (HEP/COL) LbL coatings have been studied extensively by our group [3,4]. We have previously shown that using HEP/COL bilayers can increase the human Schwann cell viability on the surface of NGCs[3]. This work aims to expand our previous research by comparing the viability of human Schwann cells on HEP/COL surfaces constructed using collagen from two different manufacturers, Integra and Biomarix. Biomatrix Collagen pretreated with acetic acid and diluted with pH 4.0 buffer yielded similar results in cell viability experiments to Integra Collagen dissolved in pH 4.0 buffer. The manufacturer protocol for biomatrix collagen in LbL also increased cell viability for hSCs. FTIR testing showed that Biomatrix Collagen and Integra Collagen were almost identical. Overall, our research demonstrate that the HEP/COL coatings are a suitable strategy to increase cell viability using collagen from different manufacturers.

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PRECIPITATION IMAGING PACKAGE (PIP): A POTENTIAL INSTRUMENT FOR MEASURING RAINDROPS

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Rain is essential for ecosystem, but measuring it fully, from tiny droplets to larger particles, remains a scientific challenge. What if there was an instrument that could capture the entire size regime of raindrops? Meet the Precipitation Imaging Package (PIP), a camera-based instrument, namely disdrometer, from NASA designed by Dr. Larry Bliven. It has been originally constructed to measure the size, fall velocity, and concentration of snowflakes. PIP participated NASA's winter field campaigns under Global Precipitation Measurement (GPM) mission nearly two decades. PIP is a reliable, cost effective, and low maintenance instrument. A new software is just being developed to improve its ability to track particles, aiming to measure the entire particle size distribution spectrum and refine its capabilities for rain.

Our project is focused on exploring the potential of the PIP to revolutionize how we measure and analyze rainfall. Through GPM field campaigns during the winters of 2023 and 2024, our team evaluated different software for processing the PIP images. We tested six methods through comparative study with the traditional rain-measuring devices including laser-optical PARSIVEL disdrometer and tipping and weighing bucket gauges. The comparisons were based on raindrop size distribution and rain accumulation diagrams.

Our initial findings reveal both promise and surprise. Certain PIP processing methods yielded higher rain totals than the traditional instruments, indicating potential for refinement. While others align closely with traditional gauges, most show higher totals than reference instruments measure. This offers an opportunity for further enhancement, increasing accuracy and establishing the PIP as an essential tool in weather research and beyond.

Particle size distribution is fundamental quantity in weather forecasting and climate models. It is also the key parameter of remote sensing of precipitation. PIP's ability to measure entire size regime of hydrometeors (raindrops, snowflakes) brings it as a potential instrument for operational use in National Weather Service's automated surface observing system across US.

This research is funded by the Michigan Space Grant Institute.

EVALUATION OF LOW-COST ALTERNATIVE BIOMATERIALS FOR MODULATION OF NEAR-FIELD PLASMON-COUPLED EMISSION TOWARDS A LOW-COST OXYGEN SENSOR

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Surface Plasmon Coupled Emission (SPCE) is an optical sensing technique that integrates two widely used techniques namely surface plasmon resonance and fluorescence. This is achieved by using a fluorophore embedded in a polymer matrix coated on a metal nano thin film. The emission couples with surface plasmons and out-couples with improved angularity and enhancements. Unique spacer materials are placed near the fluorophore to influence the emission coupling. A low-cost material – diatomaceous earth (DE) – was used as an eco-friendly alternative in this study. DE is a naturally occurring, non-depletable material that are formed as shells by single-celled algae. They have known remarkable optical modulation properties in literature towards surface enhanced Raman scattering. To evaluate its effects on near-field SPCE, DE with AgNPs were coated onto plasmonic thin film and tested on SPCE optical setup in reverse Kretschmann geometry. For comparative analysis, a control sample was tested with SiO2 beads replacing DE. The uniqueness of DE over the spherical SiO_2 is due to its complex symmetrical patterns and shape that helps in rendering additional optical effects in channeling the fluorescence. The results provide insights into the optical effects of uniquely shaped DE on plasmon-coupled emission in comparison with spherical SiO_2 materials. Further modifications in DE could lead to promising low-cost sensor assemblies that can be applied for various gas and liquid phase sensing applications.

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Q

HIGH THROUGHPUT SCREENS TO DISCOVER UNCHARACTERIZED CELL WALL SIGNALING KINASES IN ASPERGILLUS NIDULANS

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In the Marten Lab, research focuses on filamentous fungi, in particular, the cell wall and its clinical and industrial importance. This research seeks to reveal more about the underlying processes that govern cell wall properties in filamentous fungi by looking at regulatory signaling pathways, such as the cell wall integrity (CWI) signaling pathway. These signaling pathways all involve protein kinases that transmit signals by attaching phosphate groups to other proteins. To explore protein-protein interactions involving the CWI pathway, previous work in MartenLab used transcriptomic, phosphoproteomic, and phenotypic analyses. These analyses suggest cross-talk with other signaling pathways, implying that kinases outside of the established CWI pathway influence cell wall stress response. This research project seeks to identify these kinases by screening a library of all 98, non-lethal Aspergillus nidulans kinase knockout (K.O.) strains for their ability to survive 3 distinct cell wall perturbants. Within a 95% confidence interval, only 30 single K.O. strains displayed statistically significant survival rates. These included 2 under all three cell wall perturbants, 2 under just two, and 22 under only one. For screens done on double K.O. strains, 3 strains displayed statistically significant survival rates.

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R

INVESTIGATING BINDING INTERACTIONS BETWEEN THE MONOMERIC HIV-1 RNA GENOME AND CAP-DEPENDENT TRANSLATIONAL MACHINERY, EIF4E

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The human immunodeficiency virus type-1 (HIV-1) affects over 39 million people worldwide. Current treatments include a drug cocktail consisting of inhibitors that target multiple steps of the viral replication cycle. However, many patients experience disruptive side effects due to the copious amount of drugs needed to combat the high viral mutation rates. Thus, our laboratory investigates a highly conserved segment of the HIV-1 RNA genome, the 5′-Leader (5′-L), as it is less susceptible to mutations. This region controls 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. Our group focuses on the monomeric conformation's exposed 5′-cap. This exposed 5′-cap recognizes cellular cap-dependent translation machinery, such as the protein eIF4E, in order to produce HIV viral proteins. However, it is unknown how structural elements of the HIV-1 RNA genome impact binding of eIF4E. We designed and purified 5′-capped RNA oligos with varying lengths of the TAR hairpin and the unstructured poly-A to determine if these regions of the RNAs affect eIF4E binding. We investigated the binding interactions between eIF4E and these truncated RNAs both qualitatively and quantitatively; electrophoretic mobility shift assays (EMSAs) confirmed binding and isothermal titration calorimetry (ITC) measured binding affinities. Our ITC data revealed that the HIV-1 5′-capped RNA bound >2 folds tighter to eIF4E than to the 5′-cap alone, supporting our hypothesis that electrostatic interactions between structural elements of the RNA and the eIF4E protein affect recruitment and binding. This research can be utilized to pinpoint a potential drug target within the highly conserved across HIV-1 RNA genome.

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TESTING ETHANOL TREATMENT FOR THE REDUCTION OF ALZHEIMER'S DISEASE (AD) IN DROSOPHILA

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Alzheimer's disease is a neurodegenerative disease that causes loss in cognitive functions, most common being memory loss, and is shown to be fatal as well. Alzheimer's affects 7 million Americans as of 2024. Alzheimer's is determined by the accumulation of fragments (amyloid-beta) of the protein amyloid precursor protein (APP) on the outside of the neuron called plaques or of misstructured/misfolded protein tau that clumps together within the neuron called tangles. APP and its amyloid fragments help with basic functions of neuron, but the amyloid-beta is produced when the length of the fragments is incorrectly spliced. Tau proteins play an important role as the "skeleton" of the neuron, transporting nutrients and other molecules. The accumulation of these proteins impairs the function of neurons, eventually leading them to their death, which leads to permanent damage to the brain. Previous studies showed the reduction of the progression of aging-dependent phenotypes in Drosophila treated with ethanol. In a four-week experiment, this study tested different concentrations of ethanol (1%, 2.5%, and 5%) to see within what range showed reduction in the disease-associated phenotypes and to what extent as well. Using flight behavioral experiments, we compared the flight performance between treated and control aging flies. We looked at the anatomical structure of the ventral cord using dissected fly nervous systems to see the progression of the disease within the control group and the reduction of the disease within the treatment groups. We also looked at the effect of ethanol on non-infected flies to examine other effects of ethanol on aging flies.

This research was funded by the LSAMP Summer Research Program.

EXPLORING THE FATE OF RNA IN MOLONEY MURINE LEUKEMIA VIRUS

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Moloney Murine Leukemia Virus (MoMuLV) is a gammaretrovirus that causes leukemia and neurological diseases within rodentia. It has been studied since the 1950s as a model to further understand the underlying mechanisms of all retroviruses. Our laboratory mainly focuses on Human Immunodeficiency Virus type-1 (HIV-1), most particularly the segment of the HIV-1 RNA genome necessary 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 (^{Cap}1G) in which the cap is sequestered, and the monomeric conformation adapted by 5'-capped RNAs that begin with two or three guanosines (^{Cap}2G and ^{Cap}3G respectively) where the cap is exposed. We refer to viruses containing these different beginning sites as having transcriptional start site heterogeneity. Inversely, MoMuLV utilizes a promoter with a single transcriptional start site, ^{Cap}1G, from which both packaging and translation occur. We wish to understand what drives RNA packaging versus translation in a retrovirus that contains a single start site. Through our exploration of this process, we hope to gain insight into the machinery that older viruses have conserved for millennia and provide indications of possible characteristics that newer retroviruses may exhibit in the future. Like HIV-1, we suspect that MoMuLV's genome fate is driven by dimerization dependent cap sequestration. We plan to explore the behavior of MoMuLV's genome in vitro by determining the conditions needed for the RNA to function as a monomer or dimer, capping the RNA to get an accurate representation of the virus, and exploring cap sequestration via electrophoretic mobility shift assays. After capping the RNA, to confirm its conformation we will use nuclear magnetic resonance. We will then test the hypothesis that cap sequestration is necessary for packaging in MoMuLV, as previous studies have shown it is essential in HIV-1.

Support for this research was provided by Howard Hughes Medical Institute and NIH/NIAID grant (#5R01AI50498).

EVALUATION OF PRECIPITATION AMOUNT PRODUCTS IN MID-ATLANTIC AND SOUTHERN NEW ENGLAND

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Precipitation is a driving force for the water cycle and is one of the key sources of weather extremes. The changing global climate and consequent increase in extreme weather retaliates dependence of daily life to precipitation. The drought in Maryland is evident, as only 48 mm (1.9") of rainfall fell during the first 50 days of Summer 2024.This information is based on a gauge report at Baltimore Washington International airport. Unfortunately, most of the global

land is not equipped with precipitation measuring devices. This is due to topography, land use coverage, cost, and remoteness. With the addition of global ocean coverage (>70%), precipitation climatology relies on spaceborne precipitation retrievals and model outputs. NASA's multi-satellite product, IMERG, operated and funded by the Global Precipitation Measurement (GPM) mission, is widely used in scientific research and operational applications. The NOAA's Multi-Radar Multi-Sensor (MRMS) product has been widely employed to validate satellite and model precipitation estimates among many other applications.

The GPM ground validation program has been deploying Platforms for In situ Estimation Rainfall Systems (PIERS) at granted institutes across the US. This study uses six PIERS+ sites which include a PARSIVEL disdrometer and tipping bucket gauges. The sites are located in the Mid-Atlantic region with an additional site in Connecticut. Some sites have additional instrumentation, including Pluvio weighing bucket gauge, additional tipping buckets, and additional PARSIVEL disdrometers. The study focuses on event rainfall totals for January to May 2024. The PARSIVEL disdrometer was the reference for the event definition and phase identification, while its rainfall totals compared to the gauges to determine the reference instrument. In addition to MRMS, the performance of the NOAA's HRRR model, European ERA5 reanalysis, NASA's MERRA-2 reanalysis were evaluated through comparison to the reference instrument. Future study will be conducted once IMERG data is available.

Support for this research was provided by the Maryland Space Grant Consortium.

THE EFFECTS OF LOWERED EXPRESSION OF DAUGHTERLESS ON SPEED, ENDURANCE, AND FECUNDITY IN DROSOPHILA MELANOGASTER

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Variation in speed, endurance, and fecundity among individuals is a common phenomenon. One reason for this is genetic differences. While we know that genetic differences play a role in this variation, little is known about the genes that contribute to it. A genome-wide association study using the fruitfly Drosophila melanogaster identified candidate genes that contribute to variation in speed and endurance. One being Daughterless (da). Daughterless' function during development is widely known, but not its function in adults. The purpose is to validate the effects of da on physical performance and examine its influence on egg production, to gain a better understanding of the role that da plays in variation among the tested traits. We hypothesize that knocking down da would negatively affect speed, endurance, and fecundity. Expression of da

was lowered in muscle cells by mating virgin female flies with a Gal4 muscle driver and virgin male flies with a Daughterless UAS RNAi. The control was done in the same manner except with Attp2 line males, which were genetically identical to the Daughterless UAS except without the RNAi sequence. The parents were transferred from vials after 7 days. The progeny was collected after 7 more days, then separated by sex. We measured speed and endurance via a climbing assay where we took 5ml serological pipettes and measured the starting point at 3cm and marked 9cm and 27cm away from it. The flies were placed in pipettes and the time it took from starting point to each marker, or the distance traveled within 15 seconds was taken. Afterwards females from both crosses were placed in vials and the number of eggs were counted for three days. This study is ongoing, the results will be used to better understand Daughterless' function in adults and how genetic variation effects the target traits.

I'd like to acknowledge the Arnold and Mabel Beckman Scholars Program for funding this research.

DETERMINING DIFFERENTIAL PROTEIN EXPRESSION PATTERNS FOR CYP2B6, CERS2, AND CKMT1A ACROSS MURINE BRAIN REGIONS

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Doxorubicin (DOX) is an efficacious chemotherapeutic drug that is known to exert its anticancer effects through many mechanisms, including DNA intercalation, the inhibition of topoisomerase II, and the generation of reactive oxygen species, which leads to oxidative stress. Despite its anticancer effects, DOX is known to cause serious adverse effects, including neurotoxicity, which limit its clinical use. The molecular mechanisms of DOX-induced neurotoxicity are not fully elucidated. We hypothesize that DOX can be metabolized in the brain, causing metabolic alterations. Recently, we have demonstrated the involvement of an energy metabolic pathway enzyme, creatine kinase, mitochondrial 1A (CKMT1A); a drug-metabolizing enzyme, cytochrome P450 2B6 (CYP2B6); and a lipid-metabolizing enzyme, ceramide synthase 2 (CerS2) in response to neurotoxic drugs in the brain. However, the brain is a highly heterogeneous organ, and different neuroanatomical regions may have unique protein expression profiles. The regional expression of the above enzymes in the brain are unknown. To fill this knowledge gap, we performed protein expression analyses using isolated mouse brain regions. For this work, the hippocampus, cortex, thalamus, and hypothalamus were first isolated from the brain and lysed. A Bicinchoninic Acid Protein Assay was then performed to determine the concentration of total proteins in each of the four lysates. Next, immunoblots were conducted to determine the presence of CerS2, CYP2B6, and CKMT1A in the brain regions. The immunoblot

results suggest the presence of the above proteins in murine brain regions. Interestingly, the expression of CerS2 and CYP2B6 was lower in the hypothalamus compared to the other regions. However, CKMT1A exhibited similar expression levels across all four regions. Therefore, the above data reveal that proteins CerS2 and CYP2B6 are expressed differentially across the brain regions. In the future, it would be interesting to investigate the modulation of the above proteins in response to DOX treatment in mice.

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

SYNTHESIS AND PHOTOCHEMICAL CHARACTERIZATION OF NOVEL ZN(II) AZA-DIPYRRIN-BASED CHROMOPHORES

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Boron aza-dipyrromethenes (Aza-BODIPYs) is a broadly studied class of organic dyes with near-infrared absorption and emissions, which allows for their use in fluorescence imaging, photoacoustic imaging, photodynamic therapy, and solar energy conversion. Zinc(II) aza-BODIPY analogs, however, are a class of dyes that are largely unexplored. The goal of our research is to determine the photophysical characteristics of novel symmetric and dissymmetric Zn(II)-aza-dipyrrins. Unlike aza-BODIPYs, Zn(II)-aza-dipyrrins contain two aza-dipyrrin subunits, allowing for the synthesis of dissymmetric complexes with two different aza-dipyrrins, which is not possible in aza-BODIPY compounds. We hypothesize that Zn(II)-aza-dipyrrins will exhibit energy and electron transfer between dipyrrin subunits, in addition to the usual photophysical properties characteristic of aza-BODIPY, such as fluorescence. We hypothesize that energy and electron transfer will increase in the dissymmetric Zn(II)-aza-dipyrrin complex due to the structure of the ligands. We will synthesize a series of symmetrical and dissymmetrical aza-dipyrrin complexes, determine their absorption and emission properties, and perform DFT calculations to determine their electronic structures. Novel complexes can be used in developing fluorescence imaging agents and components for solar energy conversion.

This investigation was sponsored by the U-RISE Program at the University of Maryland, Baltimore County (UMBC), which is supported by the National Institute Of General Medical Sciences of the National Institutes of Health under Award Number T34GM136497, and by NSF (CHE-1955318).

CONTACTLESS HEART RATE MONITORING: UTILIZING FEDERATED LEARNING FOR ENHANCED PRIVACY

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This study presents a new way for contactless heart rate prediction using video data while addressing the critical issue of privacy in healthcare data analysis. We propose a federated learning (FL) framework to process remote photoplethysmography (rPPG) data, enabling heart rate prediction in a contactless manner that does not compromise privacy. Our approach involves collecting video and corresponding rPPG data from multiple sources. Unlike traditional centralized approaches, we set up a decentralized FL model where the initial training occurs on a central server using a portion of the existing data. The partially trained model is then sent to local devices, representing individual data collection sites. These devices continue to train the model using local rPPG data, while only sharing updated model parameters with the central server when they are done. This iterative process continues until the model achieves a specific accuracy in heart rate prediction based on video data. Our approach ensures that sensitive patient data remains on local devices, significantly decreasing privacy issues while utilizing the benefits of distributed data. This research aims to contribute to the growing field of privacy-preserving machine learning in healthcare, offering a safer, more secure solution for contactless vital sign monitoring.

Support for this research was provided by the NSF REU site grant (2050999).

S

IDENTIFICATION AND CHARACTERIZATION OF NUCLEOCAPSID BINDING SITES WITHIN THE MAL HIV-1 RNA PACKAGING SIGNAL

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Human Immunodeficiency Virus type 1 (HIV-1) targets CD4+ cells, weakening the immune system and potentially leading to AIDS. Most antiviral therapies focus on HIV-1 proteins, which frequently undergo rapid mutations. To create more effective treatments, understanding the virus's structure and focusing on its more stable regions is essential for the therapy to have long-lasting effects. During viral genome packaging, two RNA copies form a dimer; the dimerization facilitates the binding of HIV-1 Gag proteins. Genomic recognition, a highly conserved process, represents a promising drug target. Mutagenesis studies on selective HIV-1 packaging have identified the Core Encapsidation Signal (CES) as the minimal packaging unit for HIV-1, which shows native-like dimerization, nucleocapsid (NC) binding, and packaging efficiency. Ding et al. determined the highest affinity binding sites of NC on the 5' Leader of HIV are in the CES region. The central finding was that the binding of NC causes unwinding within the PSI hairpin of the viral RNA, which is important for genome packaging and viral replication. However, this work primarily focused on the NL4-3 strain of HIV-1. Our project focuses on the MAL strain of HIV-1 to determine the binding characteristics of NC on the RNA packing signal. To quantify the number of binding sites in the MAL packaging signal and the affinity of NC on those sites, we utilized Nuclear Magnetic Resonance (NMR) and Isothermal Calorimetry (ITC). 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.

This research was supported by Howard Hughes Medical Institute and NIH #5R01AI150498.

DURABLE & FLEXIBLE CHITOSAN-BASED POLYMER GEL ELECTROLYTE FOR RECHARGEABLE ZINC MANGANESE DIOXIDE BATTERIES

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With the ever increasing demand of energy around the globe, there is a need to improve the quality of electrochemical energy storage devices, in order to make them safe, efficient, and environmentally friendly. To cater for these requirements, researchers are exploring the advantages of Zn-MnO_2 batteries, so they can complement, and eventually replace the existing

Li-ion batteries. While the commercially available zinc metal batteries are being utilized for various industrial and domestic applications, they cannot be incorporated into flexible wearable devices because of their rigid design and acidic electrolytes. Herein, we present a biodegradable, flexible and safe gel electrolyte for Zn-MnO_2 batteries based on a biodegradable polymer, i.e., chitosan. Aqueous solution of chitosan and polyvinyl alcohol (PVA) prove to be a promising electrolyte when soaked in 5M (potassium hydroxide) KOH, as the high concentration of KOH provides increased ion mobility which in turn results in high ionic conductivity (IC), without compromising the flexibility and mechanical strength of the electrolyte. The obtained safe and flexible gel electrolyte can prove to be a promising addition to the Zn-MnO_2 chemistry in order to enhance the battery performance.

Support for this research was provided by FlexMeshed lab UMBC and grants through the Meyerhoff undergraduate program.

ECO-FRIENDLY MICROFLUIDIC ELECTROCHEMICAL SENSOR UTILIZING LOW-COST ANION EXCHANGE RESIN FOR SELECTIVE NITRATE DETECTION IN WATER

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The increased use of inorganic fertilizers and poor treatment of industrial wastewater, sewage, livestock manure, and landfill leachate have led to a concerning rise in freshwater nitrate levels, exceeding U.S. Environmental Protection Agency (EPA) thresholds. Recent reports highlight dangerous nitrate pollution in several U.S. agricultural regions, posing health risks like infant methemoglobinemia. This issue is acute in Maryland's Lower Eastern Shore, where high cancer and infant mortality rates are linked to nitrate in drinking water. These findings raise critical question: Are health hazards being overlooked due to inadequate testing and transparency? The most likely reason for inadequate testing is the high cost, bulkiness, and labor-intensive nature of current EPA-certified nitrate sensors.

Accurate monitoring of nitrate levels in water is essential for mitigating health and environmental issues caused by nitrate pollution. Various on-site measurement methods exist, such as absorption spectrometry, fluorescence spectrometry, chemiluminescence, electrochemistry, and chromatography. Electrochemical methods stand out for their sensitivity and flexibility but often require converting nitrate to nitrite, posing additional environmental risks. Therefore, there is a pressing need to develop simple, sensitive, selective, and cost-effective methods for nitrate detection suitable for environmental monitoring.

This led us to develop a portable microfluidic electrochemical sensor using a low-cost anion exchange resin for selective nitrate detection. The eco-friendly structural material for the microfluidic system ensures biodegradability and reduces environmental impact, while minimizing the use of samples and reagents. The anion exchange resin selectively adsorbs nitrate without generating environmental hazards. Preliminary results show a sensitive and selective response to nitrate, distinguishable from other ions. We are optimizing sensing conditions and constructing a calibration curve to validate the sensor's accuracy and reproducibility.

Support for this research was provided by the Maryland Innovation Initiative (MII) TEDCO award (0923-0003).

INVESTIGATING HYPOXIA INDUCED ZEBRAFISH RETINAL REGENERATION

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Zebrafish is a resilient organism that is both hypoxia-tolerant and regenerative. Under hypoxic environments, the zebrafish embryo can halt its development, and downregulate most energy-demanding processes to enter a metabolically arrested state until environmental conditions are right for development. Although many energy-demanding processes such as cell proliferation, gene expression and ion pumping are suppressed following exposure to anoxia, some processes are in fact up-regulated. A bulk RNA Seq analysis of zebrafish embryos exposed to 8 hours of anoxia revealed that the expression of over 1000 genes was elevated. Interestingly, a subset of these genes expressed in the eye had previously been implicated in regeneration of photoreceptor cells in the eye following mechanical damage or photodamage. Photoreceptors are the most energy-demanding cells, so it is not surprising that dramatic drop in ATP production results in vision loss in mammals. One gene, Ndrg1a, which has previously been shown to be upregulated following anoxia and help degrade sodium-potassium ATPase in the pronephric duct of zebrafish embryos to reduce energy consumption is also upregulated transcriptionally around the retina following anoxia, hinting at a potential eye protective mechanism involving Ndrg1a under anoxia. My project will be addressing the general hypotheses that; severe hypoxia causes

photoreceptor cell death, which in turn triggers a regenerative response in the eye, possibly mediated by reactive Muller glia, OR Ndrg1a is upregulated in the retina leading to the degradation of sodium potassium ATPases to reduce photoreceptor energy consumption and prevent anoxic damage. Data will be presented examining photoreceptor damage by looking at Ndrg1a, NKA, and activated Caspase 3 expression at different time points following hypoxia exposure. These studies are significant given that neovascular and degenerative diseases of the eye are the leading causes of blindness in the world, and hypoxia is considered central to the pathogenesis of these disorders.

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T

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 potentially resulting in Acquired Immunodeficiency Syndrome (AIDS). Current antiviral therapies target HIV-1 proteins that have high mutation rates. Therefore, a greater understanding of the HIV-1 structure is necessary to target more conserved regions. During viral genome packaging, two copies of the genomic viral RNA form a dimer and are bound by the HIV-1 Gag protein. Genomic recognition is a highly conserved process and a promising drug target. Mutagenesis studies of selective HIV-1 packaging identified the minimal packaging unit for HIV-1, called the Core Encapsidation Signal (CES), which exhibits native-like dimerization, nucleocapsid (NC) binding, and packaging efficiency. Keane et al. determined the three-dimensional structure of CES. Their central finding was that the splice donor (SD) region does not form a hairpin but instead forms 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. To probe the structure of the MAL packaging signal, we utilized Nuclear Magnetic Resonance (NMR) and a novel fragmentation-based labeling approach. In this approach, differentially labeled RNA fragments of the packaging signal are prepared separately and non-covalently annealed together. This technique allows for unambiguous NMR signal assignment by reducing signal overlap and selectively eliminating signals from the final NMR spectrum. Our next goal is to characterize the RNA and Gag interactions important for nucleocapsid binding, genome selection, and selective packaging.

Support for this research was provided by Hughes Medical Institute, and NIH #5R01AI150498.

OPTIMIZING PC-12 DIFFERENTIATION THROUGH SCHWANN CELL CO-CULTURE FOR APPLICATIONS IN BIOMEDICAL ENGINEERING

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Schwann cells and PC-12 cells play crucial roles in nerve regeneration and serve as valuable models for studying neuronal differentiation. PC-12 cells, derived from a pheochromocytoma of the rat adrenal medulla, are widely used in neurobiology for their ability to model neuronal differentiation. Schwann cells, glial cells of the peripheral nervous system, are essential for nerve regeneration due to their support and insulation of neurons. This study investigates the influence of Schwann cells on the differentiation of PC-12 cells within a co-culture system. By employing layer-by-layer coating techniques with various extracellular matrix components, including collagen, heparin, and poly-L-lysine (PLL), as well as varying the concentration of nerve growth factor (NGF), we assessed the optimal conditions for PC-12 cell differentiation. Our findings demonstrate that Schwann cells enhance PC-12 differentiation, with optimal NGF concentrations providing the most favorable environment. These results highlight the critical role of the cellular microenvironment, extracellular matrix, and growth factors in promoting neuronal differentiation. This research has important implications for medical applications, including the development of advanced therapies for neurodegenerative diseases and nerve regeneration, offering valuable insights for tissue engineering and regenerative medicine.

Support for this research was provided in part by the Meyerhoff Scholars Program, as well as funding from the University of Maryland, Baltimore County.

ANALYTICAL PIPELINES FOR DIFFERENTIAL EXPRESSION ANALYSIS IN MULTIFACTORIAL SINGLE NUCLEUS RNA-SEQUENCING DATA TO UNDERSTAND RELAPSE-RELEVANT TRANSCRIPTIONAL SIGNATURES

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Single nucleus RNA-sequencing (snRNA-seq) approaches disentangle the heterogeneity of complex tissues and aid in the identification of rare populations otherwise masked by conventional bulk-tissue procedures. Our lab recently developed multipleXed Population Selection and Enrichment snRNA-seq (XPoSE-seq), which expands the feasibility of complex experimental designs that integrate multiple factors. However, most snRNA analysis packages are only able to run pairwise comparisons and do not account for individual subjects. To address this limitation, we developed an analysis pipeline to perform differential gene expression analysis on multi-factorial datasets. This pipeline accepts user-defined factor metadata, biological replicate, and annotated cell type information and performs a quality-control (QC) inclusion step of nuclei counts per condition. After QC, the pipeline pseudobulks by factor(s), biological replicate, and cell type before implementing a general linear model via DESeq2 that accepts complex designs and accounts for individual subject variability and between/within subject experimental factors.

We used XPoSE-seq and this analytical pipeline to understand the transcriptional signatures of cocaine relapse. Rats that were trained on cocaine self-administration were tested for cocaine seeking 21 days after the last cocaine exposure. We observed robust cocaine seeking behavior, and we isolated behaviorally active and non-active neuronal nuclei as input for XPoSE-seq. Our analysis revealed distinct clusters corresponding to known cell types in the mPFC (excitatory and inhibitory neurons) that further subcluster into expected layer and interneuron sub-types within the medial prefrontal cortex, a reward-related region of the brain. Using this approach, we characterized differentially expressed genes between a within-subject factor (i.e. activity or brain region) while accounting for a between-subject factor (i.e. biological sex or behavior) within rats that went through the seeking test. Current work aims to apply this data's results to downstream applications such as gene ontology, gene pathway analysis, and drug repurposing.

Supported by funds from NIDA IRP (Hope lab), the NIH Center for Compulsive Behaviors, the NIH Summer Internship Program, NIDA EDUCATE (UMBC), and the NIH Graduate Data Science Summer Program.

EVALUATING CELL VIABILITY IN A 3D LIVER MODEL CONSTRUCTED WITH THIOL-MODIFIED HYDROGELS

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2D cell cultures are widely used for testing drug effectiveness and studying cellular responses to various chemicals. However, they do not accurately mimic the native cellular environment, which can limit the translatability of results to real-world applications.Hydrogels have emerged as a promising solution to this problem. By using hydrogel cell cultures, we can encapsulate cells within a cell-degradable polymer, creating a 3D environment that more closely resembles in vivo conditions. In this project, we utilized hydrogels composed of thiol-modified hyaluronic acid—a polymer abundant in the extracellular matrix found in tissues—and thiol-reactive polyethylene glycol (PEG) diacrylate as a crosslinker to encapsulate differentiated hepatocytes (liver cells) within the hyaluronic acid polymer. These components worked together to create a 3D in vitro liver model. To test the conditions of our cells we utilized MTS assays to measure cell metabolic activity, and viability. This served to assess the activity of cells encapsulated in the hydrogel and their level of interaction with the external environment. Our studies revealed that cells remain metabolically active within two weeks of being encapsulated. This 3D model holds potential for future drug testing applications with accurate and translatable results.

This investigation was sponsored by the U-RISE Program at the University of Maryland, Baltimore County (UMBC), which is supported by the National Institute Of General Medical Sciences of the National Institutes of Health under Award Number T34GM136497.

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V

REAL-TIME NON-INVASIVE MONITORING OF NADH CONCENTRATIONS IN CELL-FREE SYSTEMS

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Protein production through cell-based biomanufacturing is a pivotal manufacturing technique in the pharmaceutical industry which suffers from many downsides. Cell-based yields may be limited by inefficient energy utilization and insolubility of the final product. Cell-free protein synthesis (CFPS) is a nascent alternative manufacturing process that utilizes cellular components instead of whole cells. This allows for more process control, increased product complexity, easier purification of the final product, and redirection of energy to protein production. Nicotinamide adenine dinucleotide (NAD) is an essential component of cellular metabolism, acting as a reducing agent in the form of NADH. It is primarily utilized in the electron transport chain to generate a proton gradient which drives adenosine triphosphate (ATP) production. Currently, the biochemical processes of cell-free reactions are unpredictable and poorly understood. We hypothesize that measuring NADH levels will provide an indicator of protein synthesis potential in cell-free reactions and help to engineer higher-yield reactions.

Resazurin is a blue phenoxazine dye that rapidly reduces into resorufin, a highly-fluorescent pink compound, after reacting with NADH. The rate of this reaction has previously been used in our lab to measure microbial contamination as a function of NADH concentration. Single-use reagents, like resazurin, are undesirable for use with cell-free bioreactors because they require direct sampling which poses a contamination risk. The goal of this project is to characterize and develop real-time non-invasive sensing of NADH concentration, by way of NADH fluorescence, to avoid direct-sampling from bioreactors. We present the preliminary development of a system that measures the fluorescence of NADH directly at 340/450 nm, using a fiber-optic cable attached to the bioreactor, which will eliminate the need for direct sampling.

This investigation was sponsored by the DARPA Biological Technologies Offices under the Reimagining Protein Manufacturing grant [HR001121S0038].

IDENTIFYING AREAS OF CONVERGENCE BETWEEN DORSAL AND VENTRAL HIPPOCAMPAL PATHWAYS IN THE NUCLEUS ACCUMBENS

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Establishing learned associations between rewarding stimuli and the context under which those rewards are encountered is critical for survival. Input from the hippocampus, a brain region integral in learning and memory, to the nucleus accumbens (NAc), a key area regulating motivated behaviors, is important for establishing associations between rewarding stimuli and related contextual information. This connection consists of two independent pathways originating from the dorsal (dHipp) or ventral (vHipp) hippocampus, which have previously been considered functionally and anatomically distinct. Recent findings from our lab and others show overlap in dHipp and vHipp terminal fields in the NAc, leading us to reconsider this view and raising new questions regarding the potential interactions between these two pathways in the NAc. We used optogenetics, electrophysiology, and an innovative transsynaptic labeling technique in mouse models to investigate the anatomical innervation and physiological relevance of these two independent inputs. Our labeling technique allowed us to visualize dHipp innervated neurons, vHipp innervated neurons, and dually innervated neurons in the NAc. Optogenetic manipulation during whole-cell electrophysiology recordings confirmed the presence of dual innervation of individual neurons in the NAcSh via the dHipp and vHipp pathways and revealed heterosynaptic interactions between the two pathways. Altogether, these results confirmed that the vHipp and dHipp dually innervate a subset of neurons in the NAc, suggesting integration of vHipp and dHipp information at the level of individual neurons. Further probing of the physiological and behavioral relevance of this finding will provide novel insight as to how single neurons can integrate spatial and contextual information and how it influences learning processes.

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VOID SPOT ASSAYS AS A NONINVASIVE METHOD FOR DETECTING PROSTATE INFLAMMATION IN A MOUSE MODEL OF CHRONIC PROSTATITIS/CHRONIC PELVIC PAIN SYNDROME

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Chronic prostatitis/chronic pelvic pain syndrome (CP/CPPS) is a prevalent yet poorly understood urologic disorder that affects 35-50% of men during their lifetime. To study the etiology and pathobiology of CP/CPPS we have generated a mouse model that develops prostatic inflammation. The RIG model is characterized by the expression of three genes; the reverse Tetracycline transactivator under the control of Hoxb13 regulatory elements (R) IL1-ß, a proinflammatory cytokine (I) , a marker gene (GFP, G). Two cohorts of RIG mice were generated with different lineages to determine the lineage-dependent expressivity of the genes. We hypothesize that prostate inflammation will alter the process of micturition in RIG mice. To test this hypothesis, we performed a series of experiments to establish a correlation between abnormal urination patterns determined by Void Spot Assays (VSAs) and prostate inflammation to develop a predictive non-invasive method to detect severity of prostate inflammation. We compared micturition patterns at baseline and upon induction of inflammation by using a shape detection plugin on FIJI to quantify micturition spotting. Our preliminary data show that prostate inflammation confirmed by histological analysis correlated with altered urination patterns. This data strongly suggests that VSAs can be used as a surrogate marker for prostatic inflammation. This work will support further development of the RIG model as a system to study CP/CPPS and other prostate pathologies associated with inflammation.

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W

REDUCING DATA OVERLOAD IN OBJECT TRACKING: DIFFERENTIAL CAMERA SYSTEMS IN PHYSICAL AND SIMULATED ENVIRONMENTS

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The growing demand for machine learning in robotics and computer vision necessitates more efficient data processing methods. Currently, machine learning-based object tracking systems require the processing of large data sets, which can hinder real-time performance. The setup for this project includes two environments: a physical setup with a robotic arm controlled by an NVIDIA Jetson Nano, and a simulated environment in Gazebo with ROS2 replicating the same conditions. A camera approach that isolates moving pixels was emulated to study low-latency embedded processing, aiming to reduce data and improve the efficiency of the object tracking

algorithms in both the physical and simulated environments. OpenCV will be paired with reinforcement learning, implemented in Python, to emulate an event-driven camera that tracks an object. The initial phase of the project involved developing a dynamic vision camera system emulation that isolates pixels associated with movement. This system has been implemented and tested in the physical environment, demonstrating the feasibility of the approach in a physical setup. Additionally, a simulation environment in Gazebo with ROS2 has been established, providing a controlled environment for further experimentation. While the preliminary results are promising, indicating that the dynamic camera system can effectively reduce the volume of data for object tracking, further work is needed to integrate the reinforcement learning algorithm. Next steps include refining the motion control in the Gazebo simulation and implementing machine learning models in both the physical and simulated environments. This research aims to demonstrate that focusing on dynamic events within the visual field can significantly enhance the efficiency of machine learning-based object tracking systems.

Support for this research was provided by the NSF grant (2207374).

UNDERSTANDING THE DEGRADATION OF VERDIGRIS & DEVELOPING STRATEGIES FOR ITS CONSERVATION IN ARTWORK

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Conservation science focuses on the preservation and protection of artwork. One of the most difficult challenges faced by conservation scientists is understanding how the components of an artwork interact with the environment. For paintings in particular, pigment degradation poses a considerable threat due to altering the color profile of the artworks. The focus of this project was verdigris, an organometallic pigment used in ancient and modern artwork. It's history dates back to ancient times when it was the brightest green pigment available, making it widely used in artwork. Verdigris is known to irreversibly degrade over time. In this project, we studied the degradation profile of verdigris through various thermal and photodegradation experiments. Comparisons between verdigris in solution and as a paint with lipidic binders were studied. Analysis of the degradation was conducted using UV/Vis spectroscopy, FTIR, and NMR. Our results demonstrate that verdigris is both thermally and photosensitive. The next step in our research is employing the use of a member of a new class of transition metal carbide nanomaterials, MXenes, to determine their effects on the degradation profiles of verdigris. MXenes have demonstrated the capacity to absorb UV light which may prevent direct exposure of verdigris to harmful radiation.

This project was supported by the Baltimore SCIART research program funded by the Andrew W. Mellon Foundation under Award G-2109-11420. The students of the program would like to extend our gratitude to Dr. Joseph Bennett, Dr. Deepa Madan, Dr. Shreyasi Sengupta, Kushani Mendes. MCAC staff Josh Valencia and Cynthia Niedermeier.

X

Y

INVESTIGATING THE ROLE OF GADD45B IN ADAPTIVE RESPONSES TO ANOXIA

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The zebrafish is one of several vertebrate organisms capable of surviving environmental changes, such as hypoxia (low oxygen) or anoxia (no oxygen). The anoxia-tolerance of zebrafish embryos is due to their ability to enter a reversible state of metabolic suppression. Despite this energy-conserving response and the general suppression of transcription and translation, the expression of genes that promote anoxia survival is up-regulated. Using an RNA-Seq approach, the Brewster lab found that over 1000 genes were increased twofold or more in embryos exposed to 8 hours of anoxia compared to normoxic controls and stress response gene Growth arrest and DNA-damage-inducible beta (gadd45b) was among them. The goal of my project is to carry out a functional analysis of gadd45ba. I have so far validated the upregulation of gadd45ba using qPCR for a quantitative assessment and wholemount in situ hybridization to examine the spatial distribution of this gene. Under normoxic conditions, I found gadd45ba is expressed in the diencephalon and the hematopoietic stem cell niche. The diencephalon is a forebrain region regulating several crucial bodily functions, including circadian rhythm and respiration. In response to prolonged anoxia, I observed that gadd45ba expression intensifies in the forebrain in what appears to be the habenular nucleus. In the hematopoietic stem cell niche, newly developed stem cells undergo proliferation to increase the number of RBCs. After anoxic exposure, I

identified expression in the vasculature and noticed the red blood cells going into circulation. Based on these findings, gadd45ba could potentially mediate these adaptive responses by functioning as a DNA demethylase. Future experiments will test this hypothesis using gadd45 knockdown embryos to observe changes.

Support for this research was provided by the HHMI grant (52008090) and funding from the URISE NIH grant (PAR-21-146).

Z

EVALUATION OF LOW-COST ALTERNATIVE BIOMATERIALS FOR MODULATION OF NEAR-FIELD PLASMON-COUPLED EMISSION TOWARDS A LOW-COST OXYGEN SENSOR

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Surface Plasmon Coupled Emission (SPCE) is an optical sensing technique that integrates two widely used techniques namely surface plasmon resonance and fluorescence. This is achieved by using a fluorophore embedded in a polymer matrix coated on a metal nano thin film. The emission couples with surface plasmons and out-couples with improved angularity and enhancements. Unique spacer materials are placed near the fluorophore to influence the emission coupling. A low-cost material – diatomaceous earth (DE) – was used as an eco-friendly alternative in this study. DE is a naturally occurring, non-depletable material that are formed as shells by single-celled algae. They have known remarkable optical modulation properties in literature towards surface enhanced Raman scattering. To evaluate its effects on near-field SPCE, DE with AgNPs were coated onto plasmonic thin film and tested on SPCE optical setup in reverse Kretschmann geometry. For comparative analysis, a control sample was tested with SiO2 beads replacing DE. The uniqueness of DE over the spherical SiO_2 is due to its complex symmetrical patterns and shape that helps in rendering additional optical effects in channeling the fluorescence. The results provide insights into the optical effects of uniquely shaped DE on plasmon-coupled emission in comparison with spherical SiO_2 materials. Further modifications in DE could lead to promising low-cost sensor assemblies that can be applied for various gas and liquid phase sensing applications.

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