Summer Undergraduate Research Fest

SURF'S UP!

August 6, 2025

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

UMBC

Hosted by the

COLLEGE OF NATURAL AND MATHEMATICAL SCIENCES

surf.umbc.edu

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 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 a.m.
Poster Set-up (University Center Ballroom) & Continental Breakfast (UC Ballroom Lobby)

9 – 9:15 a.m.
SURF Opening Remarks (Robert and Jane Meyerhoff Building 030)

9:15 – 9:45 a.m.
Lightning Round Talks (Robert and Jane Meyerhoff Building 030)

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

10:45 – 11:30 a.m.
Poster Session #2 (University Center Ballroom)

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

PRESENTERS:
surf.umbc.edu/surf-presenters

ABSTRACTS:
surf.umbc.edu/abstracts

Lightning Talks!

The UMBC Beckman Scholars will host the SURF 2025 Lightning Talks. Each selected SURF presenter will have 5 minutes and up to 5 slides to deliver a fast-paced presentation designed to spark conversation and cross-disciplinary collaboration. Six presenters have been selected. Please note that there will be no 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

The Center for Women in Technology (CWIT)
orientation.umbc.edu/dawg-days-jumpstart

Dawg Days Jumpstart Summer Bridge
cwit.umbc.edu

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 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/translational-life-science-technology

Message from the Dean

Welcome to the 2025 UMBC Summer Undergraduate Research Fest (SURF)! Hosted annually by the College of Natural and Mathematical Sciences, SURF is a signature event that showcases the excellence of UMBC's summer STEM community. Here, students not only engage in high-quality STEM coursework, but also gain hands-on research and applied learning experiences, all while contributing to a vibrant scholarly community. This year, we are excited to welcome students from our existing community college partnerships, who have been invited to present their work at SURF. We are thrilled to have them join us for SURF 2025!

Throughout the summer, our students have followed in the footsteps of distinguished scientists and innovators—practicing, applying, and advancing the skills of research. Some projects were independently arranged, while many were made possible through competitive grants and funding dedicated to supporting undergraduate research.

We are proud of all that our students have accomplished. They return from this experience more skilled, more confident, and more prepared to tackle scientific challenges. Their discoveries and dedication have added to the growing body of scientific knowledge—empowering us with greater understanding, insight, and the potential for innovation.

This progress would not be possible without the exceptional mentorship, support, and encouragement provided by our faculty, staff, and research partners across campus. Thank you for your dedication to fostering the next generation of scholars.

We invite you to explore the outstanding work being presented today and to engage with these remarkable students.

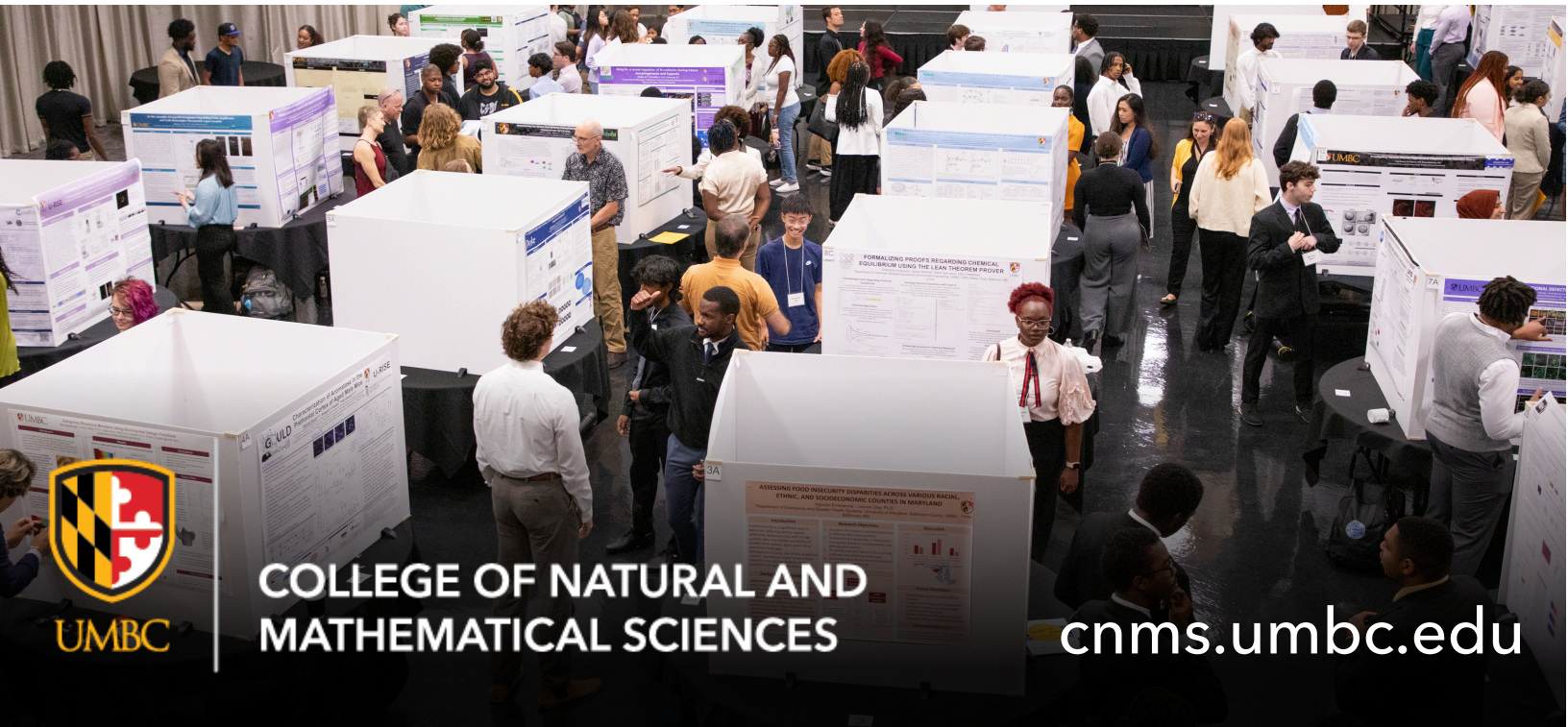
Bill LaCourse, Ph.D.
Dean and Professor of Chemistry
College of Natural and Mathematical Sciences

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 support for SURF from our alumni and friends. If you or your organization is interested in making a gift to support the program, please visit give.umbc.edu and choose College of Natural and Mathematical Sciences from the dropdown menu. If you would like to talk to someone about making a gift, please reach out to Jocelyn Kehl at jjkehl@umbc.edu. Thank you!



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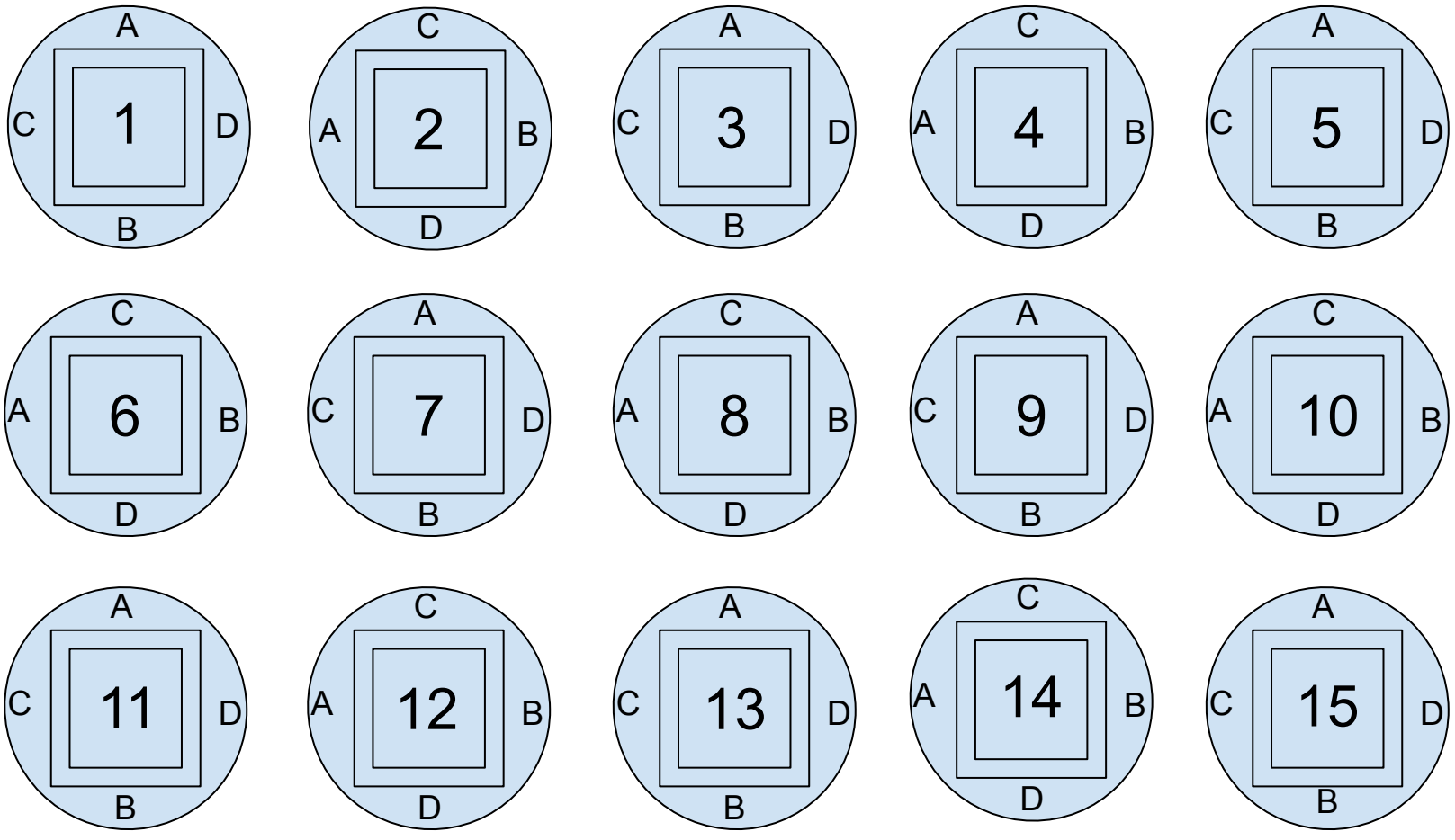
Entrance

Entrance

Entrance



STAGE

SURF 2025 Poster Session I

Board #	
19B	Abdallah, Setutsi
19A	Adesina, Ayodeji
20A	Ajibade, Tolulope
29A	Akan, Zeynep
31B	Akanji, Yonu
16A	Akhras, Lana
5A	Akinrotimi, Great
27B	Alawode, Bolu
30A	Ali, Samira
28B	Amoh-Mayes, Maxwell
1A	Anderson, Bianca
22B	Arowona, Zainab
2A	Aruna, Naomi
26A	Ashtian, Arya
4B	Bakshi, Krish
12A	Battle, De'Onna
22A	Beasley, Caitlin
7B	Beckert, Rafe
8B	Bett, Alvin
30B	Borowski, Shane
11A	Bui, Vinnie
14B	Byrd, Brianna
10B	Carter, Brenna
7A	Chia, Jane-Frances
5B	Chiduza, Tadiwa
2B	Craft, Jacob
8A	Cyrus, Azeb
16B	Davenport, Robert
13A	Dawit, Mathew
17A	Delaporte, Elise
6B	Ejimogu, Kate
24A	Elbich, Severin
25A	Foulkes, Thomas
27A	Frazie, Elana
4A	Ganesan, Dinesh
23A	Getachew, Nahom
31A	Gibson, Raine
14A	Hale, Ellis
1A	Hommel, Mary Elizabeth
12B	Howe, Gabriella
16A	Imtiaz, Nyle

Board #	
15B	Isangedighi, Xavier
17B	Kaplowitz, Aeon
16A	Kasukurthi, Avyukth
26A	Kodzwa, Tonderai
3A	Lombardo, Jacob
16A	Marszal, Stephanie
23B	Mkpasi,Kodilinye
9A	Moody, Tyler
32A	Mustafa, Wania
21B	Ndalamba, Gracia-Noël
18B	Ndiritu, Jessica
10B	Nguyen, Thanh Trieu
6A	Nkrumah, Meranda
1B	Odetayo, Saheedat
11B	Offei, Petrina
20B	Olaniyan, Ini
5A	Oshagbemi, Roseline
15A	Patel, Haley
3A	Patel, Abhinav
28A	Patrick, Rachel
24B	Poch, Emma
9B	Polyakov, Elijah
18A	Reinders, Ella
25B	Rivas, Anderson
10A	Schwanebeck, Kevin
26B	Slokan, Alexandria
29B	Srivastava, Aryan
3B	Walton-Irvin, Amir
21A	Wescoat, Jess
32B	Wroten, Nicky
13B	Zhang Kevin

SURF 2025 Poster Session II

Board #	
31D	Addai, Ryan
26D	Adesanya, Titilayomi
11D	Agyako-Wiredu, Suzi
9C	Allbritton-King, Quinn
13D	Amana, Eno
5D	Amissah, Daniel
28D	Amoa, Efua
27C	Amponsah, Desiree
14D	Arias, Yan Yu
17C	Ball, Breanna
26C	Bandi, Rishika
1C	Chen, Max
21C	Chen, Evangeline
30D	Coon, Mia
25D	Dawson, Qaiyah-Simone
11C	Ezekwesili, Ugonna
22D	Gardiner, Henry
7C	Gibson, Trevor
1C	Han, Jake
6D	Handwerger, Lily
31C	Hernandez, Emily
24C	Hoffman, Jessica
1D	Ibe, Nneamaka
17D	Iringan, Jan
13C	Isayas, Gelila
15C	Jain, Urvi
4C	Jin, Peter
27D	Johnson, Iliana
2C	Johnson, Aaron
21C	Kamalabharathy, Diya
4D	Karanja, Faith
8C	Katragunta, Aditi
11C	Kayisavera, Amedeus
24D	Khan, Maisa
14C	Lewis, Saleen
10C	Mammo, Nebiyu
3C	Mathyvannan, Mathushan
9D	Mendoza, Javan
25C	Moses, Emmanuel
23D	Natarajan, Vedanth
21C	Nguyen, Kenny

Board #	
29D	Nkansah, Nia
11C	Nwachuku, Jaden
30C	Nyanteh, Asantewaa
18D	Obas, Narah
5C	Ogungbile, Oluwagbotemi
5D	Okoye, Somgolie
10D	Olaoluwa, Chosen
22C	Omole Emmanuel
3D	Onochie, Brandon
25D	Opuni Winnifred
32D	Orellana Guzman, Jose
2D	Palmiero, Annamaria
15D	Parrales, Noeh
4C	Pathak, Sidhya
23C	Paz Menendez, David
32C	Prabakaran, Jeshuwin
19C	Quintanilla, Matthew
2C	Ravipati, Lalitha
12C	Richard, Nia
16D	Richardson, Christa
29C	Rodriguez, Ariana
16C	Ruth, Magdalen
18C	Shah, Silvi
25D	Shoola, Ashley Naomi
20C	Somerville, Jaden
7D	Swaters, Maaike
20D	Terceros, Gabriel
28C	Thorpe, Ethan
21D	Timi, Peace
12D	Trotman, Aanayah
8D	Turman, Cooke Maia
19D	Van Dyke, Ryan
6C	Webb, Blake

A

CHARACTERIZING CELLULAR PROLIFERATION AND APOPTOSIS FOLLOWING ORAL NICOTINE POUCH EXPOSURE IN A TONGUE ORGANOID MODEL SYSTEM

Setutsi Abdallah, Silvi Shah, Kafui Ameko, Ginny Murray, Sean O'Sullivan, Tatsuya Ogura, Ph.D., Weihong Lin, Ph.D.
Department of Biological Sciences, University of Maryland, Baltimore County, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

Small, tobacco-free oral nicotine pouches (ONPs) are a popular smoking cessation tool that has unintentionally reached younger audiences due to enticing flavors and discreet ease-of-use, becoming the second most used nicotine product among adolescents. Oral nicotine exposure is a significant public health concern due to its known side-effects, including dry mouth, poor oral hygiene, and altered taste sensation. The sense of taste is essential for guiding appetite, detecting harmful substances, and supporting overall quality of life. Taste dysfunction often results in significant clinical consequences, such as malnutrition, eating disorders, and decreased psychological well-being. Taste is mediated by oral taste receptor cells (TRCs), which detect various chemical tastants and relay signals to the brain. However, the effects of ONP exposure on TRCs remain unknown. To evaluate the effects of ONP exposure on TRCs, we are utilizing a novel 3D murine tongue organoid model that mimics the structure and function of human taste buds. Organoids offer a more physiologically relevant platform for studying cellular responses to ONP exposure compared to classic *in vivo* models. To simulate typical ONP usage, mature tongue organoids are exposed to a 1:10 or 1:5 dilution of Wintergreen ZYN™ ONP extract for 24 hours. We expect the higher 1:5 concentration to produce a more pronounced cellular response. After exposure, immunohistochemistry will be used to label the organoid tissue with antibodies against Ki-67 and cleaved Caspase-3 (CC3), which mark proliferating and apoptotic cells, respectively. Here, we hypothesize that ONP exposure will lead to increased CC3 activity and decreased Ki-67 activity in tongue organoids due to nicotine damaging the TRCs and impairing the regenerative and proliferative ability of stem cells. These findings will provide insight into the potential impact of flavored ONPs on taste cell viability and oral health, particularly among vulnerable youth populations.

Support for this research was provided by the UMBC START program and the Department of Biological Sciences. Setutsi Abdallah was supported in part by a grant (52008090) to the UMBC Meyerhoff Scholars Program from the Howard Hughes Medical Institute (HHMI).

INVESTIGATING OLFACTORY BULB STRUCTURE IN DROSOPHILA WITH APPL GENE DELETION

Ryan Addai, Fernando Vonhoff
Department of Biological Sciences, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD, 21250

The APPL gene in Drosophila melanogaster is homologous to the human APP gene, which is critical in the formation of amyloid plaques found in Alzheimer's disease. Although prior research indicates APPL deletion results in drosophila that demonstrate impaired olfactory behavior, the anatomical basis for this dysfunction is unexplored. This project investigates if APPL deletion is responsible for compromised olfaction due to altered structure in the olfactory bulb during development. This project investigates if deletion of the APPL gene causes structural changes in the adult Drosophila olfactory system. Brains from both wild-type and APPL deleted (APPLD) adult flies were dissected. Samples were fluorescently labeled with a series of antibodies imaged via confocal microscopy. The angles of the glomeruli that comprise the olfactory bulb were measured using image analysis software to determine structural differences between the two genotypes. Preliminary findings reveal consistent differences in glomerular orientation between wild-type and APPL-deleted brains. These results suggest that the APPL gene may play a developmental role in organizing olfactory structures in the fly brain. Since APP is strongly associated with neurodegeneration in humans, studying its Drosophila homolog will offer insight on the molecular and anatomical underpinnings of olfactory processing and neurological disorders.

Support for this research was provided to Ryan Addai by the Meyerhoff Scholars Program and conducted in the Vonhoff Lab at UMBC.

CHARACTERIZING THE ROLE OF PLEXIN A IN *DROSOPHILA MELANOGASTER* BORDER CELL MIGRATION

Titilayomi Adesanya, Christopher Welsh, and Michelle Starz-Gaiano
Department of Biological Sciences, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD, 21250

Collective cell migration is integral for various biological processes, especially in cancer metastasis, and we model this concept in *Drosophila melanogaster,* also known as fruit flies. This organism is an exemplary model for studying collective cell migration. Some advantages are the ability to identify required components using genetic tools and the use of dynamic imaging methods. In this project, we focus on an important and highly regulated process that occurs during oogenesis in Drosophila: border cell migration. Plexin A (Plex A) is a transmembrane receptor implicated in various forms of cell migration; Plex A is known to facilitate cohesion and successful neuronal cell migration. We hypothesize that overexpression of *Plex A* may cause the border cells to migrate individually instead of migrating as a cluster. The knockdown of *Plex A* may negatively impact the ability of the cluster to detach from the anterior end of the egg chamber.

To investigate these hypotheses, we employed genetic methods, immunofluorescence microscopy, and imaging analysis software. We altered the levels of Plex A genetically in the migrating cells and dissected them to extract the ovaries and egg chambers. We fixed and stained egg chambers that have different levels of Plex A expression to investigate differences in border

cell migration, adhesion, and detachment. We are quantifying this data by measuring the distance of migration relative to the stage of egg chamber development.

If our hypothesis is correct, we expect to see border cell clusters with *Plex A* expression irregularities have decreased migration distance due to a lack of cohesion and difficulties detaching from the anterior end. In the future, we aim to determine other components that interact with Plexin A in the border cells.

This research is funded by the NSF grant IOS-2303587 and the Meyerhoff Scholars Program.

USING ACOUSTIC SIGNALS IN ANDROID APP DEVELOPMENT TO MONITOR RESPIRATION IN REAL TIME

Ayodeji Adesina, Riishav Guptaa, Dong Li
Future Sensing and Interaction Lab, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD, 21250

Monitoring respiration through smartphones can offer accessible, non-invasive health insights. This project explores the use of acoustic signals for real-time respiratory monitoring using Android app development. The application integrates a custom low-latency audio API to transmit and record ultrasonic signals, which are then processed to detect subtle chest movements related to breathing. Initial development focused on understanding and integrating the new API in comparison to Android's native audio tools. Major challenges included ensuring compatibility across devices, real-time processing of sound data, and precise visualization of waveforms. The app successfully demonstrates respiration detection and visualization, with future work focusing on signal amplification and refining the detection algorithm. This project highlights the potential of mobile applications for accessible health monitoring using audio-based sensing.

This research was was supported by the Meyerhoff Scholars Program.

QUANTIFYING RELEASE OF DOXORUBICIN FROM DENDRONIZED GOLD NANORATTLES USING FLUORESCENCE SPECTROSCOPY

Suzi Agyako-Wiredu, Ayden Roberts, Marie-Christine Daniel
Department of Chemistry and Biochemistry, The University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD, 21250

Although current chemotherapy treatments have the ability to eradicate cancer cells, the biodistribution of drugs to the whole body contributes to deleterious side effects on normal tissues as well as to the development of drug resistance. This highlights the need for a directed method of drug distribution, with which gold nanorattles (AuNRTs) can help. AuNRTs consist of a gold nanoparticle (AuNP) core, a void, and a porous gold shell. In order to enhance drug delivery, selected dendrons can self-assemble onto the gold surfaces, and drugs can be covalently

added to their terminal ends. This project aims to synthesize an AuNRT drug delivery platform carrying doxorubicin (DOX) via a pH-sensitive bond and quantify the release of DOX using fluorescence spectroscopy. A ligand exchange reaction between 17 nm citrate-capped AuNPs and poly(propyleneimine) dendrons terminated with DOX form the nanorattle cores. A silver coating was nucleated around this core using a polyol reduction method. A dropwise titration of gold salt onto these structures etched away silver and replaced it with gold, forming a porous gold shell (due to the reaction's stoichiometry) and thus the final AuNRT structures. In acidic conditions (pH 4), the hydrazone bond between the dendron and DOX is cleaved, which can release drugs after endocytosis inside tumor cells. To characterize this release, the AuNP cores and the AuNRTs were separately placed in pH 4 water and release of DOX was monitored at different time intervals (up to 6 days) following initial addition of acid. Due to the fluorescent properties of DOX, fluorescence spectroscopy was utilized to record an emission spectrum for DOX at each timepoint, correlating the intensity of the emission signal to the amount of DOX released.

This research was funded by a UMBC Undergraduate Research Award (URA).

ANALYSIS OF *Eudorina elegans* TO EVALUATE THE PROCESS OF CELL DIFFERENTIATION THROUGHOUT THE VOLVOCINE ALGAE CLADE

Tolulope Ajibade, Kevin Chen, Stephen M. Miller
Department of Biological Sciences, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

Cell differentiation is a fundamental developmental mechanism important for generating specialized cell types, but very little is known about how cell differentiation evolves. The volvocine green algae clade comprises an excellent system for investigating the origins of cellular differentiation because it includes undifferentiated, conditionally differentiated, and fully differentiated species. *Eudorina elegans* and *Volvox carteri* are volvocine algae that are suited for studying the evolution of cellular differentiation. *E. elegans* produces differentiated cells (small, motile somatic cells) under cold stress, so far the only stress known to induce them. Meanwhile, *V carteri* is programmed to produce somatic cells under normal and stress conditions, and maintenance of the somatic cell fate requires the *regA* gene. *E. elegans* contains the *regA* gene, which we hypothesize to be a stress response gene that is required for somatic cell differentiation in response to stress in this species. To test this idea, we are using CRISPR-Cas9 to knock out regA in *Eudorina*. To this end, we are creating *E. elegans* guide RNA targeting vectors through a two-step process. First, we annealed pairs of complementary oligonucleotide sequences, pair p804 and pair p1009, and ligated them into the *V. carteri* guide expression plasmid. Now we are performing a double digestion and ligation to move the part of the *Volvox* plasmid containing the *E. elegans* target sequences into an *E. elegans* guide expression vector. Next, we will transform

these vectors together with a Cas9 expression into *E. elegans* and screen for *regA* mutants by genomic PCR. *RegA* mutants will be cold shocked to determine if *regA* is required for the induction of somatic cells, and to determine if it is required for tolerance to nutrient or other stresses. These studies should bring us closer toward understanding the evolution of somatic cell differentiation within the volvocine clade.

This work was supported by an REU 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).

NMR STRUCTURAL STUDIES OF THE HIV-1 5'-LEADER

Zeynep Akan[1] , Bersabel Tekle[1] , William Sakowicz[1] , Bethel Beyene[1], Brian Grossman[1] , Horasa Ji[1], Michael F. Summers[1,2]
[1]University of Maryland, Baltimore County (UMBC), 1000 Hilltop Circle, Baltimore, MD 21250
[2]Howard Hughes Medical Institute, Chevy Chase, MD, 20814

The Human Immunodeficiency Virus type 1, better known as HIV-1, is a retrovirus that weakens the host immune system and results in Acquired Immunodeficiency Syndrome, also known as AIDS, one of the deadliest pandemics in history with over 36 million deaths. Current antiviral therapies have a limited effect in controlling the replication of the virus. Therefore, a greater understanding of the HIV-1 structure is necessary to target more conserved regions. More specifically, the 5'-Leader. This highly structured and conserved region plays a central role in regulating essential steps of the viral life cycle such as transcriptional activation, genomic packaging, dimerization, and splicing targeted for future drug development. The 5'-Leader can adapt different conformations that determine the fate of the RNA. HIV-1 transcripts that begin with one guanosine (Cap1G) form dimers that sequester the cape and are selectively packaged into new virions. In contrast, RNA with three guanosines (Cap3G) are monomeric and are efficiently translated and spliced. Structural studies of the 5'-Leader by NMR are complicated by its large size. To address these complications, we're utilizing a novel segmental labeling technique with TGK, a mutant DNA polymerase. TGK enables the stepwise preparation of differentially labeled RNA segments within the packaging signal. This approach reduces signal overlaps in the NMR spectrum, allowing for clearer, unambiguous signal assignments by selectively eliminating signals.

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

INVESTIGATING THE ROLE OF JUVENILE HORMONE IN THE MATURATION OF INNATE REWARD BEHAVIOR IN *DROSOPHILA*

Yonu Akanji, Anthony Rosenthal, Dr. Fernando Vonhoff
Department of Biological Sciences, University of Maryland Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

The coordination of brain development is an essential facet in the maturation of innate reward behavior, which is necessary for survival. In *Drosophila melanogaster*, Juvenile hormone (JH) is an essential regulator that changes throughout development, but its direct impact on the development of innate non-sexual reward-driven behavior is unknown. In this study, we explore

the influence of JH on sexually dimorphic reward behavior in Drosophila by studying olfactory preference at different ages, as well as after direct manipulations of JH titer. We made use of a two-choice behavioral assay recording the preference of differently aged flies using various established attractants and repellents such as Apple Cider Vinegar, Ethyl Acetate, and Benzaldehyde. It was found that differently aged flies, specifically one day old vs five-to-six-day old flies, react differently to the same substances. Additionally, it was found that the depletion of JH via precocene treatment resulted in partially phenocopied preference probabilities between old and young flies, highlighting the essential role of JH in coordinating typical mature innate reward behavior. These results advance fundamental knowledge of maturation processes by offering insight on how hormone cues influence developmental timing that might be relevant in numerous species.

Support for this research was provided by the Louis Stokes Alliance for Minority Participation Program (LSAMP).

INVESTIGATING THE ROLE OF RNAI RHO1 ON CLIMBING SPEED AND ENDURANCE IN DROSOPHILA MELANOGASTER

Avyukth Kasukurthi[4], Lana Ahkras[3], Nyle Imtiaz[3], Stephanie Marszal[2], Dr. Jeff Leips[1]
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[2]University of Delaware, 210 South College Avenue, Newark, DE
[3]River Hill High School, 12101 Clarksville Pike, Clarksville, MD 21029
[4]Marriotts Ridge High School, 12100 Woodford Dr, Marriottsville, MD 21104

The Rho1 gene has been identified through a genome-wide analysis as a candidate gene affecting physical performance in Drosophila melanogaster. Rho1 is an evolutionarily conserved gene that encodes for proteins in the family of GTPases, which play a key role in the regulation of actin dynamics and wound healing, and therefore potentially impact physical performance. We studied the effect of the Rho1gene on climbing speed and endurance by under-expressing Rho1 in the muscle tissue of the fly by utilizing the GAL4-UAS system. Virgin females of the muscle-GAL4 line were crossed with males of the UAS Rho1RNAi responder line and males of a control line. We measured the climbing speed and endurance of the offspring of these crosses. This experiment aims to determine whether Rho1 expression in muscle tissue significantly influences locomotor performance, including speed and endurance. We hypothesize that under-expressing the Rho1 gene within flies will have a negative correlation with their speed and endurance. The results of our experiment will provide insight into the significance of the Rho1 gene in the physical ability of Drosophila melanogaster, which may suggest the role the human orthologs of Rho1 play in physical performance in humans. This could help enhance personalized healthcare as it relates to physical decline and conditions such as myopathy and muscular dystrophy. If under-expressingRho1 gene is found to lower the physical performance in Drosophila melanogaster, further research is needed to determine the underlying mechanisms behind this effect. Future research should investigate the gene's effect on other tissues and age groups, given

that Rho1 has been characterized as an age-specific gene in a genome-wide analysis of Drosophila melanogaster.

Support for this research was provided by the Department of Biological Sciences at the University of Maryland, Baltimore County.

Acknowledgement to Diya Kamalabharathy, Kenny Nguyen, and Evangeline Chen, who worked on the effects of overexpressing the Rho1 gene on the physical performance in Drosophila melanogaster. They helped in the collection of virgin females and offered support in the creation of our poster.

DESIGNING AN INCLUSIVE MICRO-PURCHASE MARKETPLACE FOR HISTORICALLY EXCLUDED FOUNDERS WITHIN THE GOVERNMENT CONTRACTING SECTOR

Great Akinrotimi[1], Roseline Oshagbemi[2] , Latoya Staten[3]
[1]Department of Computer Engineering, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD, 21250
[2]Department of Mechanical Engineering, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD, 21250
[3]Fearless Institute , 8 Market Pl, Baltimore, MD 21202

Public Procurement, particularly micro-purchases under $10,000, usually presents opportunities in order to drive economic equity by increasing contract accessibility for historically excluded small business founders. Many of these businesses usually face barriers such as limited visibility, complex registration processes and unclear procurement pathways. To address this, we created a digital marketplace to help vendors within the Hutch program (a non-profit program designed to help entrepreneurs and digital services firms build impactful businesses in the tech and government contracting sectors) showcase their services and certifications and connect with buyers from government agencies, educational institutions and nonprofit organizations. To design our digital market place with relevant features we researched procurement laws across all government levels, existing procurement platforms and portals. Using Canva.com, we designed the website layout and created a Google form where new Hutch companies can register to be included in the marketplace. Our marketplace will simplify procurement processes and empower small businesses to navigate compliance with government agencies and build institutional trust.

Great Akinrotimi and Roseline Oshagbemi were supported in part by a grant to the UMBC Meyerhoff Scholars Program from the Hutch program at Fearless Institute.

THE ROLE OF MICRO-RNA LET-7 IN BORDER CELL MIGRATION

Boluwatinsola Alawode, Michelle Starz-Gaiano
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Cell migration is fundamental. In *Drosophila melanogaster,* also known as the fruit fly, it is essential for their development. We study migration in fruit flies because they share similar genes

with humans and are easy to genetically manipulate. Studying the migration of fly cells and their genetic regulation enables a better understanding of why conditions such as cancer or birth defects in humans may occur. We specifically focus on the border cells, which are somatic cells in the ovary and follow their journey as they migrate through the developing egg chambers. The gene that we are focusing on is microRNA *let-7*. MicroRNAs are small noncoding RNAs; they are about 22 nucleotides in length, and they bind and repress target messenger RNAs to regulate specific genes' expression. This research focuses on examining how *let-7* affects border cell migration when altered. We use transgenic lines to regulate levels of gene expression or function, in this case, altering miR *let-7*, and collecting the first generation of offspring. We followed an antibody staining protocol, which consisted of feeding females, collecting the egg chambers, dissecting them, and staining them with antibodies and dyes to stain the follicle cells, DNA, and border cells. In preliminary data, we found that the experimental egg chambers' border cells migrated on time, while the control border cells did not migrate on time at younger stages but did at older stages. We found that changes in *let-7* function also led to some lethality. More experiments are underway to determine if let-*7* is needed for border cell migration in *Drosophila melanogaster* egg cell chambers.

This research is funded in part by the NSF grant IOS-2303857 to MSG. Bolu Alawode was supported by the Meyerhoff Scholars Program.

MULTIMODAL EMOTION RECOGNITION USING FACIAL, HAND AND EEG SIGNALS FOR HUMAN-ROBOT INTERACTION

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As healthcare and assistive technologies continue to develop, a deep emotional understanding is needed within these robotic systems to ensure they are as supportive, effective, and empathetic as possible for the user's experience. Emotionally responsive robots have the potential to adjust their behavior in response to user needs and enhance therapeutic interactions, but can only be so precise, as human emotion is so comprehensive. Limitations in emotion recognition exist, as most current models consider only the visual modality. These vision-only models, trained on facial video data from the DEAP dataset, have achieved accuracies ranging from 70% to 85%, depending on the classification task and model architecture. Yet, using a multimodal approach, which combines electroencephalography (EEG) data with facial emotion recognition, achieved an F1 score of 98.1%, demonstrating the importance of utilizing neurophysiological signals and multimodal fusion for human emotion recognition to obtain more feasible and reliable detection. This project aims to extend facial emotion recognition with EEG data along with hand gesture detection, to validate emotion recognition and achieve optimal results for human-robot interactions. The project uses a hand-tracking system to capture 21 hand landmarks, providing context for hand gesture recognition in the robot, as well as a convolutional neural network model trained on video data from the DEAP dataset to detect facial emotions. Future development will focus on integrating live, accurate EEG data and enabling more advanced,

real-time robotic responses based on emotion detection, to explore how such systems might improve assistive technologies in the future.

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NEONICTINOID AND PYRETHROID PESTICIDE USAGE IN THE HCC COMMUNITY

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This mixed-methods investigation involved surveying and conducting an integrative literature review regarding the usage of two pesticide classes. Neonicotinoids are a class of insecticide pesticides derived from nicotine. As this substance has been noted for its indiscriminate targeting of organisms, its manufacture and use is currently banned in the EU. Pyrethroids are another class of insecticide pesticides derived from a naturally occurring substance called pyrethrum, which is often synthesized in order to be used in conjunction with other pesticides. It has become popular for having fast-acting effects on insects and arthropods while still having a relatively low toxicity for mammals and birds.The survey consisted of a series of questions having to do with pesticide ownership, usage habits, and feelings regarding the substances as well as educational content embedded within some of the questions in order to see if participant feelings would change over the course of taking the survey. Data-collection is ongoing. The literature review addressed the usage of neonicotinoid and pyrethroid pesticides and their effects on three species: humans, the domestic dog, canis familiaris, and the common mallard. In order to build a portfolio of effects on non-target animals (i.e., animals that are not considered pests and are therefore not the main target of these substances), animals were chosen with an attempt to address a wide range of non-target species, accounting for the likelihood of a species' likelihood of accidentally consuming these substances or coming into contact with them. All species showed an increase in rates of certain cancers, such as acute myeloid leukemia and colorectal cancer in humans, malignant lymphoma in canines, and issues with reproduction, such as decreased fertility as well as reducing numbers of eggs laid in mallards.

Support for this research opportunity was provided by the Howard Community College Department of Undergraduate Research

A COMPARISON OF STRUCTURAL AND CHEMICAL DIFFERENCES IN CONSTRUCTION IMPACTED AND CULTIVATED SOILS AT PRINCE GEORGE'S COMMUNITY COLLEGE

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Soil degradation due to demolition and construction activities has been shown to significantly alter soil properties by reducing nutrient availability and disrupting soil structure. Recent trends in agricultural restoration aim to reclaim abandoned urban construction sites and convert them into gardens. This study hypothesizes that construction negatively affects soil health in reclaimed urban spaces, posing challenges for sustainable agricultural reuse.To analyze baseline productivity of reclaimed land, we conducted analysis of soil pollution metrics, specifically pH and conductivity in deciSiemens per meter (dS/m), on two soil types present at Prince George's Community College (PGCC). Both measurements are indicators of nutrient availability in soils. In addition to these tests, we also conducted sieve analysis to assess particle size distribution and evaluate soil texture. A compacted construction site and a community garden on campus were chosen as sampling sites to compare both reclaimed urban agricultural soil and severely disturbed soil. Both sites exhibited similar slightly alkaline pH values, with no significant variation in EC measurements, suggesting comparable nutrient availability in both soils. However, some textural differences were observed, with garden soil containing more fine particles, as evidenced by lower sieving losses compared to the construction site. These findings highlight the need to integrate soil health assessments into urban planning policies to ensure sustainable land use practices. By providing data-driven insights, this research aims to inform urban residents and policymakers about the potential risks posed by construction and demolition activities.

Support for this research was provided by the Department of Natural Sciences and the Student Research Club at Prince George's Community College.

BEYOND THE CLOUDS: ROLE OF ELECTRONIC CIGARETTES EFFECTS ON THE MOUSE OLFACTORY SYSTEM OVER TIME

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In recent years, electronic cigarettes (e-cigarettes) has increased, affecting millions, particularly youth and adolescents. E-cigarettes contain toxic chemicals that can harm the olfactory system. Damage to this system is a marker for neurological and cognitive disorders. There is a negative relation between vaping having an effect on the brain and functions of the olfactory system. The olfactory system is responsible for our sense of smell.. With no blood brain barrier, odors have direct access from the environment to be easily converted to signals in the brain, processing smells. Compounds in the vapor interact with the olfactory system, sending odor information to the brain, affecting the olfactory cortex, hippocampus, and amygdala. These are the sites for perception of smell, memory, and emotional responses to odors. With many channels in the nose, there are countless of smells that the brain can perceive and recognized. The lab is investigating how increased e-cigarette exposure affects these channels in the olfactory system: do they become damaged, heighted and many more questions. It is hypothesized that prolonged exposure the vapor weakens the olfactory system, affecting one's sense of smell. . To understand how e-cigarette exposure may disrupt olfaction, olfactory-guided behaviors are assessed using behavioral assays such as the Odor Threshold Test, as mice rely heavily on their sense of smell

for locomotion. In the Odor Threshold Test, varying concentrations of nicotine and e-liquid were administered to assess changes in the mice's movement, preferences, and behavioral responses. By analyzing the mice's interactions with the liquid, the lab can derive results on how their olfactory health is affected over time: does their odor sensitivity and preference increase or decrease based on e-cigarette exposure? At this time, the lab is in the process of gaining results from its research and experiments.

Support for this research was provided by the UMB Accelerated Translational Incubator Pilot (ATIP) Grant. Kafui Ameko was supported by the Meyerhoff Scholars Program. We'd also like to thank Dr. Aaron Sathyanesan for his help with the behavioral analysis.

CREATING A DIGITAL DASHBOARD THAT SUPPORTS SMALL BUSINESSES IN ACQUIRING GOVERNMENT CONTRACTS

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Securing government contracts is a critical step in scaling small business, yet many small and diverse companies face barriers in accessing these opportunities. Hutch is an incubator company that addresses this by providing business support to help companies position themselves for federal contracts. Hutch aligns company capabilities with suitable government contracts using a manual sorting system which has limited speed and efficiency. To address this inefficiency, we developed a centralized, interactive data visualization dashboard using Power BI and information gathered from surveys distributed to target companies. This innovative dashboard streamlines the matchmaking process by transforming data into a dynamic, searchable interface. This tool enables users to filter companies by expertise or view individual company profiles to support faster and more informed decision-making. This dashboard will significantly enhance operational efficiency, reduce manual workload, and increase visibility for underrepresented businesses while amplifying Hutch's mission to promote inclusive innovation and accelerate equitable access to government contracts.

This research was funded by the Meyerhoff Scholars Program at the University of Maryland, Baltimore County (UMBC)

ENHANCING RNA HOMOGENEITY VIA TEMPLATE DESIGN FOR T7LG TRANSCRIPTION

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The human immunodeficiency virus (HIV) is an infectious agent that erodes the body's immune system, impacting more than 40 million individuals worldwide. As of 2025, the most common treatments are antiretroviral therapies (ARTs) which are used to suppress HIV replication and

mitigate viral load. Our laboratory's research focuses on a highly conserved region of the HIV-1 RNA genome, particularly the 5 'Leader (5'-L), which plays a crucial role in regulating viral functions like translation and packaging.

This project aims to: 1) investigate the effects of various reverse primer DNA modifications on RNA transcription and 2) Identify and describe modifications to produce homogenous 3' ends of RNA using T7LG RNA polymerase (RNAP). To achieve these goals, we will design and optimize various DNA primers utilizing different 5' modifications. Then, using PCR we will produce DNA templates incorporating these modifications. In vitro transcription will then be used to study the modification's effect on 3' end homogeneity of the nascent transcripts. Additionally, nuclear magnetic resonance (NMR) spectroscopy will be utilized to confirm homogeneity, identity, and number of nucleotides present in the construct. The anticipated outcome of this research is to identify a method to ensure RNA transcript homogeneity for both NMR and crystallography studies using T7LG RNAP. This work will enhance current structural studies and allow new powerful techniques to be utilized in the study of the HIV-1 5' L.

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

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The human immunodeficiency virus (HIV) is an infectious agent that erodes the body's immune system, impacting more than 40 million individuals worldwide. As of 2025, the most common treatments are antiretroviral therapies (ARTs) which are used to suppress HIV replication and mitigate viral load. Our laboratory's research focuses on a highly conserved region of the HIV-1 RNA genome, particularly the 5 'Leader (5'-L), which plays a crucial role in regulating viral functions like translation and packaging.

This project aims to: 1) investigate whether and how structural elements of the 5'-L regulate binding of a cap binding protein, eIF4E, and 2) determine the identity of specific nucleotides involved in eIF4E binding. To achieve these goals, we will optimize in vitro transcription and capping to produce 5'-capped RNAs. Next, we used an electrophoretic mobility shift assay (EMSA) to confirm in vitro capping of the transcript and investigate binding affinities. Additionally, nuclear magnetic resonance (NMR) spectroscopy in conjunction with different labeling schemes for the RNA 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 capped 5'-L and the specific identities of nucleotides involved in this interaction between the 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).

DISSECTING THE ROLES OF EGFR, PVR, AND MYOSIN VI DURING DROSOPHILA BORDER CELL MIGRATION

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Collective cell migration is essential to development and disease, yet the mechanisms coordinating this process are not fully understood. These migrations are critical for healthy development and are also involved in medical conditions such as autoimmune disorders and metastatic cancer. Therefore, it is important to uncover the mechanisms that regulate these processes. *Drosophila melanogaster* border cells during oogenesis offer a well-established model for cohort-type collective migration and are amenable to genetic manipulation. In this system, a cluster of cells migrates from the anterior end of the egg chamber to the oocyte boundary, moving between the germline cells through cytoskeletal remodeling and guided by receptor tyrosine kinase (RTK) signaling. This study investigates the roles of two RTKs—Epidermal Growth Factor Receptor (EGFR) and Platelet-Derived Growth Factor/Vascular Endothelial Growth Factor Receptor (PVR)—in guiding border cell migration and examines the potential function of the motor protein Myosin VI (Jar). We and others hypothesize that EGFR and PVR function redundantly and that Jar may traffic these ligands once they are inside the border cells. Using a germline-cell-specific Gal4 driver, we drove expression of the dominant negative (DN) transgenes for EGFR and PVR in the germline. Following ovary dissection, we stained egg chambers with antibodies and imaged ovarioles using fluorescence microscopy. Migration indices were measured to assess border cell movement. Migration occurred normally in controls, while EGFR DN showed a mild delay and the double DN showed a severe delay. These results suggest that RTK signaling is both redundant and cooperative. We are investigating whether Jar traffics RTK ligands or maintains border cell polarity. This work advances understanding of collective migration and its relevance to developmental disorders and cancer.

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EVALUATING THE FEASIBILITY OF PRODUCING HIGH-PRECISION TRANSIT LIGHT CURVES WITH SUB-MINUTE TIMING UNCERTAINTIES USING GROUND-BASED TELESCOPIC PHOTOMETRY

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High-precision astronomical databases are fundamental to exoplanetary science, particularly for validating candidate transits identified by space-based observatories such as TESS, Kepler, and JWST. While these missions provide vast quantities of time-series photometric data, confirming planetary candidates requires independent ground-based follow-up to eliminate false positives

(e.g., eclipsing binaries, blended sources) and to refine ephemerides and transit depths. Acceptance into professional repositories, such as those curated by the American Association of Variable Star Observers, requires astrometric uncertainties of less than one minute, necessitating stringent observational protocols and optimized instrumentation. We present results from an ongoing ground-based campaign designed to test the hypothesis that small-scale observatories, when equipped with modern CMOS-based imaging systems, can provide photometric precision sufficient for transit validation. Our instrumentation includes equatorially harmonic mounted optical systems with advanced digital polar alignment, thermally regulated focusing, high-resolution pixel-scale autoguiding system, and scientific CMOS monochromatic detectors optimized for high quantum efficiency, large full well capacity, low gain (e^-/ADU), minimized read noise (e^- rms), low dark current (e^-/s/pix), and wide dynamic range. These specific characteristics allow for the reliable detection of shallow brightness dips associated with suspected exoplanet transits. Our recent campaigns have yielded high-resolution time-series data with image scales near 1.15 arcseconds per pixel and robust photometric stability. Preliminary reductions indicate consistency with transit depths and timings from TESS-detected candidates and exhibit sufficient temporal resolution for transit ingress/egress characterization. Calibration procedures are being refined to minimize residual systematics and enhance the detrending of atmospheric and instrumental noise. These findings support the capability of well-configured small observatories to contribute validated transit data to global archives, improving candidate confirmation rates and reducing reliance on large-telescope follow-up. We discuss implications for expanding community-driven exoplanet science and improving the efficiency of validation timelines in the current era of high-cadence, all-sky surveys.

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ANALYZING CELL PHONE AND SHOE MICROBIOMES OF SCIENCE FESTIVAL ATTENDEES

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The human microbiota is the variety of microbes that are found on and within the human body, including bacteria, fungi, and viruses. Microbes which comprise the human microbiota have been shown to play a significant role in human health, including being correlated with illnesses such as asthma, allergies, and gastric ulcers. The composition of the human microbiota can be influenced by a multitude of factors, including the environment someone interacts with. This study aimed to investigate differences in diversity and quantities of microbes, specifically bacteria, between people who attended similar scientific festivals in different locations. It was hypothesized that the Science and Engineering Festival in Washington, D.C. would produce a more diverse microbiome on phones and shoes than the Philadelphia Science Festival because Washington, D.C. has a warmer climate; thus allowing for more bacterial growth. Data on the diversity and abundance of bacterial phyla were collected through the use of Phinch software and

the Project MERCURRI data set. 248 samples were filtered from the dataset to analyze bacterial phyla present on people of all ages who attended the Philadelphia Science Festival or Science and Engineering Festival. Analysis of the dataset showed that overall, the Philadelphia attendees had 12 different phyla of bacteria present on their phones and shoes, whereas the Washington, D.C. attendees only had 10 different phyla of bacteria present on their phones and shoes. The results differed from anticipated, as the event in Washington, D.C. displayed less diversity than Philadelphia's. This study has implications for factors that could influence the composition of the human microbiota, including what bacterial populations are present on individuals' phones and shoes in different environments. Further research could explore how the microbes found on people's phones and shoes are potentially transferred to their microbiota.

This research project was funded by the College of Natural and Mathematical Sciences at UMBC.

DEVELOPMENT OF A VAGINA-ON-A-CHIP MODEL FOR STUDYING RECURRENT BACTERIAL VAGINOSIS

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Bacterial vaginosis (BV) is one of the most commonly diagnosed vaginal infections affecting women globally, with a high recurrent rate. If not treated properly, BV increases the risk of preterm birth and acquisition of sexually transmitted infections (STIs) such as HIV, making it a concern in women's reproductive health. BV is characterized by a reduction in *Lactobacillus* species and an overgrowth of anaerobic microorganisms, including *Gardnerella vaginalis*. Mechanisms underlying BV onset and recurrence remain poorly understood, primarily due to the lack of a physiologically relevant models that capture the complex nature of the microbiome's interactions within the host microenvironment. To address this, we are building a cost-effective, biomimetic vagina-on-a-chip platform that can imitate the complex interactions present within the vaginal microbiome. The device incorporates dynamic fluid flow, supports the co-coculture capacity of vaginal bacteria with host cells, and creates a relevant tissue architecture. Unlike commercial organ-on-a-chip models that require expensive mask aligners that cost ~$250,000, our platform integrates a custom-designed 3D-printed deep UV exposure system that costs only ~$200. It was validated using a UV intensity meter to optimize curing conditions at various source-detector distances while outsourcing a digital design to reduce in-house fabrication costs. The vagina-on-a-chip features dual microchannels to support the co-culture of human vaginal epithelial cells and human uterine fibroblast cells, to be colonized by *Lactobacillus iners* and *Gardnerella vaginalis* under physiologically relevant conditions. Enabling real-time monitoring of microbiome behavior by using imaging techniques, and tracking the relevant biological changes over time without disrupting the system, epithelial integrity, pH shifts, inflammation markers, and biofilm formation. The successful fabrication and preliminary validation of this model will lay the groundwork for a scalable and affordable tool that has the potential to enhance the understanding of BV pathogenesis and support the development of more effective therapies.

This research is funded in part by the UMBC Academic Opportunity Programs and the Jackman Burden (JB) Lab.

UNRAVELING THE PCOS PUZZLE: THE IMPACT OF ANDROGEN LEVELS AND ASSOCIATED FACTORS

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Hyperandrogenism is a defining characteristic of polycystic ovary syndrome (PCOS), yet the exact mechanisms that lead to androgen excess and the subsequent development of PCOS remain under studied. Gaining insight into how hyperandrogenism functions in PCOS is critical for unraveling the etiology behind increased androgen production in the ovaries and adrenal glands. Research in this area is complex and suggests that both genetic factors and environmental influences may contribute to hyperandrogenism. This literature review aims to synthesize current knowledge on hyperandrogenism in PCOS, focusing on its interaction with genetic predispositions in affected females and exploring the underlying mechanisms of androgen excess, its impact in PCOS progression, and implications for improved diagnosis and management. We discuss how both insulin resistance and environmental factors like lifestyle and diet contribute to hyperandrogenism. Furthermore, we highlight the strong association between hyperandrogenism in PCOS and insulin resistance, examining potential links to insulin signaling proteins, and adipokine signaling. Gene expression research may clarify the complex interplay between insulin resistance and hyperandrogenism. For future progress, identifying early genetic markers like SHBG, CYP11A, CYP17, CYP19 E.T.C are crucial for understanding the initiation and progression of PCOS.

Racial Microaggressions and Depressive Symptoms in Asian American Adolescents: Role of Minimization of Race and Internalized Inferiority

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Anti-Asian discrimination during the COVID-19 pandemic detrimentally impacted Asian American (AA) youth mental health. Hostile racial slights (racial microaggressions) may lead youth to internalize beliefs that their culture is inferior (internalized cultural inferiority; ICI). ICI has been associated with more depressive symptoms, as individuals who devalue their culture may have difficulties establishing a positive sense of self-worth. Moreover, parental minimization of race practices may amplify the relation between racial microaggressions and ICI. When parents avoid talking about race, youth may have difficulties acknowledging group-based oppression, which can make them susceptible to narratives that devalue their culture. However, there has been minimal research exploring these processes. The present study examined: (1) the association between AA adolescents' racial microaggression experiences and their depressive symptoms; (2) the mediating role of ICI in this association; and (3) the moderating role of parental minimization of race on the link between racial microaggressions and ICI. A moderated mediation analysis revealed that racial microaggressions were positively associated with ICI, which in turn, was associated with higher depressive symptoms. Parents' minimization of race moderated the relation between racial microaggressions and ICI, such that racial microaggression experiences were more strongly related to adolescent ICI at increasing

levels of parental engagement in minimization of race practices. AA adolescents' experiences of negative treatment due to their race were linked to more feelings of shame and denial of their culture, especially when their parents minimized the existence of racism. In turn, perceptions of inferiority about their culture were associated with more feelings of hopelessness and suicidal ideation in adolescents. Parental minimization messages may lead to dissonance when adolescents experience racism, increasing adolescents' belief in these negative messages about their culture. Our findings can inform interventions that promote positive mental health by fostering adolescents' cultural pride and supporting parents' positive racial-ethnic socialization practices.

Support for this research was provided by the Louis Stokes Alliance for Minority Participation program (LSAMP).

EFFECT OF TEMPERATURE ON THE PERFORMANCE OF AQUEOUS ZINC ION BATTERIES WITH VANADIUM OXIDE CATHODES

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Aqueous zinc-ion batteries (AZIBs) have emerged as a promising solution for large-scale energy storage applications due to their cost-effectiveness, inherent safety, favorable volumetric energy density, and environmental friendliness. Among various cathode materials explored for these batteries, vanadium pentoxide (V_2O_5) has attracted particular interest due to its multiple oxidation states and high theoretical capacity. However, widespread implementation is limited by an incomplete understanding of their charge storage behavior, low practical capacity, and poor cycling stability. Proposed charge storage mechanisms include Zn^{2+} intercalation and Zn^{2+}/H^{+} co-insertion, while activation mechanisms typically involve hydration of the pristine V_2O_5 lattice and irreversible phase transformation. The result of activation is an increase in capacity and greater capacity contributions from the lower voltage regions. The impact of temperature variations on charge storage, activation, and degradation mechanisms, as well as performance, is significantly understudied. In this study, we cycle AZIBs using V_2O_5-based cathodes across typical ambient temperatures to gain a deeper understanding of the electrochemical charge storage mechanisms and degradation processes that affect long-term battery operation. Electrochemical techniques, including cyclic voltammetry (CV), galvanostatic charge-discharge (GCD), and electrochemical impedance spectroscopy (EIS), were employed to assess the temperature-dependent behavior of V_2O_5 cathodes. It was observed that at higher temperatures, V_2O_5 undergoes activation faster, accompanied by higher capacitance and stronger peaks during discharge; however, capacity degrades more rapidly, and side reactions proliferate. Additionally, as the temperature was lowered, peak intensities shifted, suggesting a change in the electrochemical mechanism. We propose that the activation behavior of V_2O_5 is driven by a combination of chemical and electrochemical processes, which together define its charge storage mechanism and long-term cycling behavior. This study contributes to a clearer understanding of V_2O_5 cathode behavior under different thermal conditions and supports the development of more efficient and durable AZIB systems for future energy storage solutions.

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B

THE EFFECT OF LIGHT INTENSITY IN DELAYING EARLY MATURATION OF FEMALE ATLANTIC SALMON

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Atlantic salmon (Salmo salar) aquaculture is a growing industry due to increasing global demand and declining wild fish stocks. Improving efficiency and maximizing production are high priorities. Female salmon produce higher-quality and greater quantities of fish prior to maturation due to lower energy demands from the gonads. Recent studies suggest that increasing photoperiods may delay reproductive development, offering the industry a valuable tool to compete with wild fisheries. In this study, three light intensity treatments—low (<0.0016 W/m²), medium (0.02–0.1 W/m²), and high (0.1–2 W/m²)—were applied to two replicate tanks each. In total, six tanks were stocked with groups of 109–123 female Atlantic salmon at initial densities ranging from 60.88 to 89.5 kg/m². Light spectra were in the white-green range (380–760 nm). Results show that fish exposed to the lowest light levels exhibited the least maturation throughout the study, with 20% of fish at or below a maturation level of G2. However, the lowest-light group also showed the slowest growth, with an average mass increase of 143%, compared to 166% in the medium-light group and 184% in the high-light group. This significant difference may influence future aquaculture practices. The experiment demonstrated that constant exposure to low light intensity delays early maturation, which could improve production efficiency while reducing operational costs. These findings may also help production facilities save money by using less light and therefore less electricity. Future research will aim to evaluate how continuous exposure to varying light intensities at earlier life stages may affect the onset of sexual maturation in Atlantic salmon.

Support for this research was provided by the BioLED company.

ANALYZING THE EFFECT OF *SIRT2* KNOCKDOWN ON DROSOPHILA LIFESPAN

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The mammalian ortholog of *Drosophila Sirt2,* SIRT1, is a protein deacetylase that controls gene expression. The overexpression of *Sirt2* increases longevity in mammals and yeast while the reduced expression decreases longevity. However, tissue specific effects of *Sirt2* on longevity have not been studied. We analyzed differences in survival following reduced expression of *Sirt2* in two tissues that might directly affect aging: the fat body which regulates metabolism, and

hemocytes which are important for clearing apoptotic cells. We hypothesized that knocking down *Sirt2* expression in both tissues would reduce lifespan. We used the GAL4-UAS system with RNAi interference to reduce *Sirt2* expression in both tissues and compared the knockdown flies to a control group of flies with the same genetic background in a survivorship assay. 118 virgin female flies from each cross were collected and placed in survivorship cages and the number of dead flies were recorded until there were none remaining in the cage. We found in the hemocyte survivorship study, the *Sirt2* knockdown flies outlived the control. The control flies outlived the *Sirt2* knockdown flies in the fat body group. We concluded that the *Sirt2* knockdown within the fly's hemocytes increased longevity, potentially due to an increase in their ability to clear apoptotic debris, reducing inflammation. Future experiments will need to be done to test this hypothesis. The shortened lifespan of the *Sirt2* knockdown in the fly's fat body tissue could be linked to metabolism regulation being compromised. Increasing our understanding of the relationship between *Sirt2* and lifespan can provide insight into improving healthy lifespan as we age.

We would like to acknowledge the Leips lab for the provided support and mentorship.

NEXT-GEN BREATHABLE SHAKE FLASKS FOR IMPROVED CELL GROWTH AND REAL-TIME MONITORING

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Shake flasks remain a staple in academic, biotech, and pharmaceutical laboratories for early-stage cell culture due to their simplicity and low cost. However, conventional flasks provide limited gas exchange through their narrow bottleneck openings, resulting in poor oxygen transfer, carbon dioxide buildup, and reduced cell growth and protein yield. These constraints typically limit cultures to 100 mL fill volumes in 500 mL flasks. To overcome these limitations, we previously developed lab-fabricated breathable shake flasks that achieved up to 40% higher biomass and 115% greater protein yield in Escherichia coli cultures. Building on that proof of concept, we have now advanced the technology to a higher manufacturing readiness level through injection molding. This study validates the performance of these breathable flasks across varying fill volumes compared to the standard polycarbonate flasks. Cell growth was tracked through periodic sampling for optical density measurements, while real-time dissolved oxygen levels were monitored using in-house developed non-invasive optical sensors. The breathable flasks consistently maintained higher oxygen availability, supporting healthier cultures and improved biomass accumulation. With enhanced gas exchange, they enable higher working volumes in the same 500 mL format without compromising cell health. In upstream bioprocessing, where shake flasks are widely used for early-stage cell expansion, this increase in biomass offers significant operational value. For high-value biologics such as Keytruda, where a single gram exceeds $9,000 in market value, greater upstream efficiency with breathable flasks can result in substantial cost savings and accelerated time to market.

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Role Of CD68+ Monocyte-Derived Macrophages In Regulating Adipose Tissue Growth During Diet-Induced Obesity

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Severe obesity-associated type 2 diabetes is a growing public health challenge, affecting millions of individuals worldwide. During obesity, adipose tissue adopts a state of low-grade chronic inflammation, where an increased abundance of pro-inflammatory adipose tissue macrophages (ATMs) is observed. Although CD68 has been commonly used as a macrophage pro-inflammatory marker in tissues, the field has not fully elucidated its molecular role in modulating ATMs' inflammatory responses, along with its paracrine effects in adipose tissue growth and function. We hypothesize that CD68 expression in ATMs modulates activation and recruitment of inflammatory immune cells in obese adipose tissue, thereby leading to development of low-grade chronic inflammation and insulin resistance. To investigate this hypothesis, we analyzed single-nuclei RNA sequencing (snRNA-seq) data from lean vs. obese state mouse-derived adipose tissue, where we evaluated presence of CD68+ myeloid cell populations. Tissue samples were derived from mice that went through different diet treatments, which included a chow or 60% high fat diet, resulting in lean, obese, weight loss, and weight cycling phenotypes. Results showed an increased abundance of CD68+ ATMs in obese mice compared to lean. We then corroborated these results via fluorescence microscopy staining for DAPI, CD68 and F4/80 protein expression in lean vs. obese adipose tissue. Upcoming directions include evaluation of CD68 functional role in macrophages' inflammatory profile using siRNA and flow cytometric approaches. Furthermore, we will evaluate if CD68-silenced macrophages impaired adipose tissue growth, vial co-cultures of CD68-silenced macrophages with primary preadipocytes, followed by assessment of preadipocyte proliferation. This research aims to help identify early signs of inflammation in fat tissue and support new ways to improve metabolic health by targeting myeloid immune cell pathways.

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WHEN DOES SHE FLY? MEASURING BOLDNESS IN FEMALE EASTERN BLUEBIRDS

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Eastern Bluebirds are a species of songbird known for their propensity to nest in both natural cavities and artificial nest boxes. In the past few decades they have struggled with population decline and in response there have been conservation efforts across the United States. One way bluebirds may be impacted is through the urbanization of our natural landscapes, which intersect

with the habitats that bluebirds use. Bluebird behavior may be altered by urbanization, including by impacting their "boldness" and reaction to humans. Across multiple study sites in Maryland, we measured the boldness of females by measuring their flight initiation distance (FID) from their nest as researchers approach their nestbox. We will also ask whether females behave similarly after multiple disturbances, in which case that behavior would be a "repeatable individual difference", which may be an indicator of their personality. We will determine whether female bluebirds have repeatable FID behavior, and if habitat type (urban versus rural) impacts the boldness of female bluebirds.

This research was supported by the Meyerhoff Scholars Program.

TESTING THE HETEROGENEITY OF PROSTATE INFLAMMATION USING GFP AS AN EX-VIVO MARKER ON 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 twenty-five percent of all human cancers. Evidence suggests that prolonged chronic inflammation can be a precursor for prostate cancer. However, a lack of definitive data has yet to verify this. To investigate this, we developed an inducible mouse model (RIG) which localized inflammation to the prostate gland. The model is characterized by three transgenes, Interleukin-1 Beta, Green Fluorescent Protein, and a TetOn system with a reverse tetracycline transactivator under Hoxb13 promoter control. For our study, multiple lineages of RIG mice were developed to test the impact of heterogeneity of inflammation expression on pre-neoplastic lesions, which we hypothesize will result in differences. To test this, RIG mice underwent an induction phase, followed by necropsy, and then analyzed for GFP and inflammation expression using imaging and histological techniques. Our preliminary data demonstrates that prostate inflammation is strongly correlated with GFP, however, there is no conclusive data as to which lineage is most robust. Future studies will focus on understanding the molecular basis for premalignant lesions, and to also quantify and identify the specific immune cells being localized to sites of prostate inflammation.

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DETECTING PFAS IN ESTUARINE WATER USING NOVEL EQUILIBRIUM PASSIVE SAMPLERS

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Per- and polyfluoroalkyl substances (PFAS) are synthetic chemicals used in a variety of industrial and consumer products. Recent research has indicated that PFAS exhibit toxic outcomes in humans at

extremely low concentrations, mandating PFAS monitoring in water supplies. To determine long-term average PFAS concentrations in surface water, we developed novel equilibrium-based passive samplers using anion-exchange membranes. The passive samplers were calibrated using selectivity coefficients measured in the laboratory, with competition and water quality effects being incorporated into the calibration. The objective of this project was to deploy passive samplers at four sites in and around Baltimore Harbor to validate the performance of our passive sampler and universal calibration for PFAS analysis. With assistance from municipal and nonprofit partners, we first collected grab samples from ten sites in and around Baltimore Harbor. At least 9 ng/L of PFAS was detected at each site, and PFOS was the most prevalent compound detected across the entire campaign. Based on the magnitude and composition of PFAS detected, we selected four sites for passive sampler deployment. Three of those sites were co-located with litter-collecting structures at the mouths of urban streams discharging into the Harbor, while the other site was situated at a wastewater treatment plant. We deployed our samplers for two, three, and four weeks. During deployment and retrieval of the passive samplers, we also collected grab samples to measure water quality parameters needed for the universal calibration. While PFOS was the dominant PFAS in all samplers, the PFAS composition in the samplers deployed in the Harbor differed from that in wastewater effluent, which contained more PFBS and 6:2 FTS. Samplers deployed for two, three, and four weeks showed no significant differences in the mass of accumulated PFAS, indicating that our sampler reached equilibrium within two weeks of deployment. Overall, this study demonstrates successful application of a novel passive sampler to inform PFAS loading and distribution in a sensitive estuary with variable water quality.

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DESIGNING STRUCTURAL MEMBERS USING BIO-INSPIRED DESIGN PRIMITIVES

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Understanding the organizational principles behind fibrous plant structures offers valuable insight into biomechanics and bio-inspired design. This study focuses on the smilax, which is known for its resilient climbing stems and complex vascular networks. The objective is to investigate the internal fiber and vascular arrangement of the smilax and determine whether a consistent structural pattern emerges across its cross sections. To achieve this, a 3D model of a smilax sample was digitally reconstructed from multiple X-Ray computed tomography scans of a plant stem approaching branching , then segmented using ImageJ to obtain cross-sectional images. Ten representative slices were chosen at set intervals to be analyzed. Each slice was processed through MATLAB to measure the area of individual fibers to then generate graphs relating these areas to their relative radial position from the entire cluster's centroid. By graphing fiber area versus radial distance for each slice, trends were examined in fiber size distribution and spatial arrangement. Preliminary analysis suggests some amount of radial organization and a potential optimization for fiber placement, possibly reflecting mechanical or support-related adaptations. This work contributes to a deeper understanding of plant-based structural design and may inform future development of bio-inspired fibrous materials. Applications of this research extend across several disciplines. In architecture, principles derived from smilax fiber

arrangements could be used to design lightweight yet durable support structures inspired by natural load distribution. In biomedical engineering, the spatial optimization of fibers may inform prosthetic designs that require a balance of strength, flexibility, and minimal material use. Additive manufacturing could also benefit from these findings by incorporating biologically optimized geometries into 3D-printed components for increased performance and sustainability. Additionally, integrating these structural insights into design software may allow engineers and designers to apply bio-inspired rulesets directly within digital workflows, streamlining the creation of efficient, nature-informed materials and systems.

This research was funded by the UMBC Mechanical Engineering department.

ORAL IMPLANTOLOGY UTILIZING 3D PRINTING

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Three-dimensional (3D) printing is the current accepted method to create surgical devices in clinical dentistry, specifically oral implantology. 3D Printing offers an alternative method to generate customized models in periodontics, oral and maxillofacial surgery (OMFS) departments. This includes the production of dental implant materials and tissue engineering. In this study, we investigate the usage of Formlabs 3D printer combining with intraoral scanner to ultimately design a practical patient treatment plan. Intraoral scanner involves the usage of computer-aided design/computer-aided manufacturing (CAD/CAM). CAD/CAM provides a digital impression of full mouth scanning. 3D printing implements these scans into their software, harnessing solid 3D printing surgical devices in accordance. Dental implant materials and bone graft tissues are further examined upon finishing printing. The purpose of this study is to examine the effectiveness of 3D printing surgical devices on improving oral health outcomes.

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INVESTIGATING THE IMPACT OF THE GENETIC NUTRIENT DEPRIVATION ON MALE FERTILITY IN DROSOPHILA MELANOGASTER

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The Integrated Stress Response (ISR) is a pathway that helps cells adapt to stressors such as nutrient deprivation by activating an important transcription factor called ATF4. When triggered, ATF4 helps cells survive cell death in stressful conditions. In Drosophila melanogaster, nutrient deprivation has been proven to cause a reduction in fertility, but its effects on spermatogenesis across developmental stages remain unclear. The Grmai Lab previously found that overexpression of the bacterial enzyme methioninase, which mimics nutrient deprivation by metabolizing (and therefore depleting) methionine, in fat tissues compromises viability in males.

They used the GAL4/UAS system to perform methioninase expression, where a GAL4 driver expressed in fat tissues drove expression of a UAS-methioninase transgene. They found that the presence of UAS-methionine alone led to rapid fertility decline. Since other labs have reported "leaky" expression of UAS transgenes without a GAL4 driver, this project focuses on whether UAS-methioninase alone compromises spermatogenesis. To measure this, testes from control groups UAS-lacZ, Oregon^{R}, and experimental UAS-methioninase males were dissected, stained by immunofluorescence to visualize germ cells, and imaged using confocal microscopy. The rate of spermatogenesis was determined by quantifying germ cells at different stages of differentiation. We analyzed Z-stack images in ImageJ to count germline stem cells (GSCs), gonialblasts, 2-cell cysts, 4-cell cysts, 8-cell cysts, and 16-cell cysts. Preliminary data suggest that the presence of UAS-methioninase alone may reduce the rate of germ cell differentiation. Future research will identify tissues that exhibit increased ATF4 activity in UAS-methioninase animals and whether spermatogenesis defects in UAS-methioninase reduce sperm count. These findings will help clarify how nutrient deprivation stress influences male fertility.

I would like to acknowledge the Bloomington Drosophila Stock Center (BDSC, Bloomington, IN) and Dr. Andrey Parkhitko (University of Pittsburgh) for providing the fly stocks used in this project. I also want to acknowledge the Developmental Studies Hybridoma Bank (DSHB, Iowa City, IA) for supplying key reagents for this project. Finally, I am especially grateful to the Grmai Lab at Yale School of Medicine and the Vasudevan Lab at the University of Pittsburgh School of Medicine for laying the foundational work that made this project possible

C

INVESTIGATING THE ROLE OF SHANK3 GENE IN MODULATING WINNER-LOSER EFFECTS IN MANGROVE RIVULUS KILLIFISH

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Social experiences are part of our daily lives and can lead to both short-term and long-term behavioral and physiological changes. One well-documented phenomenon is the winner–loser effect, which describes how previous winning or losing experiences alter a suite of behaviors, including aggression and cognitive behaviors. However, it remains unclear how the brain translates social experiences into behavioral responses. Our previous research, using the mangrove rivulus killifish (*Kryptolebias marmoratus*), demonstrated that prior winning experiences significantly increased aggression and spatial learning ability, whereas prior losing experiences reduced aggression but enhanced risk-avoidance learning. We also discovered that winners exhibited elevated SHANK3 protein expression, while losers showed decreased expression at the whole-brain level. Despite this finding, the specific brain regions where the *shank3* gene is expressed, and whether region-specific differences in expression directly modulate the formation of winner–loser effects, remained unknown in ours as well as other model organisms. To find these brain regions, we used *in situ* hybridization to locate the regions in which *shank3* is expressed. The *shank3* gene is known for its relevance to Autism Spectrum Disorder (ASD). Homozygous knock-out mutations of this gene, in zebrafish and mice, lead to behavioral defects similar to ASD. These behaviors include reduced social interaction,

aggression, and spatial learning ability. Based on these parallels, we hypothesize that social experiences influence aggression and cognitive behaviors through modulating SHANK3 protein levels in specific brain regions, including the fish analogs for the hypothalamus, hippocampus, and amygdala. To further test this hypothesis, we will first use *in situ* hybridization to localize *shank3* expression within the brain and compare expression patterns between winners and losers at the level of individual brain nuclei. To further investigate the relationship between SHANK3 expression and behavioral outcomes, we will use CRISPR-Cas9 gene editing tools to knock out the *shank3* gene and then use behavioral assays to examine if the winner-loser effects are affected by this manipulation.

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INVESTIGATING THE EFFECT OF OVEREXPRESSION OF RHO1 ON CLIMBING SPEED AND ENDURANCE IN DROSOPHILA MELANOGASTER

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The Rho1 gene has been identified through a genome-wide analysis as a candidate gene affecting physical performance in Drosophila melanogaster. Rho1 is an evolutionarily conserved gene that encodes for proteins in the family of GTPases, which play a key role in the regulation of actin dynamics and wound healing, and therefore potentially impact physical performance. We studied the effect of the Rho1 gene on climbing speed and endurance by manipulating Rho1 expression in the muscle tissue of the fly by utilizing the GAL4-UAS system. Virgin females of the muscle-GAL4 line were crossed with males of the UAS overexpressed Rho1 responder line and males of a control line. We measured the climbing speed and endurance of the offspring of these crosses. This experiment aims to determine whether Rho1 overexpression in muscle tissue influences locomotor performance, including speed and endurance. We hypothesize that an overexpression of the Rho1 gene within flies will have a statistically significant influence on their speed and endurance compared to the control line. The results of our experiment will provide insight into the significance of the Rho1 gene in the physical ability of Drosophila melanogaster, which may suggest the role the human orthologs of Rho1 play in physical performance in humans. This could help enhance personalized healthcare as it relates to physical decline and conditions such as myopathy and muscular dystrophy. If the Rho1 gene is found to affect physical performance in Drosophila melanogaster, further research is needed to determine the underlying mechanisms behind this effect. Future research should investigate the gene's effect on other tissues and age groups, given that Rho1 has been characterized as an age-specific gene in a genome-wide analysis of Drosophila melanogaster.

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STRUCTURAL BASIS AND MECHANISM OF HIV-1 GENOME PACKAGING

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The Human Immunodeficiency Virus type 1 (HIV-1) is a retrovirus that depletes CD4+ cells, weakening the host immune system and 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 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 segmental-based labeling approach. This approach involves a mutant DNA polymerase (TGK) that is capable of extending an RNA primer. TGK enables the preparation of stepwise, differentially labeled RNA segments of the packaging signal. This technique allows for unambiguous NMR signal assignment by reducing signal overlap and selectively eliminating signals from the final NMR spectrum.

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INVESTIGATING THE ROLE OF METHYL CPG-BINDING DOMAIN ON TUMORIGENESIS IN PROSTATE CANCER USING THE BMPC MOUSE MODEL

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Prostate cancer is one of the leading causes of cancer-related deaths globally, with nearly 1.5 million new cases and around 400,000 deaths in 2022. 1 in 8 men will be diagnosed with prostate cancer in their lifetime. Methyl-CpG-binding domain (MBD) binding proteins are involved in

DNA methylation, an epigenetic modification that regulates gene expression. These proteins are involved in transcriptional silencing of genes, including tumor suppressors. MBD2 is a member of the MBD family that plays a role in gene silencing by serving as a recruiter protein and aiding in DNA methyltransferase binding to DNA. It binds to the methylated DNA region of several tumor suppressor genes with high affinity and serves as a transcriptional repressor. Previous studies have shown MBD2's role in the P13/AKT pathway responsible for cell growth and proliferation, and that the deletion of MBD2 impedes tumor progression, making it a potential therapeutic cancer target. This project aims to understand the impact of mutating MBD2 on tumor growth and metastatic profile in the BMPC transgenic mouse model of prostate cancer. This mouse model is driven by the activation of a proto-oncogene and transcription factor, MYC, and the loss of PTEN, a tumor suppressor often mutated in human prostate cancer. I hypothesize that the absence of MBD2 in FVB-BMPC mice will slow the progression of prostate cancer and highlight the vital role of MBD2 in tumor development. Through the quantification of tumor size and analysis of tumor progression and metastasis in wild-type and MBD2 knockout BMPC mice, I aim to clarify the role of MBD2 in prostate cancer. This research will provide further insight into the identification of the gene as a possible target for therapy or as a biomarker for tumor progression and has vast potential translational and clinical applications.

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EVALUATING THE IMPACT OF SUCROSE AND PACIFIER USE ON INFANT DISTRESS DURING ROP SCREENINGS

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Premature babies are susceptible to an ocular disease called retinopathy of prematurity (ROP), which requires screening using indirect ophthalmoscopy to prevent blindness. Unfortunately, neonates may experience severe pain and physiological stress from these exams, despite the fact that they are essential. This study assesses whether giving a pacifier and oral sucrose together before ROP examinations lowers pain responses and enhances physiological stability during the exam. We conducted a prospective observational study in the NICU involving infants born at or before 31 weeks gestation. One of four interventions was given to participants: no intervention, sucrose only, pacifier only, or both pacifier and sucrose. Thirty to sixty seconds before the ROP screening, the intervention (24% oral sucrose and pacifier) was given. Vital signs, such as heart rate (HR), respiration rate (RR), and oxygen saturation (SpO_2), were collected prior to, during, and following the examination. The validated Premature Infant Pain Profile (NPASS) score was used to quantify pain. Infants who received both sucrose and a pacifier had the lowest NPASS scores (mean 5.95 ± 2.56) compared to the no-intervention group (8.93 ± 2.05), indicating reduced discomfort during the test. Additionally, the physiology of this group stayed more stable: the mean minimum oxygen saturation of the sucrose + pacifier group was higher (90 ± 7%) than that of the no-intervention group (83 ± 11%). The lower minimum respiratory rate (mean 30 ± 6

bpm for both sugar and pacifier versus 41 ± 9 for controls) showed better respiratory stability. Heart rate also demonstrated a trend toward greater stability following the intervention. We found that a combination of oral sucrose and pacifier eased discomfort and improved physiologic stability in preterm newborns during ROP examinations.

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ANCHOR GENE IN DROSOPHILA MELANOGASTER: AN UNDERLYING MECHANISM OF ALCOHOL SEDATION

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Alcohol use disorder (AUD) is widespread in the United States, impacting 28.9 million individuals in 2023. Despite its prevalence and the social, economic, and medical burdens related to alcohol misuse, our understanding of pathways behind AUD remains limited. An efficient model to characterize molecular mechanisms of alcohol behaviors is Drosophila melanogaster (the fruit fly). In particular, one Drosophila study showed that the mechanistic target of rapamycin complex 1 (mTORC1), a nutrient sensor and regulator of cellular activity, modulates ethanol-induced sedation through neurons called insulin-producing cells (IPCs). Here, we consider “anchor”, the Drosophila homolog of mammalian G protein-coupled receptor 155 (GPR155). GPR155 is an integral transmembrane protein that mediates mTORC1, but no studies have investigated GPR155 or its homologs’ role in the nervous system and their influences on AUD. Our preliminary data indicates anchor expression in IPCs, suggesting that anchor would influence ethanol-induced sedation by mediating mTORC1. Therefore, we hypothesize that IPC-targeted anchor knockdown lowers mTORC1 activity, thereby decreasing insulin signaling in IPCs to produce faster ethanol-induced sedation rates in Drosophila.

Using the Gal4/UAS system, we reduce anchor expression in IPCs by crossing a driver line targeting IPCs with an anchor RNAi responder line. Then, we use an established ethanol vapor sedation assay to assess sedation over time. Interestingly, our preliminary results show slower sedation rates in anchor knockdown flies, demonstrating a lower ethanol sensitivity compared to genetic controls. This implies that anchor expression in the IPCs is directly related to ethanol sensitivity and further develops our understanding of how IPCs influence ethanol-induced sedation. Overall, our research will help us comprehend the role of anchor, inform future studies of the mTORC1 signaling pathway in Drosophila, and provide insight into the underlying mechanisms of AUD.

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PASSIVE SAMPLING OF ZWITTERIONIC PFAS USING ION-EXCHANGE MEMBRANES

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Zwitterionic per- and polyfluoroalkyl substances (PFAS) are synthetic chemicals that contain both positive and negative charges, resulting in net-neutral molecules. These compounds are incorporated into many consumer and industrial products and considered precursors of regulated perfluoroalkyl acids, which are also known as “forever chemicals”. Although precursors constitute a meaningful portion of total PFAS, zwitterions are infrequently reported in water. Currently, no passive sampling tools are specifically designed for measurement of zwitterionic PFAS. To address this knowledge gap, we evaluated the uptake of zwitterionic PFAS by anion- and cation-exchange membranes under variable water quality conditions. In particular, 1×1 cm^2 membrane coupons were placed in 100 mL of water containing three zwitterionic PFAS, namely 6:2 FTAB, 8:3 PFAQA, and N-TAmP-FHxSA, and two regulated anionic PFAS, PFOA and PFOS. While 6:2 FTAB, 8:3 PFAQA, and N-TAmP-FHxSA are zwitterions at near-neutral pH, these compounds exist as cations at low pH; furthermore, 6:2 FTAB exists as an anion at high pH. We hypothesized that these speciation profiles and other water quality parameters would influence PFAS uptake into the two membranes. To test this hypothesis, we varied solution pH (i.e., 2, 5, 12) and salinity (i.e., 10, 100, 600 mM). The batch reactors were mixed for one week, then aqueous- and membrane-phase PFAS concentrations were measured by LC-MS/MS. The results confirmed that the PFAS end group played a key role in determining the preferred membrane. While 6:2 FTAB, which has a negatively-charged end group, was preferentially accumulated in the anion-exchange membrane, 8:3 PFAQA and N-TAmP-FHxSA, which have positive end groups, favored the cation-exchange membrane. The two anionic PFAS were only detected in the anion-exchange membrane. Salinity influenced PFAS accumulation via salting-out phenomena. These findings support the development and application of passive samplers for zwitterionic precursors to better capture the full PFAS pool during environmental monitoring.

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IGFBP2-VEGF PATHWAY DRIVES AGE-RELATED RESISTANCE TO MEK INHIBITION IN ACRAL MELANOMA

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Acral melanoma (AM) is a rare and aggressive subtype of melanoma that arises on the palms, soles, and nail beds. AM primarily affects older individuals, classifying it as a disease of the elderly; however, the impact the aged microenvironment has on AM aggressiveness and therapy response remains unexplored. Targeted therapies such as Trametinib (a MEK inhibitor) have been used to target the MAPK pathway, often activated in AM. We have previously shown that older patients with cutaneous melanoma respond poorly to targeted therapy; however, how it affects AM has yet to be investigated. We aim to investigate how the aged microenvironment

(ME) influences therapy response in AM. To assess the contribution of the aged ME, we treated AM cells with trametinib in the presence of conditioned media (CM) from either young (<35) or aged fibroblasts (>55). Notably, aged CM reduced sensitivity to trametinib, as measured by viability assays. Preliminary data from a Reverse Phase Protein Array (RPPA) analysis from young and aged AM mouse tumors, showed high expression of Insulin-like Growth Factor Binding Protein 2 (IGFBP2) to be upregulated in tumors isolated from aged mice. To investigate if this is driving the lower response in the aged ME, we performed immunoblotting of AM cells treated with young or aged CM in the presence or absence of trametinib. Interestingly, Vascular Endothelial Growth Factor Receptor (VEGFR), a downstream effector of IGFBP2, was upregulated in AM treated with aged CM and further upregulated when treated with trametinib in aged CM compared to young CM. This data suggest that VEGFR is playing a role in the low therapy response of AM in the aged ME. Our next steps are to validate these results using 3D spheroid models and flow cytometry. Understanding IGFBP2-VEGF role in aged-related drug resistance will unveil new therapeutic targets and redirect treatment strategies for aging and other underserved populations.

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D

EXPLORING COMBINATIONAL METHODS OF REDUCING LONG SHORT-TERM MEMORY (LSTM) NETWORK INFERENCE SPEED FOR EDGE DEVICES

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The growing deployment of machine learning models on embedded systems has highlighted the challenge of running computationally intensive algorithms like LSTM networks on resource-limited edge devices. Three techniques were chosen to reduce inference time without significantly sacrificing prediction accuracy: quantization (reducing numerical precision), low-rank factorization (approximating weight matrices with smaller components), and hardware acceleration using parallel digital circuits. This study aims to identify if combining these techniques yielded a significant increase in inference time vs singular methods. We applied each method to a custom LSTM model for weather prediction and evaluated performance using a historical weather dataset. Quantization alone reduced inference time by approximately 33% compared to the baseline model. However, combining quantization with low-rank factorization did not yield additional improvements. Preliminary results suggest that combining hardware acceleration with quantization may offer the greatest gains.

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WHAT'S THIS LAB ABOUT? A LAB-SPECIFIC LEARNING MODEL

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The shift from a non-expert to a new researcher can take weeks, or even months, without an expert interpreting and clarifying prior work. Many labs do not have the manpower due to deadlines, and so a way to teach newcomers effectively is necessary. Proprietary Large Language Models (LLMs) such as OpenAI's ChatGPT and Google's Gemini have become a staple resource for people to learn new topics in a conversational format. However, while LLMs have been shown to do well in providing explanations and giving users space to answer follow-up questions, they lack the core principles necessary for a beginner to learn. First, they lack the domain expertise. Second, they lack the unique style, priorities, and way of presenting information of the lab. Third, proprietary LLMs cannot incorporate the most recent lab findings into their data. Moreover, it is difficult to investigate whether LLMs are actually adapting to new knowledge via prompting or if they are recycling pre-trained information. To address this, we take advantage of open-source models like EleutherAI's GPT-J-6B, GPT-Neo, and Google's Gemma by being able to see their existing knowledge. This mentorship-like dynamic shows why a conversational format shows promise for helping new researchers. For our problem, the format allows for interactive questions, can be adapted to each labs' style, and can incorporate new information seamlessly. The challenge here is not the format but aligning the content and style to the lab's work while incorporating future research. We propose a simple methodology that allows researchers to create personalized chatbots for their specific lab material. This will save time onboarding new lab members, and it will be a staple introduction for new learners.

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EXPLORING THE FATE OF RNA IN MOLONEY MURINE LEUKEMIA VIRUS (MoMuLV)

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Retroviruses must regulate the fate of their RNA genomes to balance translation and packaging. HIV-1 accomplishes this through transcriptional start site (TSS) heterogeneity, generating two distinct RNA pools, cap 1G and cap 3G, that drive either virion packaging or protein synthesis. In contrast, Moloney Murine Leukemia Virus (MoMuLV), a simple retrovirus, transcribes its RNA solely from a single TSS (coined ^{cap}1G), yet still effectively separates these functions. This suggests that MoMuLV uses a post-transcriptional mechanism to control RNA fate. We hypothesize that MLV's genome fate is driven by a dimerization-dependent cap sequestration, and we hypothesize that cap sequestration is essential for packaging. Dimerization is proposed to induce conformational changes that sequester the 5′ cap, preventing recognition by translation initiation factors like eIF4E. To test this, we use in vitro transcription to generate MoMuLV RNA, we then use Faustovirus capping enzyme (FCE) to cap the RNA, and assess cap

accessibility through electrophoretic mobility shift assays (EMSAs) with eIF4E. Because the MoMuLV leader is too large for structural analysis via NMR, we use smaller truncations that retain the native 5′ start site. We aim to find truncations that mirror the full-length RNA in dimerization and cap sequestration behavior, enabling us to validate their suitability for future NMR-based structural studies. This work aims to define a structural and behavioral mechanism by which MoMuLV regulates RNA fate in the absence of TSS heterogeneity, helping us to understand conservation of function amongst retroviruses by studying an older relative of HIV-1.

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INVESTIGATING DYSBIOTIC MICROBIAL INTERACTIONS USING ORGAN-ON-A-CHIP TECHNOLOGY

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Bacterial vaginosis (BV) is the leading cause of women's healthcare visits worldwide. It is characterized by a shift in the vaginal microbiome, specifically an overgrowth of anaerobic bacteria and a depletion of protective lactobacilli. This polymicrobial infection has been associated with serious complications, including preterm birth, and an increased risk of sexually transmitted infections (STIs). Despite its prevalence, much is unknown about the underlying mechanisms driving the onset of BV.

Three species of bacteria, *Gardnerella vaginalis*, *Lactobacillus crispatus*, and *L. iners*, have been identified as indicators of dysbiosis, a healthy state, and an intermediate state, respectively. *L. crispatus* and *G. vaginalis* exhibit an amensal relationship where *L. crispatus* inhibits *G. vaginalis* through the production of lactic acid. In contrast, *L. iners* and *G. vaginalis* appear to have a mutualistic relationship. *G. vaginalis* is strongly associated with the onset of BV, and *L. iners* is frequently detected alongside *G. vaginalis* and following treatment with antibiotics like metronidazole. This raises questions about the role of *L. iners* in either facilitating or failing to prevent BV recurrence. These microbial communities are highly unstable, with ~50% of patients experiencing a recurrence of BV within one year after treatment. Given this instability and the unclear role of *L. iners*, we aim to investigate the interactions between *L. iners* and *G. vaginalis*, focusing on their potential symbiotic relationship and its impact on vaginal health.

To simulate physiologically relevant conditions, we are developing an organ-on-a-chip technology to model microbial interactions microscale. This platform enables the coculture of human vaginal epithelial cells, uterine fibroblasts, and associated microbes, creating a biomimetic environment. By elucidating the dynamics between *L. iners* and *G. vaginalis* using a vagina-on-a-chip model system, this study has the potential to advance our understanding of BV pathogenesis and improve methods for its detection, treatment, and prevention.

Support for this research was funded by the Jackman Burden (JB) Lab.

E

OCULAR BLOOD FLOW RESPONSE TO CEREBROSPINAL FLUID REMOVAL IN NEONATES WITH POST-HEMORRHAGIC HYDROCEPHALUS

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Post-hemorrhagic hydrocephalus (PHH) following intraventricular hemorrhage (IVH) leads to excess cerebrospinal fluid (CSF) and resulting hydrocephalus in preterm infants. Increased intracranial pressure (ICP)impacts neurological development and optic nerve function. Infants with progressive hydrocephalus undergo CSF removal procedures using reservoirs and/or diverting shunts, but the direct impact of CSF removal on neonatal ocular circulation is unknown. Laser speckle contrast imaging (LSCI) is a non-invasive imaging tool that analyzes a selective, blurred pattern created as light is scattered by the movement of red blood cells. LSCI interprets dynamic ocular blood in terms of location and speed. This study aims to determine the impact of CSF removal on ocular blood flow in infants with PHH using LSCI. In this single longitudinal case, a preterm infant, born at 23.6 weeks' gestation and with a birthweight of 750 grams, underwent ocular blood flow analysis using LSCI before and after 15 mL of CSF removal from a previously placed Ommaya reservoir. Changes in ocular blood flow post-CSF removal were analyzed using paired statistical tests. Blood flow increased post-intervention in both eyes: right eye from 6.61 ± 0.44 to 7.13 ± 0.70, and left eye from 6.11 ± 0.49 to 6.33 ± 1.15, with a greater change in the right eye (right eye $\Delta = 0.52$ compared to the left eye $\Delta = 0.22$). Reducing cerebrospinal fluid resulted in increased ocular blood flow in a single infant with hydrocephalus. Non-invasive imaging could help detect and manage ICP-related pathologies. Further studies are needed to understand the impact of CSF removal on ocular blood flow.

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CAPTURING THE PROCESS OF DEGRADATION OF VERDIGRIS WITH ATR-FTIR

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Verdigris is a copper-based organometallic pigment composed of copper acetate and hydroxide in varying ratios. It's a vibrant blue-green color, and has been identified as the primary source of green paint spanning from the time of the Ancient Greeks to the Industrial Revolution. Verdigris is highly sensitive to environmental fluctuations compared to most pigments, and will degrade with a color change from green to brown in a short time on art timescales. This research focuses on determining the factors influencing the degradation process and the degradation products using Attenuated Total Reflection Fourier Transform InfraRed (ATR-FTIR) spectroscopy. ATR-FTIR spectroscopy is suitable for this study due to its high sensitivity and ability to provide

functional group information in real time, which provides great mechanistic insights on the degradation process. Ultimately, this technique could be used to detect pigment degradation before it becomes visibly perceivable. In our experiments, Verdigris was ground and mixed with linseed oil as a binder in a 2:1 (v/v) ratio, then spread onto watercolor paper to simulate paint on a canvas. Upon exposure to 120°C in an oven, the paint exhibited a color transition from blue to green within 30 minutes, followed by a shift to brown after four hours. Preliminary ATR-FTIR spectral data show an early disappearance of characteristic water absorption bands at 3470, 3365, and 3270 cm^{-1}. Additionally, the signals initially observed at 1600 and 1420 cm^{-1} exhibit shifts to 1550 and 1410 cm^{-1}, respectively, and decrease in intensity. After prolonged heat exposure, a peak emerges and grows significantly at 510 cm-1. The loss of water signals early on implies that dehydration occurs, and the decrease in intensity in the peaks at 1550 and 1410 cm^{-1} show a loss of carbonyl and methyl groups. In a separate experiment, powdered Verdigris was sealed in a round-bottom flask under an inert nitrogen atmosphere and exposed to 120°C for 19 hours. Under these conditions, Verdigris retained its characteristic blue-green color, whereas the control sample exposed to air changes to brown. These observations suggest that the thermal degradation of Verdigris may be facilitated by the presence of O2.

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POPULATION DENSITY AND MOBILE PHONE MICROBIOME DIVERSITY: A COMPARATIVE ANALYSIS ACROSS EIGHT CITIES

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The human microbiota is the community of microbes that live on and within the human body. Microbes that make up the human microbiota have been demonstrated to play a significant role in human health, such as helping to break down food, producing vitamins, and even being correlated with diseases such as obesity and diabetes. The composition of the human microbiota can be influenced by a multitude of factors, including the environment that humans interact with on a daily basis. This study aimed to investigate the diversity and abundance of microbes on phones between cities with varying populations. It was hypothesized that phone microbiomes from individuals in larger cities will yield greater microbial diversity than phones from individuals living in smaller cities. Data on the diversity of bacterial phyla and abundance was collected through the use of Phinch software and the Project MERCURRI data set. 755 samples were filtered from the dataset to analyze bacterial phyla present on mobile phones from participants across eight cities representing different population sizes: major cities (New York and Houston), large cities (San Francisco and Washington DC), medium cities (Fort Lauderdale and Palmdale), and small cities (Longmeadow and Potlatch). Analysis of the dataset showed that overall, mobile phones in bigger cities had greater diversity than their counterparts from smaller cities, with larger cities having 2 to 3 more types of phyla than smaller cities. The results align with the hypothesis that phone microbiomes from individuals in larger cities will yield greater microbial diversity than those from individuals living in smaller cities. This study has

implications for factors that could influence the composition of the human microbiota, including what bacterial populations are present on individuals' phones. Further research could explore how the microbes found on people's phones are potentially transferred to their microbiota.

This research project was funded by the College of Natural and Mathematical Sciences at UMBC.

F

DESIGN, SYNTHESIS, AND BIOLOGICAL EVALUATION OF NOVEL 4'-MODIFIED FLEXIMER NUCLEOSIDE ANALOGUES WITH BROAD-SPECTRUM ANTIVIRAL ACTIVITY

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Throughout history there have been many pandemic level outbreaks, the danger of these outbreaks is the result of three factors: the lethality and communicability of the virus and the current level of preparedness. The latter factor is completely controllable. The 2020 coronavirus outbreak may have been much less impactful if the United States had a higher level of preparedness. One way to increase preparedness for a future pandemic of an unknown virus type is to have a catalog of broad-spectrum antivirals to use as a starting point in the development of therapies against the pandemic virus.

A foundational piece of antiviral therapy are nucleoside analogues (NAs). These NAs mimic natural nucleos(t)ides and thus, through enzymatic inhibition, prevent the viral replication cycle. This type of NA, the fleximer, is a purine analogue with a single carbon-carbon bond separation between the imidazole and pyrimidine moieties. This separation introduces flexibility to the nucleobase that is not present in natural nucleosides. The flexibility grants the potential for increased potency, broad-spectrum antiviral activity, and point-mutation resistance. Modification of the 4' position of the sugar moiety with an azido functional group stabilizes the sugar moiety into the "North-type" conformation, increasing activity against viral polymerases and potentially reducing off-target effects.

In this study fleximers were modified at the 4' position yielding a series of novel 4' azido fleximer nucleoside analogues. Preliminary data shows that one compound, KAD-039, has single digit micromolar activity against DENV, EBOV, and SARS-CoV-2. This activity indicates the series' potential as broad-spectrum antivirals.

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INVESTIGATING THE ROLE OF HEPARAN SULFATE PROTEOGLYCAN BIOSYNTHESIS ENZYMES IN REGULATING BORDER CELL MIGRATION

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Collective cell migration is vitally important to development, wound healing, and cancer metastasis, yet this process is still poorly understood. Border cell (BC) migration, which occurs during egg chamber development in Drosophila melanogaster, is studied to characterize the conserved signaling pathways and regulation of collective cell migration. The BCs detach from the anterior epithelium and migrate posteriorly through the germline nurse cells by extending membrane protrusions that grapple, push, and pull on these substrate cells. Migrating cells are guided by interactions with physical structures and extracellular signals. Heparan sulfate proteoglycans (HSPGs) are common in the extracellular space, and are each composed of a core protein and glycosaminoglycan chains that perform multiple functions, including modifying the distribution of extracellular signaling molecules. Thus, the enzymes required for biosynthesis and modification of glycosaminoglycan chains attached to HSPGs interact with multiple signaling pathways, but their role in BC migration is uncharacterized. We used fluorescent in situ hybridization (FISH) to visualize the mRNA localization for individual genes that encode HSPG-related enzymes within the egg chamber. Preliminary data shows high mRNA expression in the substrate cells compared to surrounding cells for a subset of these enzymes. We used RNA interference to reduce expression of these genes in a cell-type specific manner. Reducing expression of these genes in the substrate cells led to defects in cohesive movement of the BC cluster. Reducing gene expression within the BC cluster for the same enzymes did not produce similar defects, indicating that the relevant signaling pathway(s) are likely acting non-cell autonomously. We are currently working to verify effectiveness of the RNA interference constructs and using FISH experiments with other HSPG enzymes to examine mRNA localization patterns. This project provides insight into mechanisms that guide collective cell migration in diseases like metastatic cancers.

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G

UNCOVERING THERAPEUTIC STRATEGIES FOR ACRAL MELANOMA THROUGH HIGH THROUGHPUT DRUG SCREENING

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Acral melanoma (AM) is a rare and aggressive subtype of melanoma. It has a poorer survival rate compared to other types of melanoma and has no FDA approved therapies. Part of this is due to mutational variation in these patients. AM exhibits frequent mutations in kinase-related genes, such as BRAF, NRAS, and, less commonly, EGFR among others. However, increases in the number of EGFR gene copies (called copy number variations) have also been reported. To

identify effective therapeutic targets for these patients, we performed a drug screening of approximately 130 drugs, including kinase inhibitors, cytotoxic agents, and targeted therapies. The goal was to identify drugs that significantly reduce the survivability of acral melanoma cells while not affecting normal cells. Using statistical analysis, we compared the responses of three acral melanoma cell lines (YUWERA, WM4235, and WM4234) to non-transformed control cells for each drug. Among the drugs tested, the pathways most significantly affected by targeted inhibition were EGFR signaling, microtubule stabilization, and multi-kinase activity. Notably, the compounds Gefitinib (EGFR inhibitor), Ixabepilone (microtubule stabilizer), and Regorafenib (multi-kinase inhibitor) showed the strongest effects within these respective pathways when compared to non-transformed cells. As a next step, we plan to validate our results using 3D spheroids, live and dead assays, and western blotting to better understand why melanoma cells respond to these drugs. These findings are promising for the next steps of targeted acral melanoma therapies and show the value of drug screening in identifying tumor-specific vulnerabilities.

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COLLABORATIVE ROBOT LOCALIZATION VIA NETWORK CHANNEL CHARACTERISTICS AND VISUAL SENSING IN GPS-DENIED ENVIRONMENTS

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Ground Robots require precise localization to create a scene knowledge graph for accomplishing various missions, such as situational awareness. A scene knowledge graph is essential for scene understanding, as it creates a structured representation of the objects, agents, locations, and relationships between entities present in a visual scene. While robots are equipped with GPS, they are not effective in localizing themselves in GPS-denied environments. Hence, robots need to communicate with each other to estimate their relative location in the visual scene, which is essential for applications such as collaborative scene perception and navigation, as well as distributed task execution that requires multi-robot coordination. Received Signal Strength Indicator (RSSI) is widely used for localization and inter-robot distance estimation due to its low computational overhead. However, RSSI alone is highly susceptible to interference and environmental variability, leading to significant localization errors when used in isolation. Our preliminary studies on estimating distance from RSSI values, using a dataset curated in both home and lab environments, have resulted in median errors of 5.75% using linear regression, 3.56% using KNN Classification, and 2.90% with tree-based ML models. Thus, to improve the estimation accuracy, we introduce a novel fusion framework that integrates RSSI with signal-to-noise ratio (SNR) measurements and selective RGB vision cues, yielding more robust distance estimates. Our unified model continuously fuses RSSI and SNR data, invoking visual observations selectively to account for measurement noise. We plan to test our approach on a heterogeneous multi-agent system comprising two TurtleBot3 Burger robots and a ROSbot 2 PRO. For long-range communication in GPS-denied settings, we employ Doodle Radios, which enable an extended operational range. We plan to conduct comparative evaluations against

conventional path-loss models and RSSI-based regression techniques to assess how our fusion method reduces localization error and improves distance estimation across varying environments.

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ENHANCING PHOSPHORESCENCE OF CHLORIN DERIVATIVES FOR HYPOXIA-TARGETED CANCER IMAGING

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Phosphorescent probes are noninvasive oxygen sensors used for early-stage cancer diagnostics, as small tumors create localized hypoxia (low oxygen) environments. These probes offer a greater advantage over fluorescent molecules due to their longer excited state lifetimes (milliseconds vs. nanoseconds). Upon excitation, these molecules luminesce in the red-to-near infrared window (650-900 nm), providing deeper tissue penetration and high-contrast imaging of tumor oxygen levels. We investigated three synthetic chlorin-type organic molecules, monomers, dimers, and carbonyl-substituted oxochlorins, to assess how the type of metal inserted (platinum or palladium) and structural modifications influence phosphorescence intensity. We hypothesized metal insertion and chemical modification such as dimerization, or the addition of a carbonyl group would increase phosphorescence intensity. To evaluate this hypothesis, we measured the absorption spectra of each compound to determine the excitation maxima (λ_{max} = 380-415 nm), then recorded emission under deaerated conditions to minimize quenching effects. We compared the phosphorescence intensity of the three chlorin-chlorin dimers, containing different combinations of two metals: platinum-platinum (Pt-Pt), platinum-palladium (Pt-Pd), palladium-palladium (Pd-Pd). Our results indicated that metal insertion substantially enhanced phosphorescence quantum intensity, with platinum containing compounds consistently outperforming their palladium counterparts. Among the dimers, the Pt-Pt dimer demonstrated the highest phosphorescence intensity, followed by the mixed Pt-Pd dimer, and then the Pd-Pd dimer. We additionally compared the platinum monomer, Pt-Pt dimer and platinum oxochlorin complexes. The platinum oxochlorin exhibited the strongest phosphorescent intensity followed by the Pt-Pt dimer and then the platinum monomer. These results demonstrate both metal incorporation and targeted structural modifications can enhance the phosphorescence quantum intensity and low-oxygen detection capabilities. This research will contribute to the advancement of noninvasive in vivo imaging techniques through phosphorescence-based sensing, contributing to early-stage cancer diagnostics.

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ANALYZING THE DIFFERENCES IN QUALITY BETWEEN GENOME ASSEMBLED USING DIFFERENT ASSEMBLERS

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To fully comprehend an organism, it is often necessary to analyze its genome. Current sequencing technologies like PacBio produce high quality reads, but assembling these into a whole genome requires specialized software called an assembler . Given the importance of these assembler programs we aimed to determine whether different assemblers produce assemblies that vary significantly in quality. In this study we compared the performance of two genome assemblers, Hifisasm and Flye, in assembling reads. Hifiasm is an assembler that expects high accuracy reads and works better with Hifi reads, comparatively, Flye is an assembler that can tolerate high error rates, works better with noisy reads, but is not designed for phasing. We tested the abilities of these assemblers by using both data generated in our lab as well as previously published datasets. We then polished the assemblies produced using a polishing program called Racon. These assemblies are then checked to make sure they are of quality. Quality cheers like BUSCO, which analyzes the genome based on completeness, and QUAST, which analyzes the assemblies based on accuracy. Both compared the qualities of both the raw assemblies and the polished ones. Preliminary results show that the assembly produced by Hifiasm has less contigs than the assembly produced by Flye for both the raw reads and all 3 polished variants, suggesting that Hifiasm is of better quality. Understanding the differences in quality between assemblers is important since these tools are crucial in understanding an organism's genetic makeup and how they function. Further comparisons and improvements may still be necessary.

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IMPROVING PERMANGANATE-BASED PROTOCOLS TO GENERATE HYBRID ANION-EXCHANGE RESINS FOR REMOVAL OF (ULTRA)SHORT-CHAIN PFAS IN DRINKING WATER

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Per- and polyfluoroalkyl substances (PFAS) are toxic chemicals that have contaminated global water supplies. Conventional anion-exchange resins successfully remove long-chain PFAS from water, but performance is limited for (ultra)short-chain PFAS. Metal oxide-laden hybrid anion-exchange (HAIX) resins improve PFAS uptake by adding adsorption sites and disrupting selectivity for long-chain PFAS. This study aimed to refine an HAIX resin generation protocol that involves loading parent resins with permanganate (MnO_4^-) and then introducing ferrous chloride ($FeCl_2$) to enable MnO_4^-/Cl^- exchange and oxidize Fe^{2+} to Fe^{3+} inside the resins. Two

different resins were employed. The main objective was to evaluate the impact of three MnO_4^- concentrations on the extent of iron loading and performance for removal of (ultra)short-chain PFAS. HAIX resins were generated by placing 5 g of resin in solutions containing MnO_4^- concentrations equivalent to 50%, 100%, and 150% of the resin's anion-exchange capacity. The resins were then sequentially submerged in 10% w/v $FeCl_2$, 5% w/v sodium hydroxide, and 1 M sodium chloride (NaCl) for 24 hours. Scanning electron microscopy with energy dispersive X-ray spectroscopy informed iron loading throughout the HAIX resins. Separately, ferric (oxy)hydroxide particles were synthesized and evaluated alongside granular Fe_2O_3 as controls to benchmark performance of the HAIX resins. The performance of the parent resins, HAIX media, and iron oxide controls were evaluated in solutions containing 10 mM NaCl and 0–14 mg L^{-1} of eleven (ultra)short-chain PFAS at near-neutral pH, with or without 300 mg L^{-1} of nitrate or sulfate or 8 mg_C L^{-1} of dissolved organic matter as competing species. Compared to the control materials, HAIX resins demonstrated improved uptake and selectivity for (ultra)short-chain PFAS, even in the presence of competing anions. Overall, this study highlighted the promising potential of HAIX resins to remove (ultra)short-chain PFAS and safeguard drinking water quality.

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H

CORRECTING SCEP's INADEQUATE CRYPTOGRAPHIC BINDING

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This research presents and formally verifies potential corrections of a known flaw in the custom mutual authentication protocol, the Server Connection Establishment Protocol (SCEP). Cryptographic protocols are procedures that utilize cryptographic techniques to ensure specific security goals for secure data transportation across networks. However, a common pitfall when designing these protocols is failing to cryptographically bind messages to session context. This allows an adversary to compromise confidential information and makes the protocol susceptible to man-in-the-middle (MITM) attacks. SecureDNA is an organization that provides DNA synthesis screening to detect potential hazards. During this screening, SecureDNA uses the flawed SCEP, which fails to mutually authenticate the communicants. The SCEP fails to bind a request cookie and the initiator's token to the session context. This failure potentially allows an adversary to bypass SecureDNA's request rate limiting. To examine SCEP, I used the Cryptographic Protocol Shapes Analyzer (CPSA), a model finding tool for structurally analyzing cryptographic protocols. Using CPSA, I modeled and fixed this failure in the protocol using a variety of approaches that include: manual experimentation, automatic binding, and TLS channel binding. This research highlights the importance of cryptographically binding messages to context in protocols to ensure secure communication across a network.

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STRUCTURAL BASIS AND MECHANISM OF HIV-1 GENOME PACKAGING

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The Human Immunodeficiency Virus type 1 (HIV-1) is a retrovirus that depletes CD4+ cells, weakening the host immune system and 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 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 segmental-based labeling approach. This approach involves a mutant DNA polymerase (TGK) that is capable of extending an RNA primer. TGK enables the preparation of stepwise, differentially labeled RNA segments of the packaging signal. This technique allows for unambiguous NMR signal assignment by reducing signal overlap and selectively eliminating signals from the final NMR spectrum.

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

INVESTIGATING REGULATORS OF THE TUMOR MICROENVIRONMENT USING CELL LINES DERIVED FROM A GENETICALLY ENGINEERED MOUSE MODEL OF AGGRESSIVE PROSTATE CANCER

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Prostate cancer (PCa) is the most frequently diagnosed malignancy and second leading cause of cancer deaths in American men. Nearly all cases of lethal PCa have gain of proto-oncogene *MYC* and loss of phosphatase and tensin homolog (*Pten*). To study prostate carcinogenesis and metastasis, the Bieberich laboratory developed the genetically engineered BMPC (*Hoxb13-MYC; Hoxb13-Cre; Pten*$^{fl/fl}$) mouse model. Combined prostate-specific human *MYC* overexpression and genetic deletion of mouse *Pten* synergize to promote highly aggressive carcinogenesis. We have established these transgenic lines in the FVB/N (BMPC^{FVB}) and C57BL/6J (BMPC^{B6}) mouse strains and have observed prominent differences in tumor latency, growth, and metastasis between the two genetic backgrounds. We hypothesize that cell-intrinsic factors and regulators of the tumor microenvironment (TME) are differentially modulated. To investigate such factors, we derived MPF-Li and MP6-LN1 cell lines from tumors in BMPC^{FVB} and BMPC^{B6} mice, respectively. To test this hypothesis, bulk RNA sequencing was performed and our bioinformatic data analyses revealed an increased secretory signature in MP6-LN1 than in MPF-Li that includes increased Wntless (*WLS*), the main transmembrane protein responsible for secreting *WNT* proteins, and Lysyl Oxidase (*LOX*), a central regulator of the extracellular matrix. Activation of *WNT* signaling and extracellular stromal remodeling has been implicated in many cancers, and their roles in PCa progression are being evaluated by manipulating gene expression in cell lines and characterizing phenotypic changes.

This work was supported by NIH grants 2R01CA200900-06A1 and 1U54CA274370-01.
Lily Handwerger was supported by the Meyerhoff Scholars Program.

INVESTIGATING ETHANOL AS A POTENTIAL NEUROPROTECTANT IN ALZHEIMER'S DISEASE DROSOPHILA MODEL

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Alzheimer's disease (AD) results in the neurodegeneration of individuals which impairs memory, cognition, as well as motor skills. Despite AD's impact, effective treatments are limited. This study focuses on whether ethanol can be used as a neuroprotectant to reduce neuronal degradation found in AD. Using Drosophila Melanogaster as our model organism, we exposed Wild Type and APPLd flies (a mutant gene directly correlated with AD) to various ethanol concentrations into their food and enclosed environment. Each week, behavioral flight tests would be executed to various cohorts of Drosophila to observe trends that could be concluded from collected data. Through our experiments, we are able to conclude potential findings that may support our hypothesis that the usage of ethanol may act as a neuroprotectant, given a certain concentration. With further investigation, ethanol could further be proved to be safely

used as a neuroprotectant, postponing the degradation of neurons in AD. This information could be used as an agent in treating other neurodegenerative diseases such as AD.

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

A FUNCTIONAL MAP OF INTRINSICALLY DISORDERED REGIONS ACROSS THE HUMAN PROTEOME

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How function is encoded in protein sequences is key to understanding biological systems. While many sequences of the proteome encode functional tertiary structures, a significant fraction is predicted to be disordered. Intrinsically disordered regions (IDRs) lack a fixed structure in their native state and are poorly conserved across species, hindering the use of structure- or homology-based methods to resolve their functional roles. Thus, IDRs represent a major gap in understanding how the proteome encodes for biological function.

Mutations in IDRs are frequent in genetic diseases, including cancer. Genomic analyses of tumor datasets identified that 30% of mutations occur in IDRs. However, most remain variants of uncertain clinical significance (VUS). To address this gap, gene editing screens targeting 6,171 recurrent IDR cancer mutations were performed, revealing essential residues that impact the fitness of human cells. Leveraging these datasets, we identified both known and uncharacterized functional sequences in IDRs across the human proteome.

We focused on *TBX3* – a transcription factor with essential roles in development. While mutations in *TBX3* can lead to loss-of-function in congenital disorders, *TBX3* is often overexpressed in different cancers. However, mechanisms by which mutations in *TBX3* can lead to a gain-of-function phenotype remain poorly understood. We identified several VUS targeting an IDR and conferring a significant increase in cellular fitness. Preliminary data suggests these variants could increase *TBX3* expression.

Since TBX3 activity is regulated by protein phosphorylation, we hypothesize that these variants might disrupt the phosphoregulation of TBX3. Future studies will focus on investigating the phosphorylation status of TBX3 IDR variants. Lastly, I conducted computational predictions and identified impactful mutations that result in gain or loss of a phosphorylation site. Our results identify genetic mutations impacting functionally important regions in disordered domains and suggest that altered phosphoregulation may be a widespread mechanism underlying pathogenic variants in IDRs.

This work is supported by the Howard Hughes Medical Institute, NCI Cancer Center support grant, NIH T32GM13640 training grant, and funding of MIT MSRP-Bio through the MIT Biology department.

EVALUATING THE FEASIBILITY OF PRODUCING HIGH-PRECISION TRANSIT LIGHT CURVES WITH SUB-MINUTE TIMING UNCERTAINTIES USING GROUND-BASED TELESCOPIC PHOTOMETRY

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High-precision astronomical databases are fundamental to exoplanetary science, particularly for validating candidate transits identified by space-based observatories such as *TESS*, *Kepler*, and *JWST*. While these missions provide vast quantities of time-series photometric data, confirming planetary candidates requires independent ground-based follow-up to eliminate false positives (e.g., eclipsing binaries, blended sources) and to refine ephemerides and transit depths. Acceptance into professional repositories, such as those curated by the American Association of Variable Star Observers, requires astrometric uncertainties of less than one minute, necessitating stringent observational protocols and optimized instrumentation. We present results from an ongoing ground-based campaign designed to test the hypothesis that small-scale observatories, when equipped with modern CMOS-based imaging systems, can provide photometric precision sufficient for transit validation. Our instrumentation includes equatorially harmonic mounted optical systems with advanced digital polar alignment, thermally regulated focusing, high-resolution pixel-scale autoguiding system, and scientific CMOS monochromatic detectors optimized for high quantum efficiency, large full well capacity, low gain (e^-/ADU), minimized read noise (e^- rms), low dark current (e^-/s/pix), and wide dynamic range. These specific characteristics allow for the reliable detection of shallow brightness dips associated with suspected exoplanet transits. Our recent campaigns have yielded high-resolution time-series data with image scales near 1.15 arcseconds per pixel and robust photometric stability. Preliminary reductions indicate consistency with transit depths and timings from *TESS*-detected candidates and exhibit sufficient temporal resolution for transit ingress/egress characterization. Calibration procedures are being refined to minimize residual systematics and enhance the detrending of atmospheric and instrumental noise. These findings support the capability of well-configured small observatories to contribute validated transit data to global archives, improving candidate confirmation rates and reducing reliance on large-telescope follow-up. We discuss implications for expanding community-driven exoplanet science and improving the efficiency of validation timelines in the current era of high-cadence, all-sky surveys.

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BIOENGINEERING IMMUNE-EVASIVE PANCREATIC ISLETS AS A THERAPEUTIC STRATEGY FOR TYPE 1 DIABETES

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Type 1 diabetes (T1D) is an autoimmune disease characterized by the destruction of insulin-producing pancreatic β-cells, necessitating lifelong exogenous insulin therapy. While islet transplantation offers a potential curative approach, its clinical application remains limited by immune rejection, poor engraftment, and scalability issues. This project aims to develop a strategy to mitigate alloimmune rejection of transplanted islets by engineering immune-compatible cells. We plan to use CRISPR-based genome editing to modify donor or iPSC-derived islets to express recipient-specific MHC class I molecules. We hypothesize that this personalized MHC expression will reduce alloimmune recognition and enhance long-term graft survival. Initial efforts will focus on isolating pancreatic islets from mice and optimizing protocols for MHC class I silencing as a precursor to engineering human-compatible constructs. In the long term, this approach could enable the development of a scalable, off-the-shelf source of immune-compatible islets for transplantation. By improving immune tolerance and durability of engraftment, this work has the potential to advance curative therapies and improve quality of life for individuals living with T1D.

This work was supported by the UM FIRST award, Start up funds with additional support by the Meyerhoff Scholars Program.

ENGINEERING ANTIGEN-SPECIFIC REGULATORY T CELLS (CAR TREGS) FOR TYPE 1 DIABETES IMMUNOTHERAPY

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Type 1 diabetes (T1D) is an autoimmune disease in which the immune system mistakenly attacks and destroys insulin-producing β-cells in the pancreas. Current therapies rely on insulin replacement, but they do not address the underlying immune dysregulation. Regulatory T cells (Tregs) are a specialized immune cell type that helps control inflammation and prevent autoimmunity. In this project, we aim to develop a novel cell-based therapy by engineering Tregs to express a chimeric antigen receptor (CAR) that targets pancreatic autoantigens involved in T1D. By redirecting Tregs to specifically recognize and suppress autoreactive immune cells at the site of inflammation, CAR Tregs could promote immune tolerance and protect β-cells from further destruction. Our initial work focuses on designing and cloning antigen-specific CAR constructs and introducing them into mouse-derived Tregs. We will evaluate CAR expression, stability, and suppressive function in vitro. This platform will allow us to identify promising CAR designs for further testing in animal models of T1D. In the long term, CAR Treg therapy could offer a highly targeted and durable immunotherapy for preventing or reversing T1D progression, while minimizing the need for broad immunosuppression

This work was supported by the UM FIRST award, and Start up fund.

INVESTIGATING THE ROLE OF RNAI RHO1 ON CLIMBING SPEED AND ENDURANCE IN DROSOPHILA MELANOGASTER

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The Rho1 gene has been identified through a genome-wide analysis as a candidate gene affecting physical performance in Drosophila melanogaster. Rho1 is an evolutionarily conserved gene that encodes for proteins in the family of GTPases, which play a key role in the regulation of actin dynamics and wound healing, and therefore potentially impact physical performance. We studied the effect of the Rho1gene on climbing speed and endurance by under-expressing Rho1 in the muscle tissue of the fly by utilizing the GAL4-UAS system. Virgin females of the muscle-GAL4 line were crossed with males of the UAS Rho1RNAi responder line and males of a control line. We measured the climbing speed and endurance of the offspring of these crosses. This experiment aims to determine whether Rho1 expression in muscle tissue significantly influences locomotor performance, including speed and endurance. We hypothesize that under-expressing the Rho1 gene within flies will have a negative correlation with their speed and endurance. The results of our experiment will provide insight into the significance of the Rho1 gene in the physical ability of Drosophila melanogaster, which may suggest the role the human orthologs of Rho1 play in physical performance in humans. This could help enhance personalized healthcare as it relates to physical decline and conditions such as myopathy and muscular dystrophy. If under-expressingRho1 gene is found to lower the physical performance in Drosophila melanogaster, further research is needed to determine the underlying mechanisms behind this effect. Future research should investigate the gene's effect on other tissues and age groups, given that Rho1 has been characterized as an age-specific gene in a genome-wide analysis of Drosophila melanogaster.

Support for this research was provided by the Department of Biological Sciences at the University of Maryland, Baltimore County. Acknowledgement to Diya Kamalabharathy, Kenny Nguyen, and Evangeline Chen, who worked on the effects of overexpressing the Rho1 gene on the physical performance in Drosophila melanogaster. They helped in the collection of virgin females and offered support in the creation of our poster.

EXPLORING DIFFERENT MOTIVATIONAL STATES IN THE NAC USING MINISCOPES AND DEEP LEARNING

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Environmental cues associated with drug use can drive addiction by activating brain regions involved in motivation and reward. The nucleus accumbens (NAc), composed primarily of dopamine D1- and D2-expressing medium spiny neurons (MSNs), is critically involved in the neural mechanisms underlying motivated behavior and addiction. It is theorized while D1 MSNs promote reward, D2 MSNs are linked to aversion, yet the roles of how these neuronal subpopulations shape motivation under varying effort requirements remains unclear. We hypothesized that the NAc dynamically encodes motivation as a function of effort. To test this, we administered viral injections of cre-dependent AAV-CAG-FLEX-jGCaMP8m and implanted a gradient index (GRIN) lens to enable in-vivo miniature microscope (miniscope) calcium imaging in the NAc of male and female, Drd1- and Drd2- iCre rats. Rats completed a 60-day operant reward task under food restriction, with synchronized 3D behavioral tracking in a custom operant chamber while undergoing NAc miniscope imaging. We observed that rats showed behavioral differences in motivation to obtain food rewards, which peaked at different effort thresholds. We also identified distinct behaviors associated with different degrees of effort and plan to conduct further analyses to examine NAc tuning across task phases and effort requirements. These findings offer new insights into the mechanisms that drive motivated behavior and may inform future addiction and motivation research.

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MODELING THE DISPERSION OF EMISSIONS FROM THE BRESCO WASTE INCINERATOR IN BALTIMORE USING AERMOD

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This study investigates the dispersion of the BRESCO municipal waste incinerator emissions. Using AERMOD, the EPA's atmospheric dispersion modeling program, we simulate how CO_2 and PM_{10} emissions from the facility travel across the city of Baltimore. The objective is to quantify the effects of the incinerator throughout Baltimore on the neighborhood level. One specific area (between 0 and 90 degrees extending up to 300 meters) of the facility experiences significantly higher average pollutant concentrations, while the remaining distribution is relatively symmetrical, suggesting a strong influence of wind direction and localized dispersion factors. These results can help identify the communities most affected by air pollution, supporting future environmental justice efforts and informing local policy decisions.

Xavier Isangedighi was supported in part by the Meyerhoff Scholars Program. This work builds upon prior modeling and analysis conducted by Danielle Larios. Her contributions to the development of the data processing framework were instrumental in enabling this study.

REGULATION OF EGG-LAYING BEHAVIOR BY THE INTEGRATED STRESS RESPONSE IN DROSOPHILA MELANOGASTER

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The Integrated Stress Response (ISR) is a signaling pathway that allows cells to adapt to environmental stressors such as nutrient deprivation. The downstream effector of the ISR is ATF4 (Activating Transcription Factor 4), a transcription factor that controls how cells manage stress by regulating their use of energy and nutrients. Previous studies have shown that dietary nutrient stress reduces ovulation. Additionally, the Grmai Lab has shown that ATF4 regulates ovulation during homeostasis by promoting expression of the neuropeptide CNMa in the fat body. This study aims to investigate how nutrient deprivation decreases ovulation and whether ATF4 is required for the loss of ovulation using a starvation and re-feeding assay. Female flies were subjected to either nutrient-rich or nutrient-poor food for 24, 48, or 72 hours to examine how ovulation rate changes over time. Since blocking ovulation leads to retention of stage 14 oocytes (fully mature eggs) within the ovary, we counted the number of eggs per ovary as a proxy for the rate of ovulation. To perform these quantifications, ovaries were dissected, fixed, and imaged under a microscope. Egg quantification of stage 14 oocytes (the final stage of egg maturation) in fed versus starved females is ongoing but our preliminary findings suggest that starvation leads to a block in ovulation as early as 24 hours following nutrient deprivation. The second starvation and re-feeding assay will determine whether ATF4 controls changes in ovulation following nutrient deprivation and subsequent re-feeding. To test these, we will deplete ATF4 in the fat by using the GAL4/UAS expression system to express an RNAi construct targeting ATF4 in fat cells. The results of this work will highlight the importance of ISR signaling in regulating reproductive output.

Support for this research was provided by Yale University School of Medicine, the Fly Stress Lab at University of Pittsburgh School of Medicine, and the Bloomington Drosophila 517 Stock Center (BDSC, Bloomington, IN)

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INVESTIGATING HERITABILITY OF HETEROGENEITY IN TPRA/PHRA GENE EXPRESSION IN STREPTOCOCCUS PNEUMONIAE

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Streptococcus pneumoniae is a bacterium that asymptomatically colonizes the nasopharynx, but at times disseminates to other parts of the body causing “invasive pneumococcal diseases” including pneumonia, bacteremia, meningitis, and sepsis. It is the leading cause of bacterial

pneumonia hospitalizations in the United States and is responsible for the deaths of over 300,000 children under the age of 5 and 5,000 elderly over the age of 65, annually. With increasing antibiotic resistance and the established severity of disease, understanding the cellular mechanisms driving the onset of these infections becomes imperative. Previous work has shown inherent heterogeneity in the induction levels of PphrA, a promoter of the gene regulatory network (TprA/PhrA) that contributes to pneumonia and mortality in a murine model. However, the functional role of this heterogeneity and its potential role in severity of infection is largely understudied. So, we are implementing a previously established microfluidic droplet platform to examine whether heterogeneity of PphrA is conserved across its progeny. Our ultimate goal is to investigate whether higher levels of PphrA induction leads to an increased disease state. In order to test our hypothesis, we will encapsulate single cells that are fluorescently labeled into microdroplets to track their growth and expression in real time. Prior to working with genetically modified S. pneumoniae strains, we will validate our encapsulation approach using the commensal bacterium Lactobacillus crispatus as a non-pathogenic surrogate. Results from this project will validate our approach to encapsulate singular cells using microfluidics, and ultimately provide unique insight into cell-cell communication and the consequences of heterogeneity.

Support for this research was provided by the Jackman-Burden Lab.

IMPROVING PROTON BEAM RADIOTHERAPY BY SEQUENCING SIMULATED PATIENT DATA IN COMPTON CAMERA REAL-TIME IMAGING WITH NEURAL NETWORKS

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Proton beam radiotherapy is an advanced cancer treatment technique utilizing high-energy protons to destroy tumor matter. When the proton beam interacts with the patient's body, it emits prompt gamma rays, which can be detected by a Compton camera. However, image

reconstruction of the beam path from these scatterings is plagued by mischaracterized scattering sequences and excessive image noise. To address this, machine learning models were developed to order the scattering events properly. Multiple novel datasets simulating particle interactions with human tissue were generated using Duke University CT scans and GEANT4 and Monte-Carlo Detector Effects (MCDE) software. An automated hyperparameter tuning framework was also built into the Big-Data REU Integrated Development and Experimentation (BRIDE) pipeline. This work implemented a novel event-classifier transformer and a 1D Convolutional Neural Network (CNN) to better understand spatial relationships in the data.

This work is supported by the grant "REU Site: Online Interdisciplinary Big Data Analytics in Science and Engineering" from the National Science Foundation (grant no. OAC–2348755). Co-authors Sharma and Ren additionally acknowledge support by NIH. We acknowledge the UMBC High Performance Computing Facility and the financial contributions from NIH, NSF, CIRC, and UMBC for this work.

EXPLORING THE FATE OF RNA IN MOLONEY MURINE LEUKEMIA VIRUS

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The moloney murine leukemia virus (MoMuLv), a virus that causes leukemia and neurological diseases within rodentia, has been studied since the 1950s as a model to further understand the underlying mechanisms of all retroviruses due to its easy use. Our laboratory mainly focuses on the human immunodeficiency virus type-1 (HIV-1), particularly the segment of the genome important for viral replication, known as the 5'-Leader (5'L). The 5'L exists in two conformations: the dimeric conformation adapted by 5'-capped RNAs beginning with one guanosine (^{Cap}1G) in which the cap is sequestered, and the monomeric conformation adapted by 5'-capped RNAs beginning with two or three guanosines (^{Cap}2G and ^{Cap}3G respectively) where the cap is exposed. Viruses containing these different start sites are said to have transcriptional start site heterogeneity. Inversely, MoMuLv contains a unique transcription start site, meaning the virus consists of only one start site, ^{Cap}1G from which the 5'L can still adopt a monomeric or dimeric form. The aim of this work is to explore what drives RNA packaging versus translation in retroviruses that contain unique start sites and we hypothesize that MoMuLv's genome fate is driven by dimerization dependent cap sequestration. Using electrophoretic mobility shift assays (EMSAs), cap exposure versus cap sequestration was assessed by analyzing how the monomeric and dimeric RNA interacts with eGFP-eIF4E, an enhanced green fluorescent protein attached to a protein that binds to the 5' cap of mRNA and initiates translation. By isolating and purifying the capped RNA, fully capped RNA can be obtained and used for further confirmation of cap exposure or sequestration with nuclear magnetic resonance (NMR). This work will provide more information on the conserved functions of retroviruses, which can help in finding solutions to stop their replication.

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Evaluating the Ethical Implications of Public-Sector Artificial Intelligence Solutions

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Artificial Intelligence (AI) in the public sector represents a novel use of technology with numerous advantages and disadvantages. AI can provide aid in various areas of the government, including personalized service delivery, citizen engagement, compliance and risk management, and fraud detection and prevention. However, because AI is reliant on data to recognize and execute patterns, issues with training data or the model itself can produce inequitable outcomes in government operations or public services. Essentially, any bias within a set of data used to train a model will be integrated into the AI algorithm, perpetuating any inequalities exacerbated by these biases. This research addresses these inequalities and ethical challenges that arise from the deployment of AI technologies. It also explores strategies for mitigating algorithmic bias within AI systems and their integration into the public sector. By adopting a qualitative literature review approach, I conducted a thematic synthesis of peer-reviewed articles, policy frameworks, and accredited relevant literature(2020-2025) to ensure analytical rigor. Inductive analysis was applied to derive dominant themes related to bias, accountability, and governance. Human-enhancing AI, diverse AI policy, and ethical regulatory frameworks as mitigation techniques for unethical outcomes of government-use AI were the major themes that repeatedly emerged. The synthesis highlights the need for interdisciplinary collaboration and adaptive policies to address AI ethics gaps in government. By thoroughly analyzing existing literature, this study creates a consolidation of information to serve as a frame of reference for policymakers, developers, and researchers working to design fair and effective AI models.

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INVESTIGATING THE EFFECT OF OVEREXPRESSION OF RHO1 ON CLIMBING SPEED AND ENDURANCE IN DROSOPHILA MELANOGASTER

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The Rho1 gene has been identified through a genome-wide analysis as a candidate gene affecting physical performance in Drosophila melanogaster. Rho1 is an evolutionarily conserved gene that

encodes for proteins in the family of GTPases, which play a key role in the regulation of actin dynamics and wound healing, and therefore potentially impact physical performance. We studied the effect of the Rho1 gene on climbing speed and endurance by manipulating Rho1 expression in the muscle tissue of the fly by utilizing the GAL4-UAS system. Virgin females of the muscle-GAL4 line were crossed with males of the UAS overexpressed Rho1 responder line and males of a control line. We measured the climbing speed and endurance of the offspring of these crosses. This experiment aims to determine whether Rho1 overexpression in muscle tissue influences locomotor performance, including speed and endurance. We hypothesize that an overexpression of the Rho1 gene within flies will have a statistically significant influence on their speed and endurance compared to the control line. The results of our experiment will provide insight into the significance of the Rho1 gene in the physical ability of Drosophila melanogaster, which may suggest the role the human orthologs of Rho1 play in physical performance in humans. This could help enhance personalized healthcare as it relates to physical decline and conditions such as myopathy and muscular dystrophy. If the Rho1 gene is found to affect physical performance in Drosophila melanogaster, further research is needed to determine the underlying mechanisms behind this effect. Future research should investigate the gene's effect on other tissues and age groups, given that Rho1 has been characterized as an age-specific gene in a genome-wide analysis of Drosophila melanogaster.

Support for this research was provided by the Department of Biological Sciences at the University of Maryland, Baltimore County.

CONCENTRATION-DEPENDENT ENCAPSULATION AND RELEASE OF CURCUMIN IN TBAPY-Zr MOFS

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Curcumin's therapeutic potential in anticancer, anti-inflammatory, and antioxidant applications is hindered by its poor aqueous solubility and rapid photodegradation. Metal-Organic Frameworks (MOFs), known for their high porosity, tunable chemistry, and biocompatibility, offer a promising platform for curcumin stabilization and delivery. This study investigates how varying concentrations of both curcumin and MOF influence encapsulation efficiency and release behavior; key parameters in optimizing MOF-based drug delivery systems.

We utilized a functionalized TBAPy-based zirconium MOF to load curcumin at multiple drug-to-carrier ratios and characterized the system using UV-Vis spectroscopy and fluorescence. By systematically increasing curcumin concentration while holding MOF constant, and vice versa, we assessed encapsulation capacity, saturation thresholds, and release kinetics under simulated physiological conditions (phosphate-buffered saline, pH 7.4). Release profiles were monitored over time to evaluate burst release behavior and sustained delivery potential.

Results demonstrate that both curcumin and MOF concentration significantly impact drug loading and release efficiency. Higher curcumin concentrations led to incomplete encapsulation and faster initial release, suggesting surface adsorption rather than internal pore loading. Conversely, increasing MOF concentration enhanced uptake but showed diminishing returns

beyond a critical threshold, indicating pore saturation. Notably, optimal curcumin-to-MOF ratios minimized burst release and prolonged release duration, suggesting a concentration-dependent balance between surface interactions (e.g., π-π stacking, hydrogen bonding) and pore encapsulation.

By mapping these concentration-dependent effects, this work advances understanding of structure-function relationships in MOF-based drug carriers. These findings inform future formulations targeting sustained therapeutic delivery with minimal degradation or toxicity.

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DISSECTING THE ROLE OF THE IGFBP2 PATHWAY IN ACRAL MELANOMA PROGRESSION IN THE AGED MICROENVIRONMENT

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Acral melanoma (AM) is a rare subtype of melanoma that develops on the palms, nails, and foot soles. Older patients have a higher occurrence of AM and tend to have worse prognosis than younger patients for reasons that are severely understudied. Preliminary data from AM tumors display elevated expression of insulin growth binding protein 2 (IGFB2), and the downstream protein vascular endothelial growth factor (VEGF), in tumors isolated from aged mice. Due to the role the IGFBP2-VEGF pathway plays in driving invasion and metastasis, we sought to investigate how IGFBP2 and VEGFR drive AM aggressiveness. To study this, we used conditioned media (CM) from cultured fibroblasts to replicate the aged and young tumor microenvironment (ME). In order to validate our preliminary data, we performed immunoblotting of AM cells cultured in young (<35) or aged(>55) CM. Our western blot showed that VEGFR had higher expression in the cells grown in aged CM, but interestingly IGFBP2 displayed lower expression. To understand the role the aged ME has on melanoma progression, we performed 2D migration and wound healing assays. Our data showed that aged CM promoted migration in AM as evidenced by both assays. Furthermore, when treating cells with recombinant IGFBP2 in the presence of young CM we were able to increase migration of AM cells. This data suggests that IGFBP2 plays a role in migration in the aged ME. For future studies, we plan to further validate our results with other AM cell lines and investigate how IGFBP2 impacts other steps of the metastatic cascade such as invasion. Understanding how the aged ME drives AM progression is crucial as it would lead to the development of effective therapies for older patients, who currently have no effective treatment options.

Support for this research was provided by the Meyerhoff Scholars Program, UM FIRST Program Grant, and a UMBC start up.

INVESTIGATING THE ROLE OF RNAI RHO1 ON CLIMBING SPEED AND ENDURANCE IN DROSOPHILA MELANOGASTER

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The Rho1 gene has been identified through a genome-wide analysis as a candidate gene affecting physical performance in Drosophila melanogaster. Rho1 is an evolutionarily conserved gene that encodes for proteins in the family of GTPases, which play a key role in the regulation of actin dynamics and wound healing, and therefore potentially impact physical performance. We studied the effect of the Rho1gene on climbing speed and endurance by under-expressing Rho1 in the muscle tissue of the fly by utilizing the GAL4-UAS system. Virgin females of the muscle-GAL4 line were crossed with males of the UAS Rho1RNAi responder line and males of a control line. We measured the climbing speed and endurance of the offspring of these crosses. This experiment aims to determine whether Rho1 expression in muscle tissue significantly influences locomotor performance, including speed and endurance. We hypothesize that under-expressing the Rho1 gene within flies will have a negative correlation with their speed and endurance. The results of our experiment will provide insight into the significance of the Rho1 gene in the physical ability of Drosophila melanogaster, which may suggest the role the human orthologs of Rho1 play in physical performance in humans. This could help enhance personalized healthcare as it relates to physical decline and conditions such as myopathy and muscular dystrophy. If under-expressingRho1 gene is found to lower the physical performance in Drosophila melanogaster, further research is needed to determine the underlying mechanisms behind this effect. Future research should investigate the gene's effect on other tissues and age groups, given that Rho1 has been characterized as an age-specific gene in a genome-wide analysis of Drosophila melanogaster.

Support for this research was provided by the Department of Biological Sciences at the University of Maryland, Baltimore County. Acknowledgement to Diya Kamalabharathy, Kenny Nguyen, and Evangeline Chen, who worked on the effects of overexpressing the Rho1 gene on the physical performance in Drosophila melanogaster. They helped in the collection of virgin females and offered support in the creation of our poster.

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

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Environmental change poses a significant threat to biodiversity, underscoring the need to understand how organisms adapt to diverse stressors. In zebrafish embryos, hypoxia induces a hypometabolic state mediated in part by N-myc downstream-regulated gene 1a (Ndrg1a), which conserves energy by downregulating the ATP-dependent Na^+/K^+-ATPase (NKA) pump in the pronephric duct (PD) and ionocytes - cell types with complementary roles in osmoregulation. My project tests whether *ndrg1a* responds to other stressors, specifically salinity stress, suggesting a broader role as a general environmental stress responder. To investigate this, 24-hours-post-fertilization (hpf) wild-type and *ndrg1a* mutant embryos were exposed to varying salinity levels (0–10 ppt) and examined for signs of osmotic stress, typically indicated by pericardial edema (fluid accumulation in the pericardial cavity). Mutant embryos exhibited pericardial edema across all salinities, indicating impaired osmoregulation in the absence of Ndrg1a. Wholemount immunolabeling further showed that, unlike the inverse Ndrg1a–NKA relationship observed under hypoxia, the level and distribution of both proteins changed in parallel in response to salinity. Two models were considered to explain the relationship between these proteins in response to osmotic stress: (1) Ndrg1a positively regulates NKA expression/distribution; or (2) both are regulated by a shared upstream pathway. To distinguish between them, we examined NKA expression in *ndrg1a* mutants. Rather than a uniform reduction, NKA exhibited a dramatic redistribution - between ionocytes and the PD depending on salinity - and appeared in cells lacking Ndrg1a, supporting Model 2: that loss of Ndrg1a triggers a stress signal redirecting NKA to alternate osmoregulatory cell types. Ongoing experiments are investigating whether the Hypothalamus-Pituitary-Adrenal axis contributes to this redirection. Together, these findings suggest that Ndrg1a is a generalist stress responder with context-dependent roles: conserving energy under hypoxia and promoting osmoregulation under salinity stress. Understanding such mechanisms is essential for predicting organismal responses to environmental changes.

This research was supported by the Brewster lab.

POPULATION DENSITY AND MOBILE PHONE MICROBIOME DIVERSITY: A COMPARATIVE ANALYSIS ACROSS EIGHT CITIES

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The human microbiota is the community of microbes that live on and within the human body. Microbes that make up the human microbiota have been demonstrated to play a significant role in human health, such as helping to break down food, producing vitamins, and even being correlated with diseases such as obesity and diabetes. The composition of the human microbiota can be influenced by a multitude of factors, including the environment that humans interact with on a daily basis. This study aimed to investigate the diversity and abundance of microbes on phones between cities with varying populations. It was hypothesized that phone microbiomes from individuals in larger cities will yield greater microbial diversity than phones from individuals living in smaller cities. Data on the diversity of bacterial phyla and abundance was

collected through the use of Phinch software and the Project MERCURRI data set. 755 samples were filtered from the dataset to analyze bacterial phyla present on mobile phones from participants across eight cities representing different population sizes: major cities (New York and Houston), large cities (San Francisco and Washington DC), medium cities (Fort Lauderdale and Palmdale), and small cities (Longmeadow and Potlatch). Analysis of the dataset showed that overall, mobile phones in bigger cities had greater diversity than their counterparts from smaller cities, with larger cities having 2 to 3 more types of phyla than smaller cities. The results align with the hypothesis that phone microbiomes from individuals in larger cities will yield greater microbial diversity than those from individuals living in smaller cities. This study has implications for factors that could influence the composition of the human microbiota, including what bacterial populations are present on individuals' phones. Further research could explore how the microbes found on people's phones are potentially transferred to their microbiota.

This research project was funded by the College of Natural and Mathematical Sciences at UMBC.

ROLE OF CYTOSOLIC 5'-NUCLEOTIDASE III ON FLUDARABINE METABOLISM AND ITS TISSUE-SPECIFIC LOCALIZATION MAPPING USING MASS SPECTROMETRY IMAGING

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Nucleotidases are enzymes that play vital roles in nucleotide pool balance and purine and pyrimidine metabolism across various tissues. Two major forms of nucleotidases, 5'-nucleotidases (5'-NTs) and nucleoside triphosphate diphosphohydrolases (NTPDases), dephosphorylate nucleoside monophosphates and triphosphates, respectively. Recently, our laboratory reported the dephosphorylation action of these nucleotidases towards the metabolites of clinically used nucleoside analog drugs, including gemcitabine, emtricitabine, tenofovir, and acyclovir. Here, we extended investigating the role of 5'-NTs in disposition of fludarabine, a drug used to treat B-cell chronic lymphocytic leukemia. *In vitro* incubations carried out using a range of 5'-NT including cytosolic 5'-nucleotidase 1A (NT5C1A), NT5C2, NT5C3, NT5C, and mitochondrial 5' (3')-deoxyribonucleotidase (NT5M) revealed that NT5C3 catalyzed the dephosphorylation of fludarabine. Although nucleotidases have critical roles in metabolism of endogenous nucleotides and xenobiotics, their spatial localization in tissues is not fully elucidated yet. In the present work, we employed matrix-assisted laser desorption/ionization mass spectrometry imaging (MALDI MSI) to ascertain localizations of tryptic peptides corresponding to major nucleotidases in mouse kidney, colon, and spleen tissues. First, *in silico* trypsin digestions were performed to determine the trypsin digestion patterns of the above proteins. Then, human recombinant nucleotidases were used to characterize tryptic peptides of major nucleotidases. Following this, MALDI MSI analyses were carried out to localize tryptic peptides corresponding to major nucleotidases mouse colon, kidney, and spleen tissues. The obtained tissue sections were subjected to serial washing steps and on-tissue trypsin digestions. From the above experiment, we observed unique localizations of major nucleotidases, including NT5C3, NT5C1A, and NTPDase1 in tissues.

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

EFFECT OF TEMPERATURE ON THE PERFORMANCE OF AQUEOUS ZINC ION BATTERIES WITH VANADIUM OXIDE CATHODES

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Aqueous zinc-ion batteries (AZIBs) have emerged as a promising solution for large-scale energy storage applications due to their cost-effectiveness, inherent safety, favorable volumetric energy density, and environmental friendliness. Among various cathode materials explored for these batteries, vanadium pentoxide (V_2O_5) has attracted particular interest due to its multiple oxidation states and high theoretical capacity. However, widespread implementation is limited by an incomplete understanding of their charge storage behavior, low practical capacity, and poor cycling stability. Proposed charge storage mechanisms include Zn^{2+} intercalation and Zn^{2+}/H^+ co-insertion, while activation mechanisms typically involve hydration of the pristine V_2O_5 lattice and irreversible phase transformation. The result of activation is an increase in capacity and greater capacity contributions from the lower voltage regions. The impact of temperature variations on charge storage, activation, and degradation mechanisms, as well as performance, is significantly understudied. In this study, we cycle AZIBs using V_2O_5-based cathodes across typical ambient temperatures to gain a deeper understanding of the electrochemical charge storage mechanisms and degradation processes that affect long-term battery operation. Electrochemical techniques, including cyclic voltammetry (CV), galvanostatic charge-discharge (GCD), and electrochemical impedance spectroscopy (EIS), were employed to assess the temperature-dependent behavior of V_2O_5 cathodes. It was observed that at higher temperatures, V_2O_5 undergoes activation faster, accompanied by higher capacitance and stronger peaks during discharge; however, capacity degrades more rapidly, and side reactions proliferate. Additionally, as the temperature was lowered, peak intensities shifted, suggesting a change in the electrochemical mechanism. We propose that the activation behavior of V_2O_5 is driven by a combination of chemical and electrochemical processes, which together define its charge storage mechanism and long-term cycling behavior. This study contributes to a clearer understanding of V_2O_5 cathode behavior under different thermal conditions and supports the development of more efficient and durable AZIB systems for future energy storage solutions.

We would like to acknowledge and thank the Undergraduate Research Award (URA) for providing funding for materials.

L

MENTORING AS A PUBLIC HEALTH INTERVENTION: EXPLORING THE IMPACT OF THE HOLISTIC CRITICAL MENTORSHIP ON MENTAL HEALTH AMONG BIPOC MCNAIR SCHOLARS AT UMBC

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This project investigated how the Holistic Critical Mentorship framework (HCM) acknowledges and supports the mentee's emotional needs, helping them build self-awareness, resilience, and emotional intelligence. I will look at current research, and literature on mentorship as a means to alleviate racial stressors impacting the mental health of BIPOC students in higher education. I conducted an interdisciplinary literature review analyzing empirical studies, theoretical frameworks, and narrative-based research methods. By using an Indigenous lens on how systemic racism can impact all levels of the socio-ecological model, I was able to examine the extent to which mentoring programs that include critical race theory, reciprocate, and representation can ultimately be of benefit for BIPOC undergraduate students at the University of Maryland, Baltimore County. This literature indicates that culturally affirming mentorship programs reduce isolation, enhance racial identity development, and offer protective emotional and psychological benefits for BIPOC students. Frameworks such as HCM provide multi-level support that aligns with public health strategies to mitigate minority stress and mental health disparities. By positioning HCM as a transformative framework that reframes mentorship as both a cultural and public health intervention is essential. Institutions must adopt mentorship models that are structurally embedded and culturally grounded to address the mental health crises disproportionately affecting BIPOC students in higher education.

Support for this research was provided by the SRI grant and funded by the McNair Scholars Program at UMBC.

DESIGNING AND CONSTRUCTING A THERMOELECTRIC POWERED SELF-SUSTAINING SENSOR PLATFORM

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Within the realm of art conservation, sensors play a critical role in collecting ambient environment data on metrics including temperature, humidity, and light exposure, helping to maintain optimal conditions to minimize the degradation of artwork. The ease of use of these sensors is limited by the lifespan of their batteries, which create the need for constant maintenance and human interaction. Energy harvesting technologies including thermoelectrics, piezoelectrics, and photovoltaics have been studied as supplemental power supplies for electronic devices and sensors.

However, the inherent low, variable output of these sources (50-200 mV) creates a significant power mismatch with sensor operating requirements (3.3 V), making direct, continuous power an unresolved challenge. To significantly extend sensor uptime, this work develops a low-power, self-sustaining sensor system that includes (1) a step-up circuit capable of matching the variable output of energy-harvesting materials to sensor requirements, while also (2) enabling intelligent power storage and adjustable duty cycling through the introduction of a 5 V capacitor and a voltage-controlled switch.

The system's sensor platform, built around an Arduino Nano Matter powered by a thermoelectric array, utilizes a heart rate sensor as a demonstrative load, chosen for its operational and power consumption characteristics that mimic typical environmental sensors for art conservation. The primary mechanism enabling self-sustainability is a voltage-controlled switch with adjustable hysteresis. This intelligent power management circuit manages power delivery for periodic operation, activating the Arduino-sensor system when the capacitor charges to 4.1V and disconnects power when below 3V. This intermittent duty cycle, rather than constant uptime, effectively facilitates self-sustainability. This work demonstrates the potential for a fully self-sustaining sensor platform capable of harvesting ambient energy for intermittent data collection and transmission. The innovative power management circuit overcomes the battery-life limitations of conventional sensors, offering a practical solution for the perpetual monitoring of sensitive artworks.

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M

INVESTIGATING THE INFLUENCE HAPTIC INTERFACE SHAPES ON SENSORY THRESHOLDS

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The future of prosthetics is leaning towards haptic cues delivered with wearable devices to enable users to complete tasks with more dexterity. As we pursue more natural-feeling prosthetics, we face a key challenge: user comfort. Haptic devices, so far, have included many different interface profiles, but this leaves us with the question of how we choose the interface profile that is both comfortable and effective for the user. We define comfort using the Allowable Stimulus Range (ASR), or the range of detectable and comfortable cue magnitudes, and effectiveness with the Just Noticeable Difference (JND), or how much something changes to be distinctly different. These psychophysical metrics are found using the Method of Adjustments and the Staircase Method. These metrics are found for the most prominent interface shapes in the literature for wearable indentation and skin stretch haptic devices: square, cylinder, rotated cylinder, and sphere. In addition to Psychophysical testing, indometric testing will provide elastic strain energy and the hysteresis loss factor as a model-free method of quantifying the elastic and

viscous tissue responses on the forearm and investigate correlations with the psychophysical thresholds. This work will allow the direct comparison of haptic interface profiles on comfort and haptic perceptual resolution, and assess the impact of elastic and viscous tissue properties on the results

Supported for this research was provided by the Louis Stokes Alliance for Minority Participation program.

INVESTIGATING THE ROLE OF RNAI RHO1 ON CLIMBING SPEED AND ENDURANCE IN DROSOPHILA MELANOGASTER

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The Rho1 gene has been identified through a genome-wide analysis as a candidate gene affecting physical performance in Drosophila melanogaster. Rho1 is an evolutionarily conserved gene that encodes for proteins in the family of GTPases, which play a key role in the regulation of actin dynamics and wound healing, and therefore potentially impact physical performance. We studied the effect of the Rho1gene on climbing speed and endurance by under-expressing Rho1 in the muscle tissue of the fly by utilizing the GAL4-UAS system. Virgin females of the muscle-GAL4 line were crossed with males of the UAS Rho1RNAi responder line and males of a control line. We measured the climbing speed and endurance of the offspring of these crosses. This experiment aims to determine whether Rho1 expression in muscle tissue significantly influences locomotor performance, including speed and endurance. We hypothesize that under-expressing the Rho1 gene within flies will have a negative correlation with their speed and endurance. The results of our experiment will provide insight into the significance of the Rho1 gene in the physical ability of Drosophila melanogaster, which may suggest the role the human orthologs of Rho1 play in physical performance in humans. This could help enhance personalized healthcare as it relates to physical decline and conditions such as myopathy and muscular dystrophy. If under-expressingRho1 gene is found to lower the physical performance in Drosophila melanogaster, further research is needed to determine the underlying mechanisms behind this effect. Future research should investigate the gene's effect on other tissues and age groups, given that Rho1 has been characterized as an age-specific gene in a genome-wide analysis of Drosophila melanogaster.

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LONGITUDINAL GROWTH RATES OF THE VASCULAR RETINA IN RETINOPATHY OF PREMATURITY

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Retinopathy of Prematurity (ROP) impacts premature infants born prior to complete vascularization of the infant retina. Among infants born more than 9 weeks early, with severe growth restriction or medical instability, retinal avascularity can lead to aberrant development requiring treatment to prevent retinal detachment and blindness. The purpose of this study is to quantify the retinal growth rates among preterm infants with ROP using serial fundus photography and correlate retinal growth rates with severity of ROP and treatment for ROP. In this retrospective study, images were analyzed from 14 preterm infants (28 eyes) who underwent at least 5 retinal fundus imaging sessions. Nasal and temporal distances (pixels) between the optic nerve and vascular-avascular junction were measured using ImageJ. Stage, plus score, treatment status, post-menstrual age, gestational age, and birthweight were variables evaluated as predictors of retinal vascular growth rates.

We found retinal growth rates of 0.637 +/- 0.327 optic nerve units/week. The correlation between the left and right eyes of a single subject was r=0.9 (p=0.0001). Among treated subjects, analysis of retinal growth rates before and after intravitreal anti-VEGF treatment is ongoing. Among untreated subjects, younger post-menstrual age was associated with faster retinal growth rates and more severe ROP stage or higher plus score was associated with slower retinal growth rates.

In conclusion, we found that clinical factors may influence retinal growth rates. These factors may be opportunities to enhance retinal growth and prevent persistent avascular retina, an established risk factor for lifelong risk of retinal complications. We expect that continued analysis of treatment-related changes in growth rates will strengthen these findings.

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USING ENERGY LANDSCAPE ANALYSIS TO EXPLORE FUNCTIONAL CONNECTIVITY IN PARKINSON'S DISEASE PATIENTS WITH SEVERE HYPOSMIA

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Functional connectivity of the brain refers to the relationship between different brain regions and can be studied to gain a deeper understanding of neurological disorders. Parkinson's disease is an example of a neurological disorder that affects movement and gets worse over time. Hyposmia, a decreased sense of smell, is a risk factor for dementia in Parkinson's disease. To explore this further, we use Energy Landscape (EL) Analysis on a resting state fMRI dataset to measure and compare functional connectivity among healthy control groups, Parkinson patients with no/mild hyposmia, and Parkinson patients with severe hyposmia. EL analysis is used to focus on neural dynamics in the brain, and can be useful for comparing connectivity between different control groups. Previous studies have reported a decrease in amygdala functional connectivity between Parkinson's patients with severe hyposmia and the healthy control groups. Our work aims to not only support these findings but also provide additional analysis on how functional connectivity in other regions of the brain may be impacted.

This research was supported by the Meyerhoff Scholars Program.

LONGITUDINAL ORAL HEALTH MONITORING USING IMU AND AUDIO FROM WEARABLE SENSORS

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Maintaining proper oral hygiene remains critical across all age groups. However, individuals frequently miss spots, neglect areas, apply too much pressure, or overemphasize specific areas during brushing. Incorrect brushing techniques can lead to plaque buildup, enamel abrasion, gingivitis, and other oral health issues. With increasing popularity of smartwatches, there exists significant potential to leverage these devices for monitoring brushing behavior and techniques. This research investigates application of consumer-grade smartwatches for detecting and analyzing toothbrushing activities, with a specific focus on recognizing distinct brushing techniques, including horizontal scrub, vertical scrub, and circular motion patterns, using heterogeneous sensors across various smartwatch platforms. The research addresses multiple challenges in smartwatch-based toothbrushing activity recognition, including gaps in sampling data with unequal data stream lengths, gyroscope drift during rapid motions, establishing appropriate coordinate systems to determine tooth surface locations, synchronizing video annotations with multiple IMU and audio data streams, and managing inherent variability in sensor configurations across Samsung and Apple smartwatch ecosystems. Linear interpolation was employed to resample and synchronize disparate data streams, ensuring alignment across all sensor inputs. Complementary filters were developed to extract gravity vectors from accelerometer data, thereby mitigating gyroscope drift during dynamic brushing motions. Advanced smoothing techniques are planned for implementation, including the Madgwick filter, which enhances sensor fusion and enables the extraction of roll, pitch, and yaw orientations from Samsung watch data, thereby providing comprehensive motion analysis capabilities. Custom data collection applications were developed for both Apple Watch and Samsung devices, capable of simultaneously capturing IMU and audio data during toothbrushing sessions, while accommodating the distinct sensor architectures and data acquisition protocols for each platform. This research delivers a dataset featuring fine-grained toothbrushing annotations paired with 6-9

axis IMU and audio data, providing validated data collection applications for both smartwatch platforms and establishing a foundation for future research in smartwatch-based oral health monitoring that can provide real-time feedback to improve oral health.

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LAYER-BY-LAYER IN CELL VIABILITY FOR SCHWANN CELL PERIPHERAL NERVE RECOVERY AND HMSC MANUFACTURING

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Layer-by-layer is a promising technique that shows advantages in multiple fields, including tissue engineering, drug delivery, and implants. This study aims to investigate whether layer-by-layer is a promising technique for improving cell viability and proliferation in both Schwann cells and human mesenchymal stem cells (hMSCs).
Many severe cases of peripheral nerve injuries require surgery, which can cause other complications. Schwann cells play a vital role in nerve repair in the PNS. By improving cell viability and proliferation of Schwann cells, nerve repair will be promoted.
Human mesenchymal stem cells are used in cell therapy and regenerative medicine. hMSC production can experience challenges, as often it takes a significant amount of time for sufficient cell growth. Layer-by-layer provides a promising approach for enhancing the proliferation rate of hMSC cells, thereby reducing the time before harvesting.
Layers were formed on a 96-well culture plate using the layer-by-layer technique. A solution of 1 mg/ml Polyethylenimine was used first to ensure proper coating. This was then followed by alternating 1 mg/ml solutions of heparin and then collagen. Multiple collagen solutions were prepared and tested. These two solutions were alternated for a total of 6 bilayers. Two plates were prepared: one being monitored on day 3, while the other was observed on day 6. The plates were monitored under a microscope to observe changes in cell behavior and growth.
Proliferation was evaluated through a PrestoBlue viability assay on each plate's predetermined date. Results from a PrestoBlue viability assay demonstrated increased cell proliferation and viability for both Schwann and hMSC cells, on both day 3 and day 6 of cell culture.
This study shows the versatility of layer-by-layer in nerve regeneration and hMSC production. This will lay the groundwork for future development in regenerative methods and cell-based therapeutics.

Support for this research was provided by URA.

Finite-Difference Drift-Diffusion Modeling of III/V Photodetectors: Temperature Dependence and Avalanche Photodetector Simulation

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This research aims to investigate the performance variations of III/V photodetectors under different thermal conditions and extend the modeling framework to simulate avalanche photodetectors (APDs) for single-photon detection in quantum applications. Our focus will be in two key areas. First, we want to successfully simulate APDs by properly implementing impact ionization, and then analyze potential design optimizations for the creation of future APDs. Next, we want to analyze APD performance under non-constant temperatures. Our goal is to see its effect on quantum efficiency, bandwidth, phase noise, and mechanisms such as recombination, and see how well our simulation stacks against real APDs created and used in literature.

I would like to thank both the Meyerhoff Scholars program and the QuPIDC program for funding and supporting this research.

THE EFFECT OF ANCHOR KNOCKDOWN IN DROSOPHILA CIRCADIAN RHYTHEM

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Sleeping disorders regarding Circadian Rhythms (CRSDs) affect 3% of the adult and 16% of adolescence population which leads to sleep and behaviour dysregulation. Previous studies suggest some neurological signaling pathways affect circadian rhythm, such as mTORC1. G-protein coupled receptor 155 (GPR155) is a 17-transmembrane with a GPCR-like region which works upstream of mechanistic target of rapamycin complex 1 (mTORC1) to mediate mTORC1 complex signaling; a protein complex that regulates cell growth. However, these mechanisms remain elusive so we hope to shed light on these knowledge-gaps. Since GPR155 is a mediator for mTORC1, and mTORC1 affects IPCs as well as circadian rhythm, we hypothesize that GPR155 has an increased circadian rhythm. In Drosophila mTORC1 influences release of insulin-like peptides in Insulin Producing Cells (IPCs) of the brain, which causes changes in circadian rhythm. Drosophila, as a model organism, contains orthologs such as the Anchor gene for the human GPR155 gene. We aim to study the Anchor gene to better understand the link between sleeping disorders and neurological pathways. Using the GAL4/UAS system, which controls gene expression of organisms to knock down the anchor gene, we have induced an Anchor KnockDown (AKD) in IPCs. To further gain insight into AKD's effect, we used an established circadian monitoring paradigm called a Drosophila Activity Monitor (DAM), which monitors fly activity 24/7, to allow us to study the sleeping patterns, activity, and circadian rhythm of Drosophila by comparing the flies with the anchor knockdown to the genetic controls. Preliminarily, we found AKD leads to dysregulation of the circadian rhythm. This shows a disruption of sleeping patterns in drosophila, implying that the anchor gene has an effect on the circadian rhythm. Additionally since the Anchor gene is a homolog of GPR155, the results may allow us to understand how to find solutions to CRSDs.

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LAYER-BY-LAYER SURFACE MODIFICATION OF $Ti_3C_2T_x$ USING POLY-D-LYSINE AND LAMININ: OPTIMIZATION OF POLYELECTROLYTE RATIOS AND CONCENTRATIONS

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Two-dimensional MXenes, particularly $Ti_3C_2T_x$, offer a unique combination of high electrical conductivity, hydrophilicity, and tunable surface chemistry, making them ideal candidates for a wide range of applications. However, their direct application in biological systems is limited by the need for improved biocompatibility. In this study, we present a layer-by-layer surface modification approach using biocompatible polyelectrolytes to enhance the stability of $Ti_3C_2T_x$ MXene nanosheets and films in biological media. The polyelectrolytes used for this study, poly-D-lysine (PDL) and laminin, are commonly used to promote cell adhesion and growth. To optimize the synthesis of polyelectrolyte coated MXene nanosheets, varying ratios of PDL and laminin were tested against specified concentrations of MXene nanosheets. The initial phase of the work focuses on optimizing the ratio and concentrations of PDL and laminin to achieve stable bioelectrolyte coatings. PDL–MXene nanosheets were prepared by adding PDL of carrying concentration to 0.5mg/mL MXene solution in an optimized 1:1 ratio. The resulting PDL-MXene nanosheets were washed using multiple centrifugation and resuspension cycles in DI water. The PDL-MXene nanosheets were characterized using zeta potential measurements to understand surface charge dynamics, yielding an averaged net positive change of ~50mV after the addition of PDL. Sequential layers of PDL and laminin were deposited on MXene nanosheets forming polyelectrolytic multilayers. During the remainder of the summer we plan to carry out FTIR, SEM, and AFM measurements of these modified nanofilms. Electrical conductivity measurements on Laminin-PDL MXene, PDL-MXene and unmodified MXene films were carried out to evaluate the effect of surface functionalization on MXene's electronic properties, and were found to maintain MXene's high conductivity of 10,000S/cm.

This layer-by-layer surface engineering strategy presents a promising pathway for creating biocompatible MXene-based platforms tailored for bioelectronics, tissue engineering, and other biomedical applications.

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Reducing Microbial Buildup on Corn Stover Using Atmospheric Cold Plasma Treatment

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Corn waste such as cobbs, husks, and stalks, have great potential to be a stable source of renewable energy. This is mainly due to its availability, and abundance in the carbohydrate cellulose and hemicellulose. However, when it comes to its preservation, scientists run into various issues. One of these issues, which is the one that will be addressed in this project, is the microbial build up on the corn stover. This appears to be an obstacle because as the microorganisms grow on the biomass, they feed onto it, leading to dry matter loss and the breaking of the carbohydrate bonds. This research aims at addressing this issue by using Atmospheric Cold Plasma (ACP) treatment on biomass of different moisture content. ACP treatment uses ionized gas to interact with the biomass being treated and disable microbial build up. Using ACP on the corn stover, we hope to address microbial problems. However, we are also anticipating the ionized gas to react with the carbohydrates, changing the chemical composition of the biomass. In order to monitor these changes, we will also use Fourier Transform Infrared Spectroscopy (FTIR). FTIR will allow us to see where the chemical bonds change and give us a better picture of how ACP treatment affects the corn waste. During the beginning stages of the research, we hope to see a decrease in microbial build and minimal change in the chemical structure of corn stover.

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THE IMPACT OF *SIRT2* ON AGE-SPECIFIC INNATE IMMUNE RESPONSE IN *DROSOPHILA MELANOGASTER*

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Sirtuin 2 (Sirt2), a member of the sirtuin family of protein deacetylases, is responsible for deacetylating lysine residues within proteins. Studies of mammalian sirtuins demonstrated their significant role in longevity regulation, metabolic control, and cellular inflammatory responses. We hypothesize that *Sirt2* is required for innate immune function during aging, specifically the age-specific clearance of bacteria. We generated an RNAi-mediated genetic cross to knockdown expression of *Sirt2* within the fat body of *Drosophila melanogaster*, as the fat body plays a major role in immunity. Virgin females aged 1 to 5 weeks were injected with a standard inoculation of *E. coli*, and we measured their ability to clear infection after a 24 hour period using a standard bacterial clearance assay. We anticipated that the knockdown of *Sirt2* will decrease the bacterial clearance ability for both the 1 and 5 week old flies as *Sirt2* has been shown to naturally decline with age. Additionally, we hypothesized that the further knockdown of *Sirt2* in older flies will further compromise immune function. Our results show that *Sirt2* knockdown had little to no effect on bacterial clearance in one-week old flies. However, in five week-old flies, the knockdown of *Sirt2* significantly hindered bacterial clearance, suggesting an age-dependent role

for *Sirt2* in innate immune function. These findings potentially support a model in which Sirt2 activity becomes increasingly essential for maintaining immune competence in aging flies. Understanding Sirt2's role in immunity may reveal mechanisms involved in immune decline and offer potential targets for treating age-related or immunocompromised conditions.

This research was funded by the Department of Biological Sciences at the University of Maryland, Baltimore County

INVESTIGATING THE EFFECT OF OVEREXPRESSION OF RHO1 ON CLIMBING SPEED AND ENDURANCE IN DROSOPHILA MELANOGASTER

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The Rho1 gene has been identified through a genome-wide analysis as a candidate gene affecting physical performance in Drosophila melanogaster. Rho1 is an evolutionarily conserved gene that encodes for proteins in the family of GTPases, which play a key role in the regulation of actin dynamics and wound healing, and therefore potentially impact physical performance. We studied the effect of the Rho1 gene on climbing speed and endurance by manipulating Rho1 expression in the muscle tissue of the fly by utilizing the GAL4-UAS system. Virgin females of the muscle-GAL4 line were crossed with males of the UAS overexpressed Rho1 responder line and males of a control line. We measured the climbing speed and endurance of the offspring of these crosses. This experiment aims to determine whether Rho1 overexpression in muscle tissue influences locomotor performance, including speed and endurance. We hypothesize that an overexpression of the Rho1 gene within flies will have a statistically significant influence on their speed and endurance compared to the control line. The results of our experiment will provide insight into the significance of the Rho1 gene in the physical ability of Drosophila melanogaster, which may suggest the role the human orthologs of Rho1 play in physical performance in humans. This could help enhance personalized healthcare as it relates to physical decline and conditions such as myopathy and muscular dystrophy. If the Rho1 gene is found to affect physical performance in Drosophila melanogaster, further research is needed to determine the underlying mechanisms behind this effect. Future research should investigate the gene's effect on other tissues and age groups, given that Rho1 has been characterized as an age-specific gene in a genome-wide analysis of Drosophila melanogaster.

Support for this research was provided by the Department of Biological Sciences at the University of Maryland, Baltimore County.

INVESTIGATING THE ROLE OF SHANK3 GENE IN MODULATING WINNER-LOSER EFFECTS IN MANGROVE RIVULUS KILLIFISH

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Social experiences are part of our daily lives and can lead to both short-term and long-term behavioral and physiological changes. One well-documented phenomenon is the winner–loser effect, which describes how previous winning or losing experiences alter a suite of behaviors, including aggression and cognitive behaviors. However, it remains unclear how the brain translates social experiences into behavioral responses. Our previous research, using the mangrove rivulus killifish (*Kryptolebias marmoratus*), demonstrated that prior winning experiences significantly increased aggression and spatial learning ability, whereas prior losing experiences reduced aggression but enhanced risk-avoidance learning. We also discovered that winners exhibited elevated SHANK3 protein expression, while losers showed decreased expression at the whole-brain level. Despite this finding, the specific brain regions where the *shank3* gene is expressed, and whether region-specific differences in expression directly modulate the formation of winner–loser effects, remained unknown in ours as well as other model organisms. To find these brain regions, we used *in situ* hybridization to locate the regions in which *shank3* is expressed. The *shank3* gene is known for its relevance to Autism Spectrum Disorder (ASD). Homozygous knock-out mutations of this gene, in zebrafish and mice, lead to behavioral defects similar to ASD. These behaviors include reduced social interaction, aggression, and spatial learning ability. Based on these parallels, we hypothesize that social experiences influence aggression and cognitive behaviors through modulating SHANK3 protein levels in specific brain regions, including the fish analogs for the hypothalamus, hippocampus, and amygdala. To further test this hypothesis, we will first use *in situ* hybridization to localize *shank3* expression within the brain and compare expression patterns between winners and losers at the level of individual brain nuclei. To further investigate the relationship between SHANK3 expression and behavioral outcomes, we will use CRISPR-Cas9 gene editing tools to knock out the *shank3* gene and then use behavioral assays to examine if the winner-loser effects are affected by this manipulation.

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EVALUATING ETHANOL PREFERENCE IN GPR155 KNOCKOUT MICE USING THE INTELLICAGE SYSTEM

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Alcohol use disorder (AUD) is a major public health concern affecting over 29 million Americans and contributing to significant health issues. While AUD's medical outcomes are well-studied, the underlying signaling pathways that cause alcohol-related behaviors are less understood. Among these, AUD is linked to disruptions in the mechanistic target of rapamycin complex 1 (mTORC1) signaling pathway. GPR155, a modulator of mTORC1 signaling, has an undefined role in regulating ethanol-related behaviors through this pathway. Prior findings in

Drosophila demonstrate that a homolog of GPR155, anchor, alters ethanol sensitivity, suggesting GPR155's potential role in modulating ethanol-related behavior (Vonhoff Lab). While these findings suggest a role for GPR155, its involvement in specific aspects of ethanol consumption, such as binge-like drinking and ethanol preference, remains unknown. To address this, we use a global knockout (KO) mouse model to investigate whether GPR155 deletion in mice influences voluntary consumption of ethanol in behavioral assays that measure reward.

Specifically, we use the IntelliCage system, an automated home-cage system that allows for 24/7 drinking monitoring of group-housed mice. This approach allows for constant assessment of intake and preference while avoiding experimenter bias and minimizing stress. Mice were given access to ethanol solutions ranging from 2% to 12%, with concentrations gradually increasing to observe intake across concentrations. Our results show that female GPR155 KO mice consumed less ethanol than WT mice at concentrations 8% to 10%. However, KO males show a similar ethanol preference compared to WTs at all concentrations. These results confirm that GPR155 deletion lowers ethanol consumption patterns in females. Additional experiments will further examine GPR155 KO mice in the drinking in the dark (DID) paradigm which models binge-like drinking through limited ethanol access during mice's dark cycles. These results will inform future research on signaling pathways involved in ethanol-mediated behaviors.

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ANALYZING CELL PHONE AND SHOE MICROBIOMES OF SCIENCE FESTIVAL ATTENDEES

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The human microbiota is the variety of microbes that are found on and within the human body, including bacteria, fungi, and viruses. Microbes which comprise the human microbiota have been shown to play a significant role in human health, including being correlated with illnesses such as asthma, allergies, and gastric ulcers. The composition of the human microbiota can be influenced by a multitude of factors, including the environment someone interacts with. This study aimed to investigate differences in diversity and quantities of microbes, specifically bacteria, between people who attended similar scientific festivals in different locations. It was hypothesized that the Science and Engineering Festival in Washington, D.C. would produce a more diverse microbiome on phones and shoes than the Philadelphia Science Festival because Washington, D.C. has a warmer climate; thus allowing for more bacterial growth. Data on the diversity and abundance of bacterial phyla were collected through the use of Phinch software and the Project MERCURRI data set. 248 samples were filtered from the dataset to analyze bacterial phyla present on people of all ages who attended the Philadelphia Science Festival or Science and Engineering Festival. Analysis of the dataset showed that overall, the Philadelphia attendees had 12 different phyla of bacteria present on their phones and shoes, whereas the Washington, D.C. attendees only had 10 different phyla of bacteria present on their phones and shoes. The results differed from anticipated, as the event in Washington, D.C. displayed less diversity than

Philadelphia's. This study has implications for factors that could influence the composition of the human microbiota, including what bacterial populations are present on individuals' phones and shoes in different environments. Further research could explore how the microbes found on people's phones and shoes are potentially transferred to their microbiota.

This research project was funded by the College of Natural and Mathematical Sciences at UMBC.

POPULATION DENSITY AND MOBILE PHONE MICROBIOME DIVERSITY: A COMPARATIVE ANALYSIS ACROSS EIGHT CITIES

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The human microbiota is the community of microbes that live on and within the human body. Microbes that make up the human microbiota have been demonstrated to play a significant role in human health, such as helping to break down food, producing vitamins, and even being correlated with diseases such as obesity and diabetes. The composition of the human microbiota can be influenced by a multitude of factors, including the environment that humans interact with on a daily basis. This study aimed to investigate the diversity and abundance of microbes on phones between cities with varying populations. It was hypothesized that phone microbiomes from individuals in larger cities will yield greater microbial diversity than phones from individuals living in smaller cities. Data on the diversity of bacterial phyla and abundance was collected through the use of Phinch software and the Project MERCURRI data set. 755 samples were filtered from the dataset to analyze bacterial phyla present on mobile phones from participants across eight cities representing different population sizes: major cities (New York and Houston), large cities (San Francisco and Washington DC), medium cities (Fort Lauderdale and Palmdale), and small cities (Longmeadow and Potlatch). Analysis of the dataset showed that overall, mobile phones in bigger cities had greater diversity than their counterparts from smaller cities, with larger cities having 2 to 3 more types of phyla than smaller cities. The results align with the hypothesis that phone microbiomes from individuals in larger cities will yield greater microbial diversity than those from individuals living in smaller cities. This study has implications for factors that could influence the composition of the human microbiota, including what bacterial populations are present on individuals' phones. Further research could explore how the microbes found on people's phones are potentially transferred to their microbiota.

This research project was funded by the College of Natural and Mathematical Sciences at UMBC.

EFIA: A WEARABLE ROBOTIC GLOVE FOR HAND REHABILITATION AFTER PARALYSIS

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Hand functionality is one of the most common ways that people interact with the world, and losing that ability can make navigating daily life independently difficult. A loss of hand dexterity affects millions of people who have paralysis. In addition, hand paralysis is often a result of stroke which affects millions of people every year. With over a decade of research in the Vinjamuri Lab, the Hand Exoskeleton with Embedded Synergies (HEXOES) was designed to address this issue. Originally, it was a soft-actuated robotic glove with high dexterity for the rehabilitation of people with hand paralysis. Today, this project will test the efficiency of a version of the HEXOES, the Efia, that has low dexterity, ease of use, and faster training times. It is hypothesized that the Efia could be an effective lite-weight mobile rehabilitation device if it could empower users with activities of daily living. To achieve high portability, the Efia was redesigned to be lightweight and compact. It utilizes bluetooth control through an app and prioritizes one degree of freedom instead of the original 10. The Efia will be tested with the use of finite element analysis in Solidworks and COMSOL, and loading tests to determine the structural robustness, its customizability, and the pressure it puts on the user. Through this testing, it will be determined whether or not the Efia is sturdy, comfortable, provides a good user experience, and its potential as a durable rehabilitative and assistive device.

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COMPARATIVE GROWTH ANALYSIS OF WILD-TYPE AND RHIZOFERRIN-OVEREXPRESSING MUCOR LUSITANICUS STRAIN FOR ENHANCED BIOLEACHING APPLICATIONS

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Lithium (Li), Nickel (Ni), and cobalt (Co) are critical metals in battery production, with demand expected to rise in coming decades. The growing demand for lithium-ion batteries (LIBs) necessitates sustainable battery recycling methods to address environmental concerns from traditional mining. Fungi are excellent biochemical producers of molecules like siderophores. Siderophores are iron (Fe) chelators, produced in the cell to maintain iron homeostasis, but also bind to other metals such as Ni and Co. Mucor lusitanicus is a filamentous fungal species that produces the siderophore, rhizoferrin. Given rhizoferrin's market price of approximately $290/mg, engineering fungi to enhance its biosynthesis could offer a cost-effective alternative to

traditional extraction methods for this project. When M. lusitanicus synthesizes rhizoferrin excessively, phenotypic changes can be introduced. We hypothesized phenotypic differences between NRRL3631 (wild-type) and MU636+rfs (rhizoferrin overexpressing strain) with increased siderophore synthesis. While MU636+rfs exhibits enhanced siderophore production compared to wild-type, growth profiles would differ significantly between strains. We utilized growth profiles to investigate these changes. Growth kinetics were determined by measuring dry cell weight at three-hour intervals over a 12 hour period. Analysis showed MU636+rfs grew with a greater growth rate compared to wild type. This project builds core knowledge to optimize biological networks for rhizoferrin synthesis. Based on these findings, we will develop an engineering strategy to enhance biomass production, thereby achieving higher rhizoferrin titers and improved bioleaching efficiency.

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BEYOND THE CLOUDS: ROLE OF ELECTRONIC CIGARETTES EFFECTS ON THE MOUSE OLFACTORY SYSTEM OVER TIME

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In recent years, electronic cigarettes (e-cigarettes) has increased, affecting millions, particularly youth and adolescents. E-cigarettes contain toxic chemicals that can harm the olfactory system. Damage to this system is a marker for neurological and cognitive disorders. There is a negative relation between vaping having an effect on the brain and functions of the olfactory system. The olfactory system is responsible for our sense of smell.. With no blood brain barrier, odors have direct access from the environment to be easily converted to signals in the brain, processing smells. Compounds in the vapor interact with the olfactory system, sending odor information to the brain, affecting the olfactory cortex, hippocampus, and amygdala. These are the sites for perception of smell, memory, and emotional responses to odors. With many channels in the nose, there are countless of smells that the brain can perceive and recognized. The lab is investigating how increased e-cigarette exposure affects these channels in the olfactory system: do they become damaged, heighted and many more questions. It is hypothesized that prolonged exposure the vapor weakens the olfactory system, affecting one's sense of smell. . To understand how e-cigarette exposure may disrupt olfaction, olfactory-guided behaviors are assessed using behavioral assays such as the Odor Threshold Test, as mice rely heavily on their sense of smell for locomotion. In the Odor Threshold Test, varying concentrations of nicotine and e-liquid were administered to assess changes in the mice’s movement, preferences, and behavioral responses. By analyzing the mice’s interactions with the liquid, the lab can derive results on how their olfactory health is affected over time: does their odor sensitivity and preference increase or decrease based on e-cigarette exposure? At this time, the lab is in the process of gaining results from its research and experiments.

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INVESTIGATING THE INFLUENCE OF HAPTIC INTERFACE SIZE ON SENSORY THRESHOLDS

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The human sense of touch allows us to distinguish between different sensations, and in assistive robotics we can use haptic devices to refer to touch sensations of assistive robots to their users for daily tasks. Haptic feedback technology plays a crucial role in fields such as prosthetics, virtual reality, and medical devices. However, the scientific understanding of how to replicate touch sensations is still developing, with competing design requirements such as increasing importance, user comfort, and making devices low profile. This research focuses on indentations and skin stretch cues, studying the impact of size on comfort and saliency for a diverse group of participants by measuring the allowable stimulus range and just noticeable difference for each interface, respectively. The study will include development of haptic interfaces utilizing Computer Aided Design (CAD) and 3D printing, and testing them with the Clark Lab's contact and psychophysical testbed equipped with encoders and force-torque transducers. The results from this study will allow us to determine how compact we can make devices while maintaining comfort and sufficient perceptual resolution to relay important touch sensations the robot experiences to the user.

Support for this research was provided by the Meyerhoff Scholars Program

Investigating cell survivability on Edible Gelatin Electrospun Scaffold using Electrospinning

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The development of edible scaffolds through electrospinning brings forth a promising future for biomedical and industrial applications. Electrospinning creates fibrous scaffolds from polymers that offer structural support for cell growth. In this project, the goal is to use electrospinning to create an edible scaffold using Type B gelatin – a commonly used, food safe polymer – combined with fungal particles to culture lab grown meat. The fibers themselves are created by electrospinning a solution of gelatin and the fungal particles in acetic acid and water. They are then chemically crosslinked with formaldehyde, then pH adjusted, and finally they are sterilized with UV prior to cell culture. We've successfully created electrospun fiber samples and have seeded HMSC mammalian cells to the scaffolds to test biocompatibility. Unfortunately, initial results show poor cell survival. Initially, we investigated whether pH imbalance contributed to cell death, but results showed that pH was not an issue. We then turned our attention to the scaffold composition. To test this, we pre-conditioned the scaffolds with collagen before cell

seeding, but this led to continued cell death. These findings have suggested that other factors are in play that are impacting the cells. Currently, we are exploring new approaches to improve scaffold performance and support cell survival. Part of this process requires us to continue to develop and test new electrospun fiber samples to optimize conditions for successful cell growth. Creating edible scaffolds for lab grown meat can help reduce the environmental impact of traditional farming. This approach has the potential to improve access to food and fight food insecurity by offering a more sustainable way to produce meat. In addition, what we learn from this research could also be useful in regenerative medicine, where scaffolds can help repair or grow human tissues.

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CREATING A DIGITAL DASHBOARD THAT SUPPORTS SMALL BUSINESSES IN ACQUIRING GOVERNMENT CONTRACTS

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Securing government contracts is a critical step in scaling small business, yet many small and diverse companies face barriers in accessing these opportunities. Hutch is an incubator company that addresses this by providing business support to help companies position themselves for federal contracts. Hutch aligns company capabilities with suitable government contracts using a manual sorting system which has limited speed and efficiency. To address this inefficiency, we developed a centralized, interactive data visualization dashboard using Power BI and information gathered from surveys distributed to target companies. This innovative dashboard streamlines the matchmaking process by transforming data into a dynamic, searchable interface. This tool enables users to filter companies by expertise or view individual company profiles to support faster and more informed decision-making. This dashboard will significantly enhance operational efficiency, reduce manual workload, and increase visibility for underrepresented businesses while amplifying Hutch's mission to promote inclusive innovation and accelerate equitable access to government contracts.

This research was funded by the Meyerhoff Scholars Program at the University of Maryland, Baltimore County (UMBC)

INVESTIGATING THE EFFECTS OF ESTRADIOL ON PLATELET TRACTION FORCES

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Platelets are blood cells that drive blood clotting and stop bleeding. During these processes, platelets bind, spread, and contract. Their ability to generate traction forces (i.e., contract) is crucial to prevent excessive bleeding after injury. There are notable differences in the coagulability, or ability to clot, of males and females. Female hypercoagulability has been shown, in part, to be a result of estradiol, which induces faster clot formation and increased clot strength. Coagulability is clinically significant as, after severe injury, females have an advantage in trauma-induced coagulopathy. However, whether estradiol affects platelet traction forces is unknown. This study aims to investigate the effects of estradiol on platelet traction forces to understand sex-specific variations in platelet mechanics. To explore these differences, black dots are utilized. Black dots are a fluorescent micropattern created by stamping a fluorescent protein onto a flexible substrate. Platelets are seeded on the substrate, where they bind, spread, and contract. The distortions of the micropattern are visualized via fluorescence microscopy. These distortions are used to calculate single-platelet traction forces. We seeded washed platelets from healthy human research subjects onto the black dots in the presence or absence of exogenously added estradiol. After quantifying 262 platelets from a male research subject, we found that they produced 20.1 nN per platelet with a standard deviation of 6.67 nN. It was also observed that platelets with 150 pg/mL and 1500 pg/mL exogenously added estradiol produced an average of 23.54 nN and 26.93 nN, with standard deviations of 8.23 and 11.34, respectively. These preliminary results indicate that estradiol may increase platelet force generation.

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NEW ANTIBIOTIC DISCOVERY

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The period from 1940 to 1970, known as the Golden Era, saw the discovery of numerous antibiotics, significantly increasing life expectancy to 78.8 years and shifting the leading cause of death from communicable to non-communicable diseases. However, the emergence of superbugs—antibiotic-resistant organisms—is threatening to end this era, as infections become increasingly difficult to treat. In the US, healthcare-associated infections resulted in 99,000 deaths out of 1.7 million cases in 2002, a stark rise from 13,300 deaths in 1992. This emphasizes the urgent need for new interventions.

This study investigates the problems of antibiotic resistance, challenges in culturing archaea and bacteria, and innovative approaches to overcome the limitations of traditional culturing techniques. The hypothesis posits that novel culturing methods for bacteria and archaea could mitigate the rise of superbugs.

This quantitative research involved a literature review of five peer-reviewed scholarly articles published in the last decade. The study found that the scarcity of new antibiotics is largely due to the difficulty in culturing bacteria and archaea. To address this, new methods such as growing microbes in their natural environments and then isolating them for study were explored. Techniques like deep learning and diffusion chambers were identified as promising solutions. Notably, the deep learning technique led to the discovery of halicin, which has been effective in treating infections in mice.

Investigating USP15 as a Regulator In Ovarian Cancer Cells

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Due to the lack of effective therapeutics and late diagnosis, ovarian cancer is the second most lethal gynecologic cancer and the sixth leading cause of cancer-associated deaths among women in the United States. To improve clinical outcomes, it is crucial to identify key factors that drive ovarian cancer progression and understand the mechanisms that regulate these factors within cells. USP15 expression is elevated in several cancers, including ovarian cancer, and high USP15 levels are associated with poor clinical outcomes in these patients. Despite its established role in several cellular functions and impact on cancer, there are no reports investigating the mechanisms that regulate USP15 protein stability and levels in cells. My project aims to address this knowledge gap. Our preliminary data show that a small molecule called MCB-613, depletes USP15 protein in the TYK-Nu ovarian cancer cells. Cycloheximide chase assay also revealed a reduction in USP15 half-life upon MCB-613 treatment, confirming the effect is post-translational. We will ascertain the broader biological relevance of these results by expanding these experiments to various ovarian cancer cell lines. We will then combine chemical biological approaches, and structure-function analyses to identify the precise mechanism through which MCB-613 regulates USP15 in ovarian cancer cells.

This research was supported by the Meyerhoff Scholars Program.

ULTRASTRUCTURAL CHARACTERIZATION OF STEROID-RESPONSIVE CATARACTS: IDENTIFYING CELLULAR PATHWAYS FOR TARGETED THERAPEUTIC DEVELOPMENT

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Steroid-responsive cataracts are characterized by an increased presence of vacuoles in the lens capsule compared to non-steroid cataracts, suggesting a distinct cellular pathway involved in their formation. Gaining insight into this pathway may pave the way for targeted treatments for steroid-induced cataracts, which would be a major clinical advance if those treatments are additionally utilized for steroid-induced glaucoma. Finding ultrastructural and molecular variations in lens capsule tissues linked to steroid-responsive versus non-steroid cataracts is the goal of this study. We will evaluate the size and quantity of organelles in tissue samples taken from patients undergoing cataract surgery using intracellular imaging methods such as transmission electron microscopy (TEM) and immunofluorescence staining. Data will be analyzed across variables such as age and cataract type to uncover potential biomarkers or mechanistic clues. We anticipate that steroid-responsive cataracts will exhibit distinct organelle profiles, providing not only foundational insights into their pathogenesis but furthermore informing future therapeutic development.

Support for this research was provided by the UMSoM Grant K23EY03525 to Janet Alexander.

Exploring the Fate of RNA in Moloney Murine Leukemia Virus (MoMuLV)

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Retroviruses must regulate the fate of their RNA genomes to balance translation and packaging. HIV-1 accomplishes this through transcriptional start site (TSS) heterogeneity, generating two distinct RNA pools, cap 1G and cap 3G, that drive either virion packaging or protein synthesis. In contrast, Moloney Murine Leukemia Virus (MoMuLV), a simple retrovirus, transcribes its RNA solely from a single TSS (coined ^{cap}1G), yet still effectively separates these functions. This suggests that MoMuLV uses a post-transcriptional mechanism to control RNA fate. We hypothesize that MLV's genome fate is driven by a dimerization-dependent cap sequestration, and we hypothesize that cap sequestration is essential for packaging. Dimerization is proposed to induce conformational changes that sequester the 5′ cap, preventing recognition by translation initiation factors like eIF4E. To test this, we use in vitro transcription to generate MoMuLV RNA, we then use Faustovirus capping enzyme (FCE) to cap the RNA, and assess cap accessibility through electrophoretic mobility shift assays (EMSAs) with eIF4E. Because the MoMuLV leader is too large for structural analysis via NMR, we use smaller truncations that retain the native 5′ start site. We aim to find truncations that mirror the full-length RNA in dimerization and cap sequestration behavior, enabling us to validate their suitability for future NMR-based structural studies. This work aims to define a structural and behavioral mechanism by which MoMuLV regulates RNA fate in the absence of TSS heterogeneity, helping us to understand conservation of function amongst retroviruses by studying an older relative of HIV-1.

Support for this research was provided by the Howard Hughes Medical Institute and funding from the National Institute of Health/NICHD (R01AI150498)

EMPOWERING SMALL BUSINESSES: SIMPLIFYING SBIR/STTR FUNDING FOR TECHNOLOGICAL INNOVATION AND COMMERCIAL GROWTH

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Enhancing the understanding of Small Business Innovation Research (SBIR) and Small Business Technology Transfer (STTR) programs can stimulate significant improvements for small businesses, research institutions, governments, and other stakeholders. A total of 11 federal agencies maintain SBIR programs, while only 5 of those agencies maintain STTR programs. SBIR and STTR programs are made to support small businesses by determining product feasibility, providing funding for a period of time, and ultimately commercializing a business idea into a viable product for the marketplace. While this process may not seem complex, an incredible amount of requirements are needed for a small business or research institution to gain the funding necessary. This project aims to dive deep into SBIR/STTR policies, primarily the Department of Defense, and create a resourceful guide to help small businesses and research institutions with the process of gaining federal funding and providing marketable solutions with their research. The guide is made to serve current and future entrepreneurs and researchers to simplify the commercialization pathway through a federal agency. Using the Department of Defense as a foundation, the information examined is crucial to create a generalized view on comprehending agency requirements to minimize any trouble that may occur when trying to earn funding. A commercialization strategy is provided within the guide as well as solutions to common concerns entrepreneurs and researchers face. With the summarized findings of SBIR/STTR policies, market opportunities, and proposal submissions, small businesses and research institutions will be able to strive toward success and scale their technologies.

This research was funded by the Meyerhoff Scholars Program at the University of Maryland, Baltimore County (UMBC).

DESIGNING AN INCLUSIVE MICRO-PURCHASE MARKETPLACE FOR HISTORICALLY EXCLUDED FOUNDERS WITHIN THE GOVERNMENT CONTRACTING SECTOR

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Public Procurement, particularly micro-purchases under $10,000, usually presents opportunities in order to drive economic equity by increasing contract accessibility for historically excluded small business founders. Many of these businesses usually face barriers such as limited visibility, complex registration processes and unclear procurement pathways. To address this, we created a digital marketplace to help vendors within the Hutch program (a non-profit program designed to help entrepreneurs and digital services firms build impactful businesses in the tech and government contracting sectors) showcase their services and certifications and connect with buyers from government agencies, educational institutions and nonprofit organizations. To design our digital market place with relevant features we researched procurement laws across all government levels, existing procurement platforms and portals. Using Canva.com, we designed the website layout and created a Google form where new Hutch companies can register to be included in the marketplace. Our marketplace will simplify procurement processes and empower small businesses to navigate compliance with government agencies and build institutional trust.

Roseline Oshagbemi and Great Akinrotimi were supported in part by a grant to the UMBC Meyerhoff Scholars Program from the Hutch program at Fearless Institute.

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MATRIX DECOMPOSITION AND TIME-SERIES PREDICTION FOR COMPLEX VORTEX STRUCTURE CHARACTERIZATION

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The accurate characterization of complex spatiotemporal structures, such as coherent vortices in high-speed turbulent boundary layers, poses a significant challenge due to the high dimensionality and nonlinear nature of the governing Navier-Stokes equations.
To circumvent these issues, flows are computer-simulated over a grid, yielding discrete data which captures physical characteristics of the flow at each grid-point. Through the decomposition of select attributes of this physical data, lower-dimensional matrices of temporal coefficients and spatial modes can be derived. Our work focuses on optimizing matrix decomposition such that the resulting spatial modes best capture dominant physical structures within the fluid flow, then implementing time-series prediction on the corresponding temporal coefficients to predict the future behavior of the flow. The main issue encountered when using a dimensionality reduction technique in this manner is the appearance of pseudo-vortices, a truncation error from the unresolved high-frequency spatial modes.
In this study, we explore various matrix decomposition techniques to reconstruct complex vortex structures while minimizing pseudo-vortices. We extend the use of Non-negative Matrix Factorization (NMF) into the domain of Fluid Dynamics and compare the performance of NMF to Principal Component Analysis (PCA) in accurately reconstructing the fluid flow. NMF visually eliminates pseudo-vortices better than PCA when reconstructing fluid flows, however

spatial modes generated using NMF have a tendency to exactly replicate physical features of the original fluid flow, rather than capturing abstract components which are not seen in the original vortex structure, like PCA. Additionally, we implement an open-source time-series prediction model, MOMENT, for the first time on Computational Fluid Dynamics data to facilitate the prediction of future spatiotemporal behavior of complex fluid flows.

Support for this research project was provided by the University of Maryland, Baltimore County Department of Mathematics and Statistics.

DESIGNING INTERACTIVE TOOLS FOR ANALYZING GLACIER TRAJECTORY THROUGH COMPUTER VISION OUTPUTS

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The increasing use of satellite imagery and machine learning techniques in polar science has created a demand for user-centered tools that help researchers interpret complex model outputs. This project focuses on designing user interfaces to support polar scientists investigating glacier trajectory. By using automated image segmentation of satellite data, we aim to provide intuitive ways for users to explore computer vision predictions and evaluate spatial and temporal patterns. Our goal is to align interface elements with scientific reasoning practices such as comparison, pattern recognition, and hypothesis development. Through iterative prototyping and researcher feedback, we are developing interactive visualizations that highlight model metrics and segmentation results. These tools are intended to enhance the interpretability and usability of AI-assisted workflows in environmental science and contribute to broader efforts in transparent and collaborative scientific computing.

Support for this research was provided by the NSF HDR Institute for Harnessing Data and Model Revolution in the Polar Regions

DESIGNING AND CONSTRUCTING A THERMOELECTRIC POWERED SELF-SUSTAINING SENSOR PLATFORM

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Within the realm of art conservation, sensors play a critical role in collecting ambient environment data on metrics including temperature, humidity, and light exposure, helping to maintain optimal conditions to minimize the degradation of artwork. The ease of use of these sensors is limited by the lifespan of their batteries, which create the need for constant maintenance and human interaction. Energy harvesting technologies including thermoelectrics, piezoelectrics, and photovoltaics have been studied as supplemental power supplies for electronic devices and sensors.

However, the inherent low, variable output of these sources (50-200 mV) creates a significant power mismatch with sensor operating requirements (3.3 V), making direct, continuous power an unresolved challenge. To significantly extend sensor uptime, this work develops a low-power, self-sustaining sensor system that includes (1) a step-up circuit capable of matching the variable output of energy-harvesting materials to sensor requirements, while also (2) enabling intelligent power storage and adjustable duty cycling through the introduction of a 5 V capacitor and a voltage-controlled switch.

The system's sensor platform, built around an Arduino Nano Matter powered by a thermoelectric array, utilizes a heart rate sensor as a demonstrative load, chosen for its operational and power consumption characteristics that mimic typical environmental sensors for art conservation. The primary mechanism enabling self-sustainability is a voltage-controlled switch with adjustable hysteresis. This intelligent power management circuit manages power delivery for periodic operation, activating the Arduino-sensor system when the capacitor charges to 4.1V and disconnects power when below 3V. This intermittent duty cycle, rather than constant uptime, effectively facilitates self-sustainability. This work demonstrates the potential for a fully self-sustaining sensor platform capable of harvesting ambient energy for intermittent data collection and transmission. The innovative power management circuit overcomes the battery-life limitations of conventional sensors, offering a practical solution for the perpetual monitoring of sensitive artworks.

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RESPIRATORY ROI LOCALIZATION IN VIDEO-BASED CONTACTLESS RR ESTIMATION

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Contactless respiratory rate (RR) estimation is an emerging technology that uses video to measure breathing, offering a noninvasive alternative for monitoring patients across a range of applications, including neonatal and critical care, long-term care, sleep studies, and sleep apnea monitoring. However, accurately capturing respiratory motion is challenging due to its variability across individuals and conditions. Factors such as distance, posture, occlusion, camera angle, clothing, and background significantly affect which body region–chest, shoulder, or abdomen–provides the most reliable motion cues. This study aims to investigate how some of these factors affect the respiratory motion visibility and to identify the most dominant region of interest (ROI) for robust and efficient RR estimation across diverse conditions.
We use diverse video datasets comprising public sources (MPSC-RR, AIR-125, IR/NIR sleep videos) and lab-collected using a fisheye camera under varying distances and setups. Our methodology involves evaluating and benchmarking multiple optical flow models to extract motion magnitude heatmaps from video frame pairs. These heatmaps are analyzed to localize ROI and assess each model’s performance in terms of accuracy, consistency, and computational cost.

Our results show that RAFT optical flow estimation provides a stable and accurate flow under varied conditions, while lighter-weight models trade off some accuracy for efficiency. We also analyze how factors like subject distance and sensor type (e.g., IR, NIR, RGB) influence signal quality and ROI visibility. This work helps guide existing and future respiratory rate models to focus their computation on the most informative body regions. Understanding how signal quality varies across conditions enables more efficient and reliable contactless monitoring in real-world healthcare settings.

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IMPROVING PROTON BEAM RADIOTHERAPY BY SEQUENCING SIMULATED PATIENT DATA IN COMPTON CAMERA REAL-TIME IMAGING WITH NEURAL NETWORKS

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Proton beam radiotherapy is an advanced cancer treatment technique utilizing high-energy protons to destroy tumor matter. When the proton beam interacts with the patient's body, it emits prompt gamma rays, which can be detected by a Compton camera. However, image reconstruction of the beam path from these scatterings is plagued by mischaracterized scattering sequences and excessive image noise. To address this, machine learning models were developed to order the scattering events properly. Multiple novel datasets simulating particle interactions with human tissue were generated using Duke University CT scans and GEANT4 and Monte-Carlo Detector Effects (MCDE) software. An automated hyperparameter tuning framework was also built into the Big-Data REU Integrated Development and Experimentation (BRIDE) pipeline. This work implemented a novel event-classifier transformer and a 1D Convolutional Neural Network (CNN) to better understand spatial relationships in the data.

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INVESTIGATING MARKET STRATEGIES THAT BEST SUPPORT TECHNOLOGISTS AND ENTREPRENEURS IN COMMERCIALIZING ARTIFICIAL INTELLIGENCE CHATBOTS IN HEALTHCARE FIELDS

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Artificial Intelligence (AI) chatbots are software applications that utilize artificial intelligence, machine learning, and language processing to simulate human-like conversations either verbally or through written text. AI chatbot usage has increasingly grown in the following years, in both the private and public sectors, offering aid in areas such as health care, customer support, education, and government services. While these developments are notable, early-stage entrepreneurs are faced with issues surrounding commercializing chatbot products. With challenges such as ethical and regulatory concerns and technical limitations. This project is aimed at creating innovative strategies for commercialization that also respect both the customer and regulations. This research analyzes how technologists and entrepreneurs can commercialize AI chatbots most effectively, balancing profitability and ethical responsibility. This research investigated how chatbots currently operate in the healthcare field and analyzed the intellectual property laws, licensing models, and emerging policies. This project also involved analyzing market trends, growth potential, and risks through SWOT analysis and feasibility assessments. Ultimately, producing practical start-up strategies. The findings show that successful commercialization relies on three core strategies. First, prioritizing a design that puts humans at the center fosters trust and makes the chatbot easier to use. The next is an emphasis on intellectual property, along with compliance with the law. The third is tailoring a marketing strategy based on the needs and expectations of the target industry. These strategies aim to increase the real-world implementation of AI chatbots to make these technologies more sustainable commercially.

This research was supported by the Meyerhoff Scholars Program at the University of Maryland, Baltimore County (UMBC).

CROSS-MODAL KEY POINT TRANSFER FROM LAND RGB-DEPTH TO UNDERWATER RGB-SONAR FOR OCCLUDED HUMAN RECOGNITION

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Recognizing divers in low-light, underwater environments is challenging due to visual obstructions from diving gear, murky conditions, and occlusion by debris or coral. This study presents a framework for human recognition that extracts anthropometric and skeletal key points from land-based RGB-D data using the Kinect V2 sensor and transfers this knowledge for underwater recognition using the BlueROV2's onboard RGB camera and sonar. While the BlueROV2 lacks native 3D skeletal mapping capabilities, raw sonar video stream (via RTSP) is utilized for feature matching in the aquatic domain. This research addresses the following challenges: (a) **Extracting rich key points from RGB-D images and resolving hallucinations**: Unlike face-dependent models like OpenPose, which often fail underwater due to obscured facial features, our approach focuses on stable body regions—chest, torso, hips, and legs. To improve robustness under partial occlusion, anatomically adjacent key points (e.g., left shoulder, elbow, clavicle) are clustered and used to train a deep neural network (DNN). This clustering enables models to identify individuals when only partial body segments are visible in RGB or sonar data. We evaluate both clustering-based (KNN, K-means, DBSCAN) and graph-based (GNN) classification techniques using a dataset of over 1,000 labeled RGB-D images from six volunteers collected to support training and validation. We also conduct a comparative analysis between Kinect-derived skeletal data and OpenPose to find suitable key point extraction methods for occlusion-resilient underwater recognition. Our preliminary findings indicate Kinect-derived key points are prone to hallucinations; to mitigate this, we constrain key point extraction to visible regions identified via RGB imagery. (b) **Recognizing Occluded Individuals Underwater:** In future work, this project aims to develop a transfer learning model that maps depth-based key point representations to sonar data, enabling reliable estimation of occluded human key points in underwater environments. Finally, we will integrate autonomous navigation in the Blue ROV2, enabling movement towards recognized individuals.

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EVALUATING CURRENT AND FUTURE CAPACITY FOR SOLAR PANEL INSTALLATIONS IN MONTGOMERY COUNTY, MD

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In Montgomery County, MD, increasing demands for sustainable sources of energy require a thorough inventory of the county's capacity for both current and future solar panel usage. Through Montgomery College's DATA 205 capstone course, we spent a semester collaborating with Montgomery County Government mentors to evaluate the county's current solar panel coverage and to establish a foundation for future development of rooftop panels and carports. We utilized ESRI's ArcGIS Pro software to create two end products: a trained model capable of detecting solar panels within overhead imagery; and an assessment of the most feasible rooftops and parking lots for future panel construction based on their levels of received solar radiation.

We used ESRI's built-in Solar Panel Detection computer vision model, with an accuracy of 0.76, as a foundation which we then trained to produce a refined model with an improved accuracy of 0.86. Our updated model enabled us to successfully identify solar panels from overhead imagery of the county with significantly fewer false negatives than in the untrained model. To assess feasibility for future solar installations, we used the Raster Solar Radiation tool on a digital surface model (DSM) of the county. The data yielded by the tool reflected the total amount of solar radiation to which each area would be exposed over a year-long period. When factoring in solar panel efficiency and practical constraints, we found that the county could theoretically harness up to 8.4 million MWh of energy from rooftops and 260,000 MWh from parking lots annually. Our research was successful in providing Montgomery County with an inventory of its solar capacity, and it will be a valuable resource to factor into future planning projects.

Support for this project and access to ArcGIS Pro licenses was provided by the Montgomery County Department of Environmental Protection.

DETERRING WILD ANIMALS FROM AGRICULTURAL AND RESIDENTIAL SETTINGS USING ACOUSTICS

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Human-wildlife conflicts have risen over the past decade, with wildlife causing an estimated $600 million in crop losses (corn, soybeans, wheat, cotton) in the U.S. between 2015 and 2019. Beyond agriculture, animals like deer and foxes also damage gardens in urban and peri-urban areas, and most control methods remain harmful to them. This project seeks to develop humane and effective deterrent solutions to reduce wildlife intrusion in both agricultural and residential areas. Given the varying coverage requirements of these environments, different technologies must be employed to deliver sound-based deterrents tailored to each context. For the agricultural setting, we create two 'sound pod' devices: Sound pod A, which only produces tones, and Sound pod B, which can play sound files. For the residential setting, we create a phased array of speakers, which can only generate tones. This will enable us to control the direction of sound propagation, ensuring minimal disruption to pets and neighboring areas. All devices employ Arduino Nano ESP32 microcontroller and the MCP4151 digital potentiometer for controlling the volume. For sound creation, the phased array and sound pod A utilize AD9833 function generators, whereas sound pod B employs MAX98357 I^2S amplifiers. We observed that the phased array was able to steer the sound with an accuracy of 15° and had a 10 dB (SPL) decrease in volume outside of the beam (in both left and right directions). The general pattern of sound propagation created by our phased array matched simulations using MATLAB, although the real phased array had a beam width 20^o wider than the simulation. We also observed, using sound pod A, that a 2 kHz square wave tone was able to deter deer within approximately 2 meters of the device. Some directions of future research include increasing the precision of the phased array

and determining whether tones, predator recordings, or a mix of both are more effective in deterring animals.

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Deep Learning-Based Quantification of Mammary Gland Architecture and Adipose Remodeling in Breast Cancer

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Breast cancer is one of the most commonly diagnosed cancers in women and a leading cause of cancer-related deaths worldwide. While tumor cells drive disease progression, the surrounding stromal microenvironment, particularly changes in adipose tissue and mammary gland architecture, plays a crucial role in tumor growth and metastasis. Emerging evidence suggests that cancer-associated adipose tissue undergoes structural remodeling, potentially serving as an early indicator of tumor presence. However, current assessment methods are often subjective and lack scalable computational tools. To address this gap, we are actively developing a deep-learning-based computational framework to analyze histopathological images of mammary adipose tissue and mammary glands. Our pipeline incorporates automated image segmentation and machine learning methods to quantify key morphological features such as adipocyte size, shape irregularity, spatial distribution, and mammary gland area with the goal of distinguishing tumor-associated from healthy regions. Preliminary analysis suggests statistically significant differences in both adipocyte and mammary gland morphology between tumor microenvironments and distal (healthy) regions, supporting earlier manual findings. Once completed, this framework could provide a scalable, objective tool for detecting cancer-associated stromal and glandular remodeling in breast tissue, with potential clinical applications in early detection, risk stratification, and treatment planning.

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ISOLATING THE EFFECTS OF CONIDIATION REVEALS THAT CELL WALL STRENGTH EFFECTS THE MECHANICAL STRENGTH OF MYCELIAL MATERIALS

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Mycelial materials (MMs) grown from filamentous fungi are an emerging class of renewable biomaterials which have seen broad applications. This versatility, particularly in comparison to

other biomaterials, make them an especially attractive alternative to traditional, non-renewable materials. While MMs have shown promise, their widespread use is hindered by their limited material properties, particularly their mechanical strength. Existing approaches to mitigating this issue require the use of additives, post processing, and composite designs. Although these approaches have successfully made MMs commercially viable for some limited applications in foam and insulation, they do not address the biology that limits their mechanical strength. Thus, our research aims to uncover how various features of the mycelium influence mechanical strength, with the ultimate goal of contributing to the development of tuneable, novel MMs. Our lab has focused on one feature, cell wall strength, in the ascomycete, *Aspergillus nidulans* where weakened cell walls result in greater mycelial fragmentation. We found that MMs grown from a mutant strain with weakened cell walls displayed stronger mechanical strength. To understand this result, we conducted further analysis with SEM imaging, which revealed a secondary contributing factor. Alongside having weakened cell walls, the mutant strain also had fewer reproductive structures, resulting in a denser and more uniform material made entirely of filaments. To isolate the effect of cell wall strength on mechanical strength, we aim to eliminate reproduction while growing MMs. Namely, from mutant strains that lack reproductive pathways, and through growth in submerged cultures, where reproduction is naturally suppressed. This dual approach will help clarify how multiple phenotypes interact to influence mechanical properties.

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EXPLORING THE FATE OF RNA IN MOLONEY MURINE LEUKEMIA VIRUS

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The Moloney murine leukemia virus (MoMuLv), a virus that causes leukemia and neurological diseases within rodentia, has been studied since the 1950s as a model to further understand the underlying mechanisms of all retroviruses due to its easy use. Our laboratory mainly focuses on the human immunodeficiency virus type-1 (HIV-1), particularly the segment of the genome important for viral replication, known as the 5'-Leader (5'L). The 5'L exists in two conformations: the dimeric conformation adapted by 5'-capped RNAs beginning with one guanosine (^{Cap}1G) in which the cap is sequestered, and the monomeric conformation adapted by 5'-capped RNAs beginning with two or three guanosines (^{Cap}2G and ^{Cap}3G respectively) where the cap is exposed. Viruses containing these different start sites are said to have transcriptional start site heterogeneity. Inversely, MoMuLv contains a unique transcription start site, meaning the virus consists of only one start site, ^{Cap}1G from which the 5'L can still adopt a monomeric or dimeric form. We hypothesize that dimerization dependent cap sequestration influences packaging. To investigate this, we tested cap accessibility using eIF4E, a cap binding protein that initiates translation. Electrophoretic mobility shift assays (EMSAs) allow us to detect eIF4E

binding and indicate cap accessibility. A consistent challenge throughout has been ensuring that only fully capped RNA was present to remove confounding variables of eIF4E binding. Thus, we employed a new method using an eGFP (enhanced green fluorescent protein)-eIF4E protein complex to isolate capped RNA. Performing an EMSA with this, the shifted RNA–protein complex was excised from the gel, then isolated and purified to yield fully capped RNA, which was subsequently used for further studies. We anticipate that confirming dimerization dependent cap sequestration will provide further insights into broader strategies for targeting retroviral replication.

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EXAMINING LEARNED ASSOCIATIONS BETWEEN CONTEXTUAL CUES AND STRESS-INDUCING EXPERIENCES

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The ability to establish learned associations between stressful and contextual stimuli is important for survival, but it remains unclear how the brain integrates this information to guide behavior. We used a behavioral paradigm, Conditioned Place Aversion (CPA), to train mice to learn to associate an ethologically-relevant aversive stimulus with contextual cues in an arena. Briefly, mice received an aversive stimulus in 1 of 2 chambers that are distinguished by visual cues. We tested physical restraint as the aversive stimulus and found that it was effective in inducing CPA as measured by a reduction in the time spent in the conditioned chamber. We recently repeated this with footshock as the aversive stimulus, but additional trials are necessary to determine its effectiveness in inducing CPA.

To determine what brain regions may underlie CPA, we used immunohistochemistry to measure cFos expression, a marker of cell activation, during several restraint/context conditions. We focused on the dorsal and ventral hippocampus (dHipp/vHipp), medial nucleus accumbens (NAc), and basolateral amygdala (BLA) due to their prominent roles in contextual learning and memory, motivated behaviors, and fear, respectively. In the NAc and BLA, we observed a significant increase in cFos expression in mice that were restrained in the CPA arena. In the vHipp, mice exposed to the arena with or without restraint showed a significant increase in cFos expression. Overall, these activation patterns implicate the potential involvement of all three hypothesized brain regions in CPA behavior, with the vHipp facilitating contextual processing. Our findings establish a novel method for inducing CPA and identify potential brain regions involved in mediating this behavior. This sets up future experiments utilizing optogenetics to identify the specific neural circuits between these regions involved in facilitating contextually-dependent aversive behaviors, with implications for neuropsychiatric disorders, such as anxiety and post-traumatic stress disorders.

Support for this research was provided by a grant to UMBC from the Howard Hughes Medical Institute through the Driving Change Initiative, 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 funding from the UMBC Startup Package.

ASK THE PAPER: BUILDING A CONVERSATIONAL AGENT THAT SPEAKS FOR THE AUTHOR

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Research is fast paced and researchers are always pursuing new discoveries which includes reading and expanding on findings made in academic papers. The problem begins when researchers have questions about papers, but the authors do not have the ability to respond in a timely manner. Therefore, we propose a conversational agent that interacts with the researcher as if they were talking directly to the author. This is designed to reduce the communication burden on authors while improving ease of access to academic knowledge. We were motivated by the challenge researchers face in fully understanding and building upon complex academic papers, such as computational biology, quantum computing, etc, and aimed to create a tool that supports deeper learning without the need for author clarification. To develop this conversational agent, we fine-tuned a LLM using Supervised Fine-Tuning (SFT) and Low-Rank Adaptation (LoRA), and integrated it with a Retrieval-Augmented Generation (RAG) pipeline. LoRA was chosen to fine-tune the model because it doesn't overwrite the general knowledge of an LLM, which decreases the likelihood of catastrophic forgetting, and creates a compact model so that noisy information in the LLM is not transferred to the small model. The small model fine-tuned with LoRA was integrated into a RAG pipeline to improve the model's response by providing it with contextual information to respond to researchers' inquiries. The fine-tuning process used multiple custom datasets: one focused on section-level summarization, another included simple and complex question and answer pairs, and a third simulated multi-turn dialogues. The resulting conversational agent is capable of engaging in conversations, as if speaking directly to the author. This approach is meant to reveal an efficient solution that improves scholarly communication, which allows inquiring researchers to interact directly with academic papers without waiting on the author's availability.

This research was supported by the Louis Stokes Alliance for Minority Participation Program.

THE EFFECTS OF THE JAK/STAT PATHWAY ON HOST SURVIVAL FOLLOWING PARASITOID INFECTION IN DROSOPHILA MELANOGASTOR

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Parasites have evolved a multitude of ways to manipulate host physiology in order to evade the immune responses of hosts. For instance, parasites such as *Trypanosoma cruzi* and *Leishmania*, alter or override the JAK/STAT pathway in order to successfully evade immune response and infect the host. Parasitoid wasps offer a relatively unexplored avenue for studying the effects of parasitic infection on the immune system. Female wasps lay their eggs in *Drosophila* larvae where the parasitoid offspring will consume the larvae until it forms a pupa case and emerges as an adult wasp. When a parasitoid egg has been placed in a larva the immune system has the ability to respond by encapsulating the wasp egg, stopping it from being able to hatch. This encapsulation response is heavily regulated by the JAK/STAT pathway. However there are species of parasitoid wasps that evade the immune response by manipulating the JAK/STAT pathway. The JAK/STAT pathway is an important pathway that regulates immune response, blood cell production, apoptosis, differentiation and more[2]. This pathway is also highly conserved between humans and *Drosophila*[3]. My study aims to collect and establish a colony of parasitoid wasps to use a model of infection to study the effects of parasitic infection on the JAK/STAT pathway. In particular my study will analyze the manipulation of the genes *domeless* and *unpaired* (*upd*) *1*, *upd2*, and *upd3*, which have been implicated as likely candidates for how parasitoids interfere with the JAK/STAT pathway[1]. Overall, the findings of this study will help to better understand suppression of the JAK/STAT, as well as how parasitic infection affects the immune system.

This research was funded in part by the Arnold and Mabel Beckman Scholars Program.

MASS-SPECTROMETRY PROTEOMICS AND IMMUNOBLOTS REVEAL DYSREGULATION OF CERAMIDE METABOLISM IN THE AGING MOUSE BRAIN

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Neurodegenerative diseases are an emerging global health burden, for which aging is the principal risk factor. The brain is a highly heterogenous organ mainly composed of lipids, playing major roles in structure and signaling. However, it is not fully elucidated how lipid metabolism changes in the brain during aging. We hypothesize that the levels of key lipid metabolizing proteins are perturbed during aging. First, to decipher alterations in lipid metabolic pathways during aging, we obtained brain tissues from young and aged female mice, aged 3-4 months (n = 3) and 17-19 months (n = 3), respectively. To elucidate the protein levels of lipid metabolic pathways, we conducted a proteomics experiment. Brain tissues were prepared into lysates by adding a cell lysis buffer and a serine protease inhibitor. Then, they were sonicated and centrifuged, before the supernatant was extracted. Following, proteins were isolated from each of the lysates and digested into peptides, which were analyzed via a bottom-up mass spectrometry-based proteomics approach. The resulting data were analyzed by PEAKS Studio. Over 4500 proteins were detected, of which eight were found to exhibit a fold change of at least two and statistical significance of at least 20. To corroborate our findings and correlate with stress and energy metabolism pathways, we carried out immunoblots using the lysates. From the proteomics experiment, lipid metabolizing proteins acid ceramidase 1 and fatty acid-binding protein 7 were found to be significant. In addition, immunoblotting data demonstrate a

statistically significant reduction of lipid metabolizing enzyme ceramide synthase 2. Preliminary immunoblot findings demonstrate an increase in the abundance levels of phosphorylated c-Jun N-terminal kinase and a consistency in levels of creatine kinase, mitochondrial 1A. The future work is underway to follow up the current study with enzymatic activity assays and knockdown experiments to investigate the functional impact of these findings.

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

EXPLORING THE STRUCTURE AND MECHANISMS OF HIV-1 VIRION ASSEMBLY THROUGH GAG-RNA INTERACTIONS

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Human Immunodeficiency Virus-1 (HIV-1) affects over 39 million people worldwide and can lead to acquired immune deficiency syndrome (AIDS). There are antiretroviral therapies (ART) that manage infection, however ART is not a cure and HIV's high mutation rate makes long term treatment difficult. These challenges necessitate further study of the different stages of the HIV-1 replication cycle.

The Gag polyprotein is crucial for virion assembly, forming a shell encapsulating two copies of viral genomic RNA (gRNA). Gag is a multi-domain protein consisting of matrix (MA) for plasma membrane targeting, capsid (CA) for hexagonal lattice assembly, nucleocapsid (NC) for RNA binding, P6 for host ESCRT recruitment, and two spacer peptides (SP1 & SP2) linking CA-NC and NC-P6, respectively. The recognition between Gag and the packaging signal (Psi) on the 5'-leader of gRNA is critical for virion assembly initiation and selective gRNA packaging. However, the exact Gag/Psi recognition mechanisms remain elusive.

To elucidate Gag/Psi recognition mechanisms, the interactions between Gag fragments and gRNA will be studied. Gag fragments containing CA and/or NC will be constructed since both domains are necessary for Psi recognition. The binding and assembly behavior of these Gag derivatives onto the core encapsulation signal (CES), a region of Psi with high affinity Gag binding sites, will be evaluated through electrophoretic mobility shift assays (EMSAs) and negative stain electron microscopy (EM). These techniques will determine conditions for CES-mediated Gag assembly, such as protein to RNA ratio and assembly co-factors. Cryogenic electron microscopy (cryo-EM) data collection and analysis will be performed with a suitable Gag/CES complex for atomic structure determination. The three-dimensional structure will provide the detailed Gag/Psi recognition mechanism underlying Gag assembly initiation and selective gRNA packaging. Gaining a better understanding of these processes will facilitate future development of therapeutics targeting Gag-gRNA interactions during genome packaging and virion assembly.

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STRUCTURAL CHARACTERIZATION OF AICHI VIRUS IRES USING FAB-ASSISTED RNA CRYSTALLOGRAPHY

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Internal ribosome entry site (IRES)-dependent translation enables positive-sense, single-stranded RNA viruses to hijack host cellular machinery. Picornaviridae is a large family of viruses that has evolved to contain different types of IRESs and follow different RNA structure-based mechanisms to initiate viral protein translation. Understanding the structure of these IRES elements is crucial for developing antiviral strategies targeting viral translation. This study focuses on the structural characterization of RNA domains of the type V IRES found in Aichi virus, aiming to identify features essential for its function. We prepared Aichi virus IRES RNA constructs containing key stem-loop regions for crystallization. A synthetic antibody fragment (Fab BL3-6) was employed to facilitate chaperone-assisted crystallography. The RNA constructs were prepared by replacing functionally unimportant loop sequences that allow the Fab to bind and stabilize the RNA. Following RNA synthesis and purification, binding assays confirmed high-affinity interactions between the RNA and Fab, as well as RNA purity. A concentrated RNA–Fab complex was subjected to crystallization trials, screening approximately 400 conditions via the sitting-drop vapor-diffusion method using the SPT Labtech Mosquito Xtal3 system. Multiple crystal hits appeared within one week. However, initial crystals were too small and of insufficient quality for high-resolution X-ray diffraction. Ongoing optimization focuses on improving crystal size and quality by varying parameters such as pH and precipitant concentration, employing vapor diffusion with large hanging drop plates. Achieving high-quality crystals will enable detailed structural analysis to clarify the architecture of the Aichi virus IRES domains. Structural insights from these studies are expected to advance understanding of viral translation initiation and inform the development of antiviral therapies targeting IRES-dependent mechanisms.

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FIRST PRINCIPLES INVESTIGATION OF $TI_3T_2C_2$ MXENE WITH SMALL MOLECULE ADSORBATES (T=O, F, H, OH)

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The lifetime of art is often measured in hundreds, if not thousands of years. During this lifetime, art is constantly under threat from water, pests, physical damage, etc. In today's world, the threat from small molecules such as those produced by car emissions, wood treatment processes, and various cleaners is larger than ever. The development of sensors specifically targeted towards these different small molecules, or adsorbates, is critical to the future of art preservation. MXenes, a recently emerged family of 2D materials, shows promise in this area. We will be investigating how a variety of potential adsorbates interact with different MXenes. This investigation will be performed by using computational methods along with first-principle thermodynamic analysis. Preliminary results indicate that surface atom arrangement and identity influence adsorption strength. Surface atom terminations with octahedral geometry have higher adsorption energies when compared to terminations with tetrahedral geometries. These results also reveal that adsorbates generally favor MXenes terminated with -H and -OH rather than -F and -O. These trends from first principle analysis can be used to guide the experimental design/ synthesis of surface-specific MXenes that can be used in an array of microsensors.

This work was performed as part of the Baltimore SCIART Program, which is supported by the Andrew W. Mellon Foundation under Award G-2109-11420. 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.

ROLE OF ELECTRONIC CIGARETTE VAPE ON OLFACTION AND MENTAL DISORDERS IN MICE

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Electronic cigarette (e-cigarette) usage has become a growing public health concern, affecting millions of people worldwide, especially youth and adolescent populations. E-cigarettes are marketed as attractive alternatives to nicotine in traditional cigarettes that come in many alluring flavors. However, second-hand exposure to vaping is harmful as it transports toxic chemicals, such as nicotine and heavy metals, through the olfactory system. Repeated exposure to these chemicals may damage the olfactory system, potentially contributing to the development and increasing severity of anxiety and depressive behaviors. Although adolescent e-cigarette usage and diagnoses of anxiety and depression are on the rise, a direct connection between the phenomena remains unclear. This study investigates the adverse effects of vaping on the olfactory system and mental behaviors. We utilize knockout (KO) mice that lack a crucial smell-dependent ion channel to observe the role of proper olfaction in transporting vape-derived toxicants into the brain. We will compare behaviors between the KO mice, which have limited exposure to heavy metals, and the wild-type (WT) mice, which exhibit normal olfaction. We have exposed these mice to e-cigarette vape with flavor and metal to observe how second-hand exposure to vaping may manipulate their behaviors. We will analyze these anxiety and depressive-like behaviors via a variety of behavioral assays, including the Open Field Test, Tail

Suspension Test, Elevated Plus Maze, and Sucrose Preference Test. We hypothesize that KO mice with reduced olfaction will not experience transportation of toxic chemicals from e-cigarettes, exhibiting milder anxiety and depression-like behaviors compared to WT mice. This research is especially relevant to younger people as they typically have a strong sense of smell; therefore, they are susceptible to anxiety and depressive behaviors, and addiction. As a result, young people will continue to expose themselves to the various appealing flavors of e-cigarettes, reinforcing a harmful cycle.

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EXPLORING THE FATE OF RNA IN MOLONEY MURINE LEUKEMIA VIRUS

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Retroviruses must regulate the fate of their RNA genomes to balance translation and packaging. HIV-1 accomplishes this through transcriptional start site (TSS) heterogeneity, generating two distinct RNA pools, cap 1G and cap 3G, that drive either virion packaging or protein synthesis. In contrast, Moloney Murine Leukemia Virus (MoMuLV), a simple retrovirus, transcribes its RNA solely from a single TSS (coined ^{cap}1G), yet still effectively separates these functions. This suggests that MoMuLV uses a post-transcriptional mechanism to control RNA fate. We hypothesize that MLV's genome fate is driven by a dimerization-dependent cap sequestration, and we hypothesize that cap sequestration is essential for packaging. Dimerization is proposed to induce conformational changes that sequester the 5′ cap, preventing recognition by translation initiation factors like eIF4E. To test this, we use in vitro transcription to generate MoMuLV RNA, we then use Faustovirus capping enzyme (FCE) to cap the RNA, and assess cap accessibility through electrophoretic mobility shift assays (EMSAs) with eIF4E. Because the MoMuLV leader is too large for structural analysis via NMR, we use smaller truncations that retain the native 5′ start site. We aim to find truncations that mirror the full-length RNA in dimerization and cap sequestration behavior, enabling us to validate their suitability for future NMR-based structural studies. This work aims to define a structural and behavioral mechanism by which MoMuLV regulates RNA fate in the absence of TSS heterogeneity, helping us to understand conservation of function amongst retroviruses by studying an older relative of HIV-1.

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DIFFUSION-ENHANCED T-FLASKS FOR IMPROVED CANCER CELL CULTURES

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Traditional cell culture methods struggle to replicate the 3D architecture and microenvironment of solid tumors, limiting the physiological relevance of in vitro models. When used for spheroid culture under static conditions, T-flasks often lead to oxygen and nutrient depletion in large spheroids, resulting in core necrosis and limited cell expansion. We present a novel breathable T-flask that incorporates a gas-permeable silicone membrane into the standard T-75 design, enabling efficient oxygen and carbon dioxide diffusion throughout the medium under static conditions. In our preliminary study, A375 melanoma cells were seeded at 5.0e+04 cells/mL (20 mL volume) and cultured for 3 days at 37 °C and 5% carbon dioxide. The breathable T-flask achieved a cell density of 1.82e+06 cells/mL, a five-fold increase over the 3.65e+05 cells/mL observed in standard polystyrene T-75 flasks under the same conditions. Moreover, extended cultures of up to 10 days showed minimal lactate accumulation, indicating reduced metabolic stress and stable pH. These productivity gains enhance downstream drug screening and reproducibility while reducing time, labor, and consumables. To further enhance breathability, surface micro-patterns were introduced on the gas-permeable silicone membrane to increase the effective diffusion area and improve oxygen transfer. We used a micron-resolution resin 3D printer to create molds for micro-patterned silicone, which were adapted onto T-flasks. As an added advantage of breathability, dissolved oxygen and carbon dioxide levels could be monitored continuously, non-invasively, and in real-time throughout the entire culture period. The breathable T-flask represents a cost-effective, high-performance tool for preclinical cancer research and 3D cell biology.

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INTEGRIN AIIBB3 ACTIVATION AND PLATELET TRACTION FORCES

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Platelets are blood cells responsible for stopping bleeding and reinforcing a hemostatic plug. Upon activation, platelets bind to a wound site and to each other through receptors, spread, and generate force through the actin cytoskeleton. Platelet-generated contractile forces are crucial for blood clot consolidation, yet the molecular factors that drive force generation remain poorly defined. The most prevalent receptor on the platelet surface is integrin αIIbβ3, which provides the primary mechanical linkage between the actin cytoskeleton and proteins surrounding the cell. We investigated whether the surface abundance and activation of αIIbβ3 can predict the strength

with which an individual platelet contracts. We use black dots traction-force microscopy, in which flexible (6.5 kPa) polydimethylsiloxane substrates are cast from a Sylgard 184/Sylgard 527 blend onto plasma-treated coverslips, stamped with a 2 μm-spaced grid of bovine serum albumin (BSA)-Alexa Fluor 594 dots, and coated with fibrinogen.

Washed platelets from healthy donors are incubated with the conformation-specific unconjugated monoclonal antibody MBC 370.2, seeded for 10 min, and allowed to spread for 80 minutes. After fixation, permeabilization, and phalloidin staining, imaging supplies single-cell maps of F-actin, activated αIIbβ3, and black dot deformation. Secondary antibody fluorescence yields per-cell integrin density, while MATLAB algorithms convert dot-displacement to traction-stress maps. We anticipate a broad distribution of αIIbβ3 density numbers and a corresponding range of peak stresses. Analysis is expected to reveal a positive correlation between integrin density and platelet contractility. Such findings would link receptor expression to clot mechanics and suggest quantitative αIIbβ3 measurements as functional biomarkers for bleeding or thrombotic risk. To date, I have mastered all protocols, fabricated calibrated substrates, optimized platelet seeding density, selected and titrated the antibody, and imaged αIIbβ3-labeled platelets on the black dots. Image analysis is underway to understand the effects of integrin activation on platelet traction forces.

This project was partially supported by the American Heart Association (24CDA1268959), UMBC START, and the Meyerhoff Scholars Program.

STRUCTURAL AND MECHANISTIC INSIGHTS INTO HIV-1 GAG-RNA INTERACTIONS FOR VIRAL ASSEMBLY

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The Human Immunodeficiency Virus-1 (HIV-1) pandemic, ongoing for over 40 years and affecting 40 million individuals with 1 million new diagnoses yearly, necessitates continuous development of novel therapeutics to combat drug-resistant strains that emerge against current Antiretroviral Therapies (ARTs). HIV-1 assembly is a crucial, yet incompletely understood, stage in the viral life cycle, representing a promising target for intervention. The major structural protein Gag orchestrates this process through specific interactions with an RNA region located at the 5' leader of the viral genomic RNA (also known as the core encapsidation signal or Ψ^{CES}). This protein-RNA interaction is critical for the initiation of virion assembly and the selective incorporation of the viral genome. While the roles of individual Gag domains—such as matrix (MA) for membrane targeting, capsid (CA) for Gag-Gag interactions, and nucleocapsid (NC) for RNA binding—have been studied, the precise molecular mechanisms for the Gag-Ψ^{CES} recognition governing selective RNA packaging and efficient virion assembly remain largely elusive. This study aims to elucidate the recognition mechanism of Gag with genomic RNA. The interdependent behavior between Gag assembly and RNA packaging is characterized using Ψ^{CES} and Gag constructs containing the CA and NC domains. To identify the key factors that are

required for Gag-Ψ^{CES} nucleation complex formation and check the morphology of these complexes, we utilize Electrophoretic Mobility Shift Assays (EMSAs) and negative-stain Electron Microscopy (EM). These results will guide the preparation of suitable protein/RNA samples for Cryogenic Electron Microscopy (Cryo-EM) study to determine the atomic structure of the Gag-Ψ^{CES} nucleation complex. The detailed structural information should provide mechanistic insights on the recognition between Gag and Ψ^{CES}. This study will advance our fundamental understanding of key aspects of HIV-1 virion assembly, offering opportunities for the development of novel antiviral strategies that target this essential viral process.

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INFLUENCE OF ION-EXCHANGE MEMBRANE CHARACTERISTICS AND OPERATING CONDITIONS ON NUTRIENT RECOVERY FROM POULTRY LITTER USING TUBE-IN-TUBE DONNAN DIALYSIS REACTORS

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Nutrient pollution continues to threaten the health of the Chesapeake Bay watershed. To address this challenge, we developed a novel tube-in-tube Donnan dialysis reactor that leverages electrochemical potential gradients across ion-exchange membranes to selectively recover nutrients from poultry litter slurries. The main objectives of this study were as follows: (1) measure the physicochemical properties of ion-exchange membranes; (2) develop modular tube-in-tube Donnan dialysis reactors with high membrane surface area; (3) apply those reactors for simultaneous recovery of both anionic (*e.g.*, orthophosphate) and cationic (*e.g.*, ammonium, magnesium) nutrients in poultry litter slurries; and (4) benchmark performance for different poultry litter doses and draw solution compositions. We characterized the water uptake, ion-exchange capacity, and selectivity coefficients of the membranes to facilitate first principles-based modeling of nutrient transport. In particular, these parameters were used to model nutrient removal and recovery as a function of time in the tube-in-tube Donnan dialysis reactors to calculate diffusion coefficients for each ion. Using two anion- and two cation-exchange tube-in-tube modules and 2-L draw solutions containing 270-315 mM sodium chloride, we successfully recovered 43.9% orthophosphate, 29.9% ammonium, and 31.3% magnesium from 4 L of 10 g L^{-1} poultry litter slurry. Throughput was not affected by waste volume or poultry litter dose, highlighting the robust performance of the tube-in-tube Donnan dialysis system. Overall, modular Donnan dialysis reactors have great potential to contribute to circular nutrient economies by enabling sustainable nutrient recovery from agricultural waste.

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ENABLING MALWARE EVOLUTION ANALYSIS THROUGH A CURATED DATASET AND CROSS-LANGUAGE CLONE DETECTION

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Understanding the evolution of malware families is crucial for improving detection and attribution. While prior work has focused on collecting and analyzing malware source code, existing datasets are often relatively outdated, have a small sample size, lack manual review, and lack family tags. This work introduces a curated dataset of 6,032 Windows-based malware specimens, with 2,259 C/C++ samples manually annotated with family and behavior tags. To support deeper analysis of malware lineage, we explore the use of cross-language code clone detection tools to identify semantically similar malware written in different programming languages. These tools help uncover evolutionary links between malware samples, even when code is rewritten across languages to evade detection. Our combined dataset and analysis framework enable future research on the evolution and development of malware through the detection of cross-language code reuse.

This work was supported by the DREAM lab at the University of Maryland, Baltimore County. Gabriel Terceros was also supported by the Meyerhoff Scholars Program.

MARKET RESEARCH & COMPETITIVE ANALYSIS FOR GOVTECH SOLUTIONS

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Over the past decade, permit approval processes in major U.S. cities, such as Baltimore and New York, have faced increasing delays due to outdated systems, staff shortages, and inefficient routing protocols. These issues hinder housing and business development, particularly in high-demand urban areas. Recent Gov Tech analyses indicate that AI-driven automation tools may significantly streamline the permitting process by reducing manual errors, improving code compliance checks, and enhancing real-time communication with applicants. Strategic market research was conducted using a structured approach that focused on understanding agency needs, evaluating competitive offerings, and exploring procurement pathways. The findings revealed that low-risk permits, such as residential renovations and minor mechanical upgrades, could be accelerated through AI-powered prioritization. Additionally, competitor mapping helped identify existing gaps in speed, user experience, and communication tools among existing vendors. Through the system of analyzing real-world problems of how permitting systems operate in different cities and states, this project highlights the opportunity for new tech vendors to position themselves as impactful GovTech partners by offering tools tailored to city and state workflows.

This research was supported by the Fearless Hutch Program and Meyerhoff Scholar Program at the University of Maryland, Baltimore County (UMBC).

DIFFERENCES IN CLUTCH SIZES BETWEEN SECOND YEAR AND OLDER FEMALE EASTERN BLUEBIRDS

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Eastern Bluebirds are songbirds that commonly nest in cavities in trees or human-built bird boxes throughout the eastern United States and Canada. There are many factors that play a role in the number of eggs laid in a given nest attempt. We will compare "clutch sizes" by comparing the number of eggs laid by females of different ages. Second-year birds are those that hatched the previous calendar year, while older birds hatched two or more years before. Our team banded adult Eastern Bluebirds of active nest attempts with band ID numbers as well as color bands. We determined the ages of these adults by evaluating their plumage coloration. We gathered data of nest attempts from eight study sites across Montgomery and Howard Counties. We will compare the average clutch sizes of second-year and older females and use a T-test to determine whether there is a significant difference between clutch sizes. This study will enable us to further understand the factors that influence the reproductive success of Eastern Bluebirds.

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BRAIN BREAK PREFERENCES IN CHILDREN WITH ADHD: EXPLORING GENDER DIFFERENCES AND PERCEIVED EFFECTIVENESS

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Selective sustained attention (SSA), the ability to maintain focus on relevant information while filtering distractions, is critical for academic success. Brain Breaks are a crucial strategy to support SSA, particularly in children facing attentional challenges. This study aims to identify brain break preferences in children with Attention-Deficit/Hyperactivity Disorder (ADHD) and investigate how these preferences differentiate by gender, given the known sex-based variations in ADHD symptom manifestation.

This study utilizes a secondary data analysis approach, drawing upon data from an ongoing study titled "Brain Breaks: Teacher Usage And Child Preference" conducted within the same research lab (Kumaravelan, Leroux, & Godwin, 2024). The original study, which includes elementary and middle school children (Grades 1-6; M=9.37 years; ~53% female) recruited from museums in the Mid-Atlantic US, employs a forced-choice task to assess preferences for six brain break types (cognitive engagement, mindfulness, physical activity, nature videos, coloring, mind wandering),

along with a ranking task for overall preference and perceived focus benefit. For the purpose of this analysis, data will be extracted specifically from participants whose parents have identified them as having Attention-Deficit/Hyperactivity Disorder (ADHD) within this ongoing dataset. Data will be analyzed using SPSS Statistics Version], using descriptive statistics and independent samples chi-squared tests to compare brain break preferences and perceived focusing ability by gender, with a significance level of $\alpha=0.05$. Based on existing literature on selective sustained attention and the differential manifestation of ADHD symptoms by gender, we anticipate several key findings from this study. We hypothesize that children with Attention-Deficit/Hyperactivity Disorder (ADHD) will demonstrate distinct preferences for certain types of brain breaks, with a particular emphasis on those that provide a clear shift in cognitive or physical demands. Furthermore, we predict significant gender differences in these preferences, with males potentially favoring more active or physically engaging breaks, while females may prefer more cognitively engaging or mindfulness-based activities. We also expect to identify variations in how different genders perceive the effectiveness of various brain breaks for improving focus. These anticipated findings will contribute to a more nuanced understanding of how to tailor brain break interventions to meet the specific attentional needs and preferences of children with ADHD, considering their gender. This proposed study aims to critically examine brain break preferences among children with ADHD, specifically investigating how these preferences may vary by gender. By leveraging an existing dataset and focusing on this often-underserved population, we anticipate identifying specific brain break types that are most preferred and perceived as effective by different genders. These findings are crucial for developing more personalized and effective brain break interventions, ultimately enhancing selective sustained attention and academic success for children with ADHD.

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THE LANGUAGE OF DECRIMINALIZATION: DRUG POLICY RHETORIC AND PUBLIC HEALTH IN 21ST CENTURY CANADA

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By January 2026, Canada's landmark three-year exemption from the Controlled Drugs and Substances Act may come to a close—an experiment that temporarily decriminalized possession of small amounts of heroin, fentanyl, cocaine, and methamphetamine. But what does it mean, rhetorically and ethically, to decriminalize without truly humanizing? This project analyzes the rhetoric of Canadian drug policy reform through a comparative lens with the United States, examining how language, accountability, and narrative shape public perception and state action. At stake are not semantics, but lives. Drawing from archival records, policy statements, and media coverage, this research traces the shift from punitive language—such as "addict," "crackhead," and "war on drugs"—toward people-first frameworks like "people who use drugs" and "harm reduction." It interrogates how rhetorical choices influence who we protect, who we punish, and who we pretend not to see. Decriminalization alone will never be liberation. This is a call to reimagine community, care, and justice—not through incarceration, but through healing spaces that honor life over law.

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V

Characterization of Flagella Associated Protein 417 Mutants in *Volvox carteri*

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Phototaxis in spheroidal volvocine algae, such as *Volvox carteri,* is a complex and highly coordinated behavior driven by differential ciliary beating in response to light. This behavior is essential for optimizing photosynthetic efficiency and survival in dynamic environments. Previous studies suggest that the gene *rlsA* plays a critical regulatory role in phototaxis, potentially through its influence on *FAP417*, a flagella-associated protein containing a Per-Arnt-Sim (PAS) domain. Expression analyses have shown that *FAP417* is significantly downregulated in *rlsA* mutants, which also exhibit reduced motility compared to wild-type strains, implicating a functional connection between the two genes. To investigate the role of *FAP417* in phototactic behavior, two guide RNA sequences targeting the *FAP417* coding region were designed and cloned into a *V. carteri* sgRNA expression plasmid. These constructs were transformed along with a Cas9-expressing plasmid to generate *FAP417* mutants in the wild-type *V. carteri* genetic background mutants in the population were then identified through genomic DNA extraction, followed by PCR amplification of the guide/target region and sequencing. Pure mutant clones are currently being isolated by culturing single individual spheroids for further study. Additionally, we are generating two additional guide RNA vectors that target different regions of FAP417, in an effort to generate different FAP417 mutants. To this end, two pairs of complementary oligonucleotide sequences matching the coding region of *FAP417* have been annealed and then ligated into the expression vector plasmid. These plasmids will later be transformed into *V. carteri* along with the Cas9 expression plasmid.. Once we have isolated pure FAP417 mutants, we will conduct phototaxis and motility assays to characterize the function of FAP417. Ultimately, these findings should provide new insights into the molecular regulation of cilia function and its possible genetic regulation via *rlsA*.

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W

ANALYSIS OF FMRI DATA TO CHARACTERIZE BRAIN CONNECTIVITY ACROSS SOCIOECONOMIC AND RACIAL BACKGROUNDS

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Neurological conditions such as dementia and stroke disproportionately affect African American and low socioeconomic status (SES) populations, yet remain underexplored. This study employs a data-driven framework to investigate subclinical brain health disparities by using resting-state functional magnetic resonance imaging (rs-fMRI) from 176 participants in the *Healthy Aging in Neighborhoods of Diversity Across the Life Span (HANDLS)* Scan study to examine differences in brain connectivity across groups. This sample includes High SES (n = 121), Low SES (n = 55), African American (n = 65), and White (n = 111) subjects. This work applied Independent Component Analysis (ICA) to reveal brain networks by performing blind source separation on rs-fMRI data, a process that decomposes fMRI signals into functional networks and their time courses based on the assumption of independence. For the 176-subject cohort, group-level dependencies were preserved using the Adaptive Reverse Constrained Entropy Bound Minimization (arc-EBM) algorithm, with Neuromark fMRI 1.0 templates as constraints. To assess algorithmic stability and result reproducibility, multiple independent runs were performed and analyzed using Cross-Intersymbol Interference (Cross ISI) values across the constrained components. With the most stable run (lowest Cross-ISI), Functional Network Connectivity (FNC) matrices reflecting temporal correlations among independent brain networks were generated. Results indicated 10 runs to be sufficient for reproducible results, as the distribution of Cross-ISI values was unimodal and skewed towards 0. FNC matrices indicate that Low SES individuals exhibit increased connectivity in sensorimotor and auditory networks, whereas high SES individuals show greater Default Mode connectivity. Additionally, African Americans exhibited increased connectivity in auditory, sensorimotor, and subcortical regions when compared with White participants. The next step of this work is multimodal fusion of rs-fMRI with structural MRI, and potentially other magnetic resonance imaging modalities, to analyze structure-related connectivity across groups to identify subclinical neuropathology predictive of neurological disease.

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ANALYSIS OF SURFACE TRANSFORMATIONS AND ELECTRONIC STATES OF OXYGEN, HYDROGEN, FLUORIDE, AND HYDROXIDE TERMINATED MXENES

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Museums house historically significant works of art, and they can be susceptible to a variety of harmful contaminants and exposed to a wide variety of chemical conditions. Museums require sophisticated sensors to monitor each of the different environments they contain, but they need to be small enough that they do not obstruct the artworks. Therefore, we designed adsorbent microsensors using atomically layered MXenes that could identify the pollutants that come in contact with the artwork in museums. First principles thermodynamics, paired with computational methods, were used to observe how MXenes interact with different small molecule adsorbates such as volatile organics, water, and salt. The trends from our first principles study can be used to guide the experimental synthesis of surface functionalized MXenes that can be used on an array of microsensors. This research aims to equip art museums in urban areas with more robust microsensors to prevent irreversible damage to works of art.

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COMPARING EASTERN BLUEBIRD CLUTCH SIZES BETWEEN URBAN AND RURAL LOCATIONS

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Eastern bluebirds are a species of songbird that declined during the 1900s. With the extensive use of artificial nest boxes, the population stabilized. However, the species has started to decline once more in recent decades. Bluebirds nest in both rural and urban environments. Previous studies show that the species prefers areas that have been “disturbed”, for example, choosing mowed areas as opposed to natural grasses. We set out to determine whether birds differ in their nest productivity in urban versus rural study sites. Our team is analyzing their current breeding success (number of eggs laid, babies hatched, and babies that successfully leave the nest) across study sites in Maryland, including a mix of urban and rural locations. Specifically, we are comparing how these different environments affect the maximum number of eggs produced within clutches (the number of eggs produced at one given time). We compared clutch sizes between four different parks (mostly rural) and three college campuses (more urban). We analyzed the mean clutch size across the two habitat types using a t-test. This resulted in a p-value of 0.77, meaning that it is very likely that the null hypothesis is correct (which states

there is no correlation between location and clutch size). Therefore, we found no statistically significant difference between clutch size in urban versus rural habitats.

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ROLE OF FIBROBLASTS IN REPROGRAMING MACROPHAGES FOR TUMOR CELL INVASION

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Breast cancer is one of the most diagnosed cancers in women and is a top contributor to cancer deaths in the US. While it is well-documented that tumors recruit and reprogram other cell types to aid in tumor invasion and metastasis, the mechanism by which this occurs remains unknown. Tumors weaponize normal tissue repair processes in the body, such as angiogenesis and ECM remodeling, to facilitate their growth and invasion into surrounding tissues. Under normal conditions, fibroblasts—mesenchymal cells that contribute to the formation of connective tissue by secreting collagen and other ECM proteins—and M2 macrophages—anti-inflammatory immune cells that promote tissue remodeling and angiogenesis—are key players in tissue repair following illness and/or injury. Fibroblasts and M2 macrophages are also among the cells recruited/reprogrammed by tumors. Our current hypothesis states that breast cancer tumors utilize extracellular vesicles (EVs) to reprogram normal fibroblasts into cancer-associated fibroblasts (CAFs), which in turn utilize EVs to reprogram M2 macrophages into tumor-associated macrophages (TAMs), thus increasing ECM breakdown through the upregulation of matrix metalloproteinases (MMPs) in the reprogrammed M2 macrophages. Using hepatocellular carcinoma (HCC) CAFs as our model, we performed a collagen degradation assay and an inflammation cytokine array. In the collagen degradation assay, we observed that when compared to M2 macrophages alone, M2 macrophages exposed to HCC fibroblast EVs treated with the proto-oncogene BMI-1 (M2+HCC BMI-1s) had a near-2-fold increase in collagenase activity. In the inflammation cytokine array, we observed that the M2+HCC BMI-1s have an increased expression of some cytokines associated with the upregulation of MMPs expressed in M2 macrophages. The results of these two experiments suggest that CAFs contribute to the breakdown of ECM, thereby facilitating tumor invasion.

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Z

DEEP LEARNING APPROACHES FOR CLOUD PROPERTY RETRIEVAL: COMPARING FINE-TUNING WITH DOMAIN-SPECIFIC ARCHITECTURES

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Accurate and timely retrieval of cloud properties is essential for near real-time weather forecasting. The GOES-R satellites are equipped with the ABI imager which is newer, detects 16 spectral bands, and offers higher temporal resolution than MODIS. SatVision-TOA is a foundation model trained on data from 14 MODIS spectral bands. This study aims to leverage both ABI's enhanced capabilities and the SatVision-TOA foundation model. Two different approaches were explored: fine-tuning SatVision-TOA on ABI data and training models from scratch. Models were trained to predict four cloud properties: cloud mask, phase, optical depth, and particle size. For each approach, we developed both single-task and multitask models while employing various deep learning frameworks. Finally, we evaluated model performances to assess trade-offs between foundation model adaptation and domain-specific architectures.

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