UMBC

24th Annual Summer Undergraduate Research Fest

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

August 11 to 24, 2021

https://surf.umbc.edu/

A message from the Dean

Welcome to the 2021 Summer Undergraduate Research Fest (SURF) at UMBC. Although many restrictions on campus have relaxed as it relates to COVID-19, the College of Natural and Mathematical Sciences is hosting a virtual and unique SURF event from August 11 – August 24.

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

We are delighted to be able to offer this virtual SURF event so that our students who have worked so diligently all throughout the academic year and summer will have the opportunity to participate in our distinctive annual SURF event. During the event, you will have the opportunity to view student research presentations using VoiceThread. As an attendee, you will be able to leave video, voice, or text feedback for the presenters thus affirming your personal "presence" with our students. Our presenters will be responding to your questions and interacting with you throughout the scheduled event.

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

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

Welcome to the **Virtual SURF 2021** event,

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

ACKNOWLEDGEMENTS

The Summer Undergraduate Research Fest (SURF) is truly a collaborative effort. Each year many people contribute to the success of this event. We would like to recognize the following groups and individuals for their dedication and hardwork:

We acknowledge the long-standing support of the College of Natural and Mathematical Sciences (CNMS) and Dean Dr. William R. LaCourse. Special thanks to Dawn Stoute for design support and administrative coordination.

We are grateful to the Program directors, Program coordinators and Research mentors who provided research opportunities for undergraduate students.

We are grateful for the Division of Information Technology (DoIT) who provided guidance and direction in hosting this virtual event. Special thanks to Josh Abrams, Instructional Design Specialist, for being such an invaluable resource.

We are appreciative of faculty, staff and interns for their willingness to provide assistance. Special thanks to April Henry for editing support.

We would like to recognize family, friends and peers of this year's presenters. Your continued support helps ensure the success of these future researchers.

And most of all, we would like to thank the Student Presenters for SURF 2021. This event would not be possible without you!

Ms. Justine Johnson, Associate Director, Meyerhoff Graduate Program & Executive Director, UMBC STEM BUILD

Ms. Meika Samuel, Program Specialist, UMBC STEM BUILD

MENTORS

Special thanks to the mentors who supported this year's SURF presenters. We recognize that there are many types of mentors who support the research training such as student peers, program staff, graduate students, laboratory personnel, and research scientists. While space prohibits inclusion of all the mentors who made SURF 2021 possible, we would like to acknowledge the following primary research mentors:

Dr. Michael **Betenbaugh** | Johns Hopkins University | Chemical and Biomolecular Engineering

Dr. Rachel **Brewster** | University of Maryland, Baltimore County | Biological Sciences

Dr. Stephen K. **Burley** | Rutgers, The State University of New Jersey | Chemistry and Chemical Biology

Dr. Maria **Cambraia** | University of Maryland, Baltimore County | College of Natural and Mathematical Sciences

Dr. Steven **Caruso** | University of Maryland, Baltimore County | Biological Sciences

Dr. Zewei **Chen** | Purdue University | Chemical Engineering

Dr. Zhiyuan **Chen** | University of Maryland, Baltimore County | Information Systems

Dr. Steven Andrew **Culpepper** | University of Illinois Urbana Champaign | Statistics

Dr. Matthew **Davenport** | The Rockefeller University | Neuroscience

Dr. Joshua **Dehlinger** | Towson University | Computer and Information Sciences

Dr. Pengfei **Ding** | University of Maryland, Baltimore County | Chemistry and Biochemistry

Dr. Yonghui **Ding** | Northwestern University | Biomedical Engineering

Dr. Xinmei **Dong** | University of Maryland, Baltimore County | Chemistry and Biochemistry

Dr. Phoebe **Fechtmeyer** | Johns Hopkins University | Chemical and Biomolecular Engineering

Dr. Nele **Hollmann** | University of Maryland, Baltimore County | Chemistry and Biochemistry

Dr. Michael **Hughes** | Tufts University | Computer Science

Dr. Sabeen **Ikram** | University of Maryland, Baltimore County | Biological Sciences

Dr. Vandana **Janeja** | University of Maryland, Baltimore County | Information Systems

Dr. Laundette **Jones** | University of Maryland, School of Medicine | Epidemiology and Public Health

Dr. Naima **Khan** | University of Maryland, Baltimore County | Information Systems

Dr. Andrea **Kleinsmith** | University of Maryland, Baltimore County | Information Systems

Dr. Deepak **Koirala** | University of Maryland, Baltimore County | Chemistry and Biochemistry

Dr. Minjoung **Kyoung** | University of Maryland, Baltimore County | Chemistry and Biochemistry

Dr. Erin **Lavik** | University of Maryland, Baltimore County | Chemical, Biochemical and Environmental Engineering

Dr. Steven **Leeb** | Massachusetts Institute of Technology | Electrical Engineering and Computer Science

Dr. Tara **LeGates** | University of Maryland, Baltimore County | Biological Sciences

Dr. Jeff **Leips** | University of Maryland, Baltimore County | Biological Sciences

Dr. Weihong **Lin** | University of Maryland, Baltimore County | Biological Sciences

Dr. Bing **Ma** | University of Maryland, School of Medicine | Microbiology and Immunology

Dr. Stephen **Miller** | University of Maryland, Baltimore County | Biological Sciences

Dr. Kasso **Okoudjou** | Tufts University | Mathematics

Dr. Kevin **Omland** | University of Maryland, Baltimore County | Biological Sciences

Dr. Achuth **Padmanabhan** | University of Maryland, Baltimore County | Biological Sciences

Dr. Bradford **Peercy** | University of Maryland, Baltimore County | Mathematics and Statistics

Dr. Sara **Pezeshk** | Florida International University | Architecture

Dr. Sanjay **Purushotham** | University of Maryland, Baltimore County | Information Systems

Dr. Maryam **Rahnemoonfar** | University of Maryland, Baltimore County | Information Systems

Dr. Fausto **Reyher** | Johns Hopkins University | Chemical and Biomolecular Engineering

Dr. Nirmalya **Roy** | University of Maryland, Baltimore County | Information Systems

Dr. Katherine **Seley-Radtke** | University of Maryland, Baltimore County | Chemistry and Biochemistry

Dr. Gymama **Slaughter** | Old Dominion University | Electrical and Computer Engineering

Dr. Aaron **Smith** | University of Maryland, Baltimore County | Chemistry and Biochemistry

Dr. Michael **Summers** | University of Maryland, Baltimore County and Howard Hughes Medical Institute | Chemistry & Biochemistry

Dr. Jean-Francois **Van Huele** | Brigham Young University | Physics and Astronomy

Dr. Fernando **Vonhoff** | University of Maryland, Baltimore County | Biological Sciences

Dr. Nykia **Walker** | University of Maryland, Baltimore County | Biological Sciences

Dr. Jenna **Wolfanger** | Johns Hopkins University | Chemical and Biomolecular Engineering

PARTICIPATING PROGRAMS

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

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

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

HHMI Scholars Program | *Howard Hughes Medical Institute* | https://meyerhoff.umbc.edu/

Louis Stokes Alliance for Minority Participation Research Programs | *UMBC & University System of Maryland* | https://lsamp.umbc.edu/

U-RISE (MARC) Program | *National Institute of General Medical Sciences (NIGMS) at the NIH* | https://urise.umbc.edu/

McNair Scholars | *U.S. Department of Education TRIO Program* | https://mcnair.umbc.edu/

Meyerhoff Scholars at UMBC | *Supported by a network of institutional partners and friends* | https://meyerhoff.umbc.edu/

NSF Research Experiences for Undergraduates | *National Science Foundation* | https://www.nsf.gov/crssprgm/reu/

STEM BUILD 2.0 at UMBC | *NIH Common Fund and NIGMS* | https://stembuild.umbc.edu/

SURF 2021

Presenters and Abstracts

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

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

INVESTIGATING POTENTIAL SUBSTRATE OF LYSINE METHYLTRANSFERASE SET5

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The SMYD family of proteins, defined by characteristic SET and MYND domain, have shown to be responsible for lysine methylation of target proteins. This project focuses on Set5, a member of the SMYD family of lysine methyltransferase in *Saccharomyces cerevisiae*. Set5 is the yeast ortholog to the mammalian SMYD3 that is overexpressed in cancers including breast, prostate, pancreatic, etc. This project involves testing Set5's methylation activity with a potential substrate, Vps13. Through previous literature, it has been established that Set5 can methylate histone H4K5 in the nucleus. However, fluorescence microscopy has revealed localization of Set5 in the cytoplasm as well. Set5 recognizes specific amino acid sequences on its substrates—a GGKGG sequence. We are testing a substrate with a similar sequence to that recognized by Set5. This may prove useful in understanding further substrates of Set5 within the cell. Hence, we are testing the lysine methyltransferase activity of Set5 against a putative substrate, Vps 13 using purified, recombinant proteins and performing an in-vitro methylation assay.

Special thanks to Dr. Erin Green, Sabeen Ikram and all the green lab members at the Department of Biological sciences, UMBC.

MODEL OF ELECTRIFIED ETHANE DEHYDROGENATION REACTOR

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To meet the ever-growing demand for energy consumption for the 21st century, humans must come up with new strategies and new ways to meet the energy demands, while reducing carbon emission. A way proposed to meet this demand could be attributed to efficient shale gas valorization. In the last decade, the United States' production of gas has increased exponentially. Shale gas could be found in shale formations. Shale foundations are the sedimentary rocks in the crust of the Earth. Previous research has communicated a new approach that has been taking to try to reduce CO2 emissions and resolving the low thermal conductivity for endothermic processes. For this research, we sought to build upon research already conducted on a new approach to convert shale gas into liquid gas. We will be modeling the reaction utilizing the equations for energy & mass transfer. The model will be implemented using MATLAB to evaluate the electrified steam methane reforming reactor. This study aims to compare the results that will be obtained from the MATLAB model to the results obtained from previous research.

EFFECTS OF APPL MUTATION GENE ON MALE DROSOPHILA'S RESPONSE TO ODOR

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The Appl gene encodes for a protein that is similar to one found in humans, the amyloid precursor protein APP, which has been implicated in Alzheimer's disease. We hypothesized that appl is involved in neurodevelopment, and more specifically, that a deletion of the appl gene would cause an increase in the effectiveness of the olfactory system in *Drosophila melanogaster*. Olfactory assays were run via t-mazes to study their responses with one side containing a scent and the other side containing a control, water or paraffin oil respectively. We used scents that are known to be attractive, apple cider vinegar, and repulsive, benzaldehyde, and recorded their responses. The flies used to run these assays were control W1118 and Appld mutant male flies. Regardless of concentration or scent applied, W1118 flies had higher response rates than the mutant male flies. Consequently, Appld flies put in assays with Apple cider vinegar had dramatically lower response rates in one day old flies. Conversely, Appld flies exposed to t-mazes containing benzaldehyde had lower response rates to W1118 with the lowest response rates being recorded in 4 day old flies. At lower concentrations of apple cider vinegar, Appld flies were less likely to respond positively to attractive odors. An increase in concentration of apple cider vinegar led to a response that was similar to that of the W1118 flies. For benzaldehyde at a lower concentration, Appld flies had a less negative response as compared to W118 flies except for one day old flies which showed strong repulsion. For higher concentrations both flies had a strong negative response but Appld flies still showed a decreased response. Appld flies do respond to stimulus at rates comparable to W1118 flies however the response rate is lower or the preference index is altered meaning that there is an observable change in their olfactory system during development. Future studies will focus on identifying the neuronal cell types and anatomical features that require Appl function for proper network function.

We would like to acknowledge Victor Omoniyi for his work collecting data for this project. This investigation was sponsored by the U-RISE Program at the University of Maryland, Baltimore County (UMBC), which is supported by the National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 136497"

BIOINFORMATIC ANALYSIS OF THE ACTIVE SITE DIVERSITY FOR SARS-COV-2 AND OTHER CORONAVIRUSES

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Coronaviruses have been a source of significant risk to global health. Almost four million lives have been lost to SARS-CoV-2 (COVID-19). Major efforts are ongoing to mitigate the current pandemic and future outbreaks by designing broad-spectrum drugs to target coronaviruses across species. We identified the positions of residues that participate in binding by using the 3D visualization tool Mol* (https://molstar.org/) to view known inhibitors interacting with the active site of SARS-CoV-2 proteases, two essential enzymes to virus maturation. Experimental structures from the Protein Data Bank (PDB) were used where available and additional models were generated using Robetta (https://robetta.bakerlab.org/).
Sequences for additional coronaviridae proteases were obtained from NCBI (https://blast.ncbi.nlm.nih.gov/Blast.cgi). A sequence-based comparison was performed using Clustal (https://www.ebi.ac.uk/Tools/msa/clustalo/) and a structure-based comparison was performed using Dali (http://ekhidna2.biocenter.helsinki.fi/dali/), both using SARS-CoV-2 as the template.

The preliminary results show some positions with mutations that remain within the same amino acid classification, groupings by structural, chemical, and functional similarity. Other mutations result in a different classification in that position that may have a significant impact on the active site structure and binding. We will continue to analyze these changes to identify patterns in the mutations and to identify which mutations have the most impact and are most relevant to potential viral evasion of broad-spectrum drugs.

This investigation was sponsored in part by the U-RISE Program at the University of Maryland, Baltimore County (UMBC), which is supported by the National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 136497 and the RCSB PDB, which is supported by the National Science Foundation (DBI-1832184), the US Department of Energy (DE-SC0019749), and the National Cancer Institute, National Institute of Allergy and Infectious Diseases, and National Institute of General Medical Sciences of the National Institutes of Health under grant R01GM133198

DETERMINING THE EFFECT OF PHYSIOLOGICAL SYNCHRONY ON MENTAL STATES AND PERFORMANCE DURING IN-SITU TRAINING

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The goal of this research project is to understand the effect that physiological synchrony has on a group's stress, mental load, and performance in high stakes situations. Physiological synchrony is the linking of subconscious physiological responses between humans and has previously been studied at the dyadic social interaction level. This project extends it to higher stakes situations and can be used as the foundation for future research of physiological synchrony in larger groups or more stressful situations.

The project uses in-house physiological data gathered via Empatica E4 bands from medical trainee dyads during in-situ training. The data includes the trainee's heart rate, temperature, movement, and electrodermal activity (EDA). At the end of training sessions, the trainees completed a survey on their mental states on the criteria of their stress, anxiety, and mental effort. The trained paramedic instructors who oversaw the trainees filled out a survey on the trainees' performance on the criteria of patient care, crew interaction, and timing.

To analyze the data a system was created to produce a full report based on the raw E4 data sets of two trainees and the completed surveys. The E4 data is segmented by time to cover just the period of training, then cleaned, smoothed, and normalized. To model the synchrony of the two E4 data sets an analysis of Pearson's Correlation and Directional Agreement is applied. A machine learning model was then applied to the synchrony model to determine the effects that synchrony had on the trainees' mental state and performance.

Early analysis suggests that synchrony is linked to both stress and performance. We note that higher synchrony rates are correlated to lower stress and higher performance rates. In the future, we plan to evaluate the machine learning model in different contexts which may provide deeper insights in our analysis.

This research is supported by the NSF REU Site grant CNS-2050999

EXAMINING FACTORS THAT MOTIVATE LEARNING USING CONDITIONED PLACE PREFERENCE AND AVERSION PARADIGMS

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The pursuit of rewarding stimuli and aversion to threatening stimuli are evolutionarily conserved behaviors critical to the survival of organisms. The ability of organisms to associate these motivating stimuli with contextual cues within their environment is necessary to anticipate and effectively respond in the future. This contextual learning is necessary for survival, as it aids in the search for rewards such as food or avoiding harm like predation. Altered motivation, deficits in learning, and disrupted processing of motivating stimuli are all associated with psychiatric disorders. However, the mechanisms by which contextual learning occurs remain elusive. By conditioning mice to associate different environments with a positive rewarding stimulus (social interaction) or an aversive stimulus (physical restraint), we hope to develop a model of contextual based learning so we can study the neuronal mechanisms that mediate this behavior. We utilized a three-chamber arena with two chambers distinguished by visual cues and one middle corridor. Mice were conditioned to associate visual cues in one chamber with a rewarding stimulus, social interaction. We found that the mice spent more time in this interaction-associated chamber, also known as a conditioned place preference (CPP). Additionally, we found that mice only displayed CPP after being housed in isolation, suggesting they must be deprived of social interaction in order to seek a social reward. A separate group of mice were conditioned in the three-chamber arena to associate visual cues with an aversive stimulus, physical restraint. We found that the mice spent less time with the restraint-associated cue, also known as conditioned place aversion (CPA). These data suggest that restraint and social reward following brief isolation can elicit contextual-based learning. In the future, we aim to dissect the neuronal circuitry in the hippocampus that underlies contextual-based reward learning.

This investigation was sponsored by the U-RISE Program at the University of Maryland, Baltimore County (UMBC), which is supported by the National Institute of General Medical Sciences, National Institutes of Health (NIGMS/NIH) under National Research Service Award T34 GM 136497. This research was supported in part by a grant to UMBC from the Howard Hughes Medical Institute through the HHMI Adaptation Project. This research was supported in part by a grant to UMBC from the NIDA through the EDUCATE Scholar Program.

Synthesis of Flex-Remdesivir Analogues as Potential Antiviral Therapeutics

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Nucleoside analogues remain prevalent within modern medicine today as effective therapeutics against numerous diseases. Some are used as anticancer therapeutics, meant to target leukemias and melanomas; where others act as antivirals, targeting numerous viruses such as Hepatitis, HIV, Ebola, Dengue, and Yellow Fever viruses just to name a few.

Currently, efforts are underway to develop antiviral therapeutics against Severe Acute Respiratory Syndrome-Coronavirus-2 (SARS-CoV-2), the cause of the COVID-19 pandemic. One nucleotide that has shown potential is Remdesivir (RDV). RDV has shown antiviral activity against Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS), and was approved for emergency use against SARS-CoV-2.

The Seley-Radtke lab has long focused on the development of nucleoside analogues that possess flexible purine-base moieties, called Fleximers. This flexibility is advantageous, as it allows for the nucleoside to adapt conformations that are unavailable to the parent nucleoside, and remain active against resistance variants, as well as to show potent activity. This was shown with the fleximer of acyclovir, which has displayed activity against Ebola, SARS, MERS, Dengue, and yellow fever, unlike the parent compound, which only exhibits activity against Herpes Simplex Virus. This project seeks to synthesize a series of Flex-RDV analogues to explore their antiviral activity against SARS-CoV-2 and other viruses.

CHARLIE: A CHATBOT THAT ANALYZES DAILY ACTIVITY TO DETERMINE EFFICIENT DIETS AND FITNESS PLANS

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Managing a work-life balance has always been challenging especially after the recent trend of working from home, which has made maintaining one's fitness and diet regime strenuous. Failing to adhere to a fitness and diet plan has shown to cause long-term effects on a person's health including obesity and shortened lifespans. Currently, people plan their fitness and diet plans around their schedule, however, it is very challenging to keep up with and users tend to give up these plans due to lack of time and planning. To help with better planning for a fitness and diet regime, we propose "CHARLIE", a chatbot that works around a user's schedule to intelligently recommend diets and fitness goals based on their calendar. In this paper, we leverage NLP techniques to derive the context of the request from the chatbot, combine them with the user's calendar/schedule, map it with calories burnt data, and recommend a fitness and diet plan based on the Recipes 1M+ dataset. We evaluate "CHARLIE" on a real calendar/schedule dataset collected from a population of students as well as a dataset that tracks the number of calories a user loses doing certain activities. The chatbot will use a recommender system that will recommend the user certain meals and fitness activities based on the amount of time they have left in their day and the number of calories they lose. The research covers background on fitness and nutritional needs, data sets, data collection, and the making of the algorithm to determine the best diet and fitness for the user.

This research is supported by the NSF REU Site grant CNS-2050999.

Developing a fully synthetic non-degradable hydrogel with tunable mechanical properties to guide neural stem cell migration and differentiation

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A disruption of neurogenesis in the neurovascular niche (NVN) in the adult brain is linked to early signs of Alzheimer's disease (AD) and other neurodegenerative diseases. A reproducible in vitro model of the human NVN would allow for high throughput screening of diseased phenotypes for therapeutic intervention. As an alternative to traditional 3D printing, members of the Lavik Lab have developed a screen-printing method that is more sensitive, customizable, and cost-effective than other current bio-printing techniques. We first attempt to apply this screen-printing method to a customizable hydrogel based patterned coculture of endothelial cells and neural stem cells (NSC) to generate a murine model of the NVN. Previously, a synthetic poly (ethylene glycol) (PEG) based non-degradable hydrogel scaffold was first designed to behave as a biomimetic extracellular matrix to facilitate the cross-talk in the co-culture, but significantly limited the migration of cells with in the hydrogel due to the non-degradable nature. However, NSC attachment and migration was observed on top of the hydrogel indicating its potential use for reproducible NSC expansion in 2D. Optimizing the gel conditions is essential for the project. The aim is to examine different ratios of the PEG based hydrogels and measure the distance of the NSCs migration, proliferation, and differentiation. By controlling the mechanical properties of the hydrogel, we plan to maintain the stem state of the NPCs while increasing proliferation relative to standard NSC cultures.

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

PROGNOSTIC BIOMARKERS OF DISEASE SEVERITY IN ELDERLY COVID-19 PATIENTS

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Coronavirus disease 2019 (COVID-19) is the cause of the greatest pandemic in a century. One of the factors that make this virus a public health emergency is the varying, unpredictable level of severity observed in patients with otherwise similar health backgrounds. The gut microbiota is known to play an important role in disease progression and regulating immune response to illness. While often the gut microbiota has been evaluated as changing in response to an illness, in this project we proposed that the microbiota drives the progression and severity of COVID-19. Eighty-seven stool, oral, and nasal samples from thirty-five COVID-19 patients aged twenty-six to eighty-five years old that visited the University of Maryland Medical Center between January and March of 2021 were collected and sequenced using whole community shotgun metagenomic sequencing on Ilumina HiSeq 4000 platform. We correlate clinical factors including age, gender, ICU status, survival status, use of ventilator, and BMI to gut microbiome. MetaPhlAn and StrainPhlAn were used to profile the composition of the samples at a high taxonomic resolution. Phyloseq R package was employed to evaluate community alpha and beta diversity and LEfSe was used to determine the significantly different features, or biomarkers correlated with clinical features. COVID-19 viral load at each body site was determined using Bowtie package. The results of this study do indicate a significant difference in the makeup of the microbiome at these three sites. The stool samples had significantly more bacteria of the bifidobacterium, anaerococcus, and lachnoclostridum genera. Patients with severe cases, indicated by being on a ventilator or in the ICU, had a significantly lower Shannon diversity score. While this study does not address a temporal relationship between the significant differences in the microbiome as they relate to severity, the presence of these differences indicate that further study of this area is warranted.

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

CELL MEMBRANE FORCE BALANCE MATHEMATICAL MODEL

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Cell migration is the progression of uni or multicellular units in response to chemical gradients or signals. It is an integral part of daily cellular functions; moreover, development and pathologies in migration can lead to discoveries in cancer metastasis. This research focuses on movement of a cluster of migratory border cells through nurse cells in the egg chambers of drosophila melanogaster, also known as the fruit fly. Due to its short life span, this organism is often used in research.The lab aims to answer: How does one represent membrane tension interactions in a mathematical model for individual cells? How can the lab combine these membrane forces with forces of migration and stochasticity to affect cell migration in a mathematical model for clustered border cells? Furthermore, what parameters are needed to correctly simulate cell migration?

The research utilizes MATLAB to simulate the egg chamber, border cells, and migratory cells. Specifically, it focuses on the dynamic interactions between cell membranes and the forces that arise from them, including the adhesive, repulsive, and membrane spring-like forces. The migratory force is also used, which stems from a chemical gradient that sends signals to the migratory cells. These cells respond to these forces from other cells and the egg chamber boundary. In MATLAB, cell boundaries are coded around centers to represent the cell membrane and egg chamber perimeter. The previous model implementation only includes the cell centers and interactions between neighboring cells without well-defined cell boundaries. Within this model, parameters, equations, and coefficients are manipulated to more accurately depict cell migration with more detailed boundaries.

While research is ongoing, the research team has been able to progress in an understanding of the model and further incorporation of more complexities, striving to achieve a simulation that accurately mirrors real life observation of the migratory cells.

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EXPRESSING THE DYNAMICS OF A QUANTUM SZILARD ENGINE USING QUANTUM INFORMATION

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Quantum information offers the possibility of advancing computation, communication, and cryptography. Quantum circuits combine qubits and quantum gates to perform informational tasks. Quantum resources allow quantum computers to perform certain tasks faster than classical computers.

Szilard expanded on the concept of Maxwell's demon to design a single-temperature engine that challenges the second law of thermodynamics by extracting work from information. In doing so, Szilard brought together thermodynamics, information theory, and computation. We are interested in the quantum version of the Szilard engine, which we model, following Zurek and others (ref.) as an infinite rigid box. By partitioning the box, measuring occupancy, and moving the boundaries of the box, we reproduce the steps of the Szilard engine as a quantum mechanical problem.

We analyze the dependence of the solutions on the parameters of the boxes. Additionally, we encode the information contained in the properties of the solution into qubits on a quantum circuit to illustrate how quantum computation can handle fundamental questions in quantum thermodynamics.

Thank you, Dr. Van Huele, for mentoring me this summer, the rest of the BYU REU mentors for their guidance, the Meyerhoff Scholars Program, Louis Stokes Alliances for Minority Participation, and Western Alliance to Expand Student Opportunities (WAESO). This research was supported by NSF grant #2051129 and WAESO.

THE AGE-SPECIFIC EFFECT OF *COFILIN2* GENE EXPRESSION ON BACTERIAL CLEARANCE ABILITY IN *DROSOPHILA MELANOGASTER.*

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As organisms age, especially humans, components of the innate immune response begin to decline and susceptibility to infection is higher. In the adult fruit fly, *Drosophila melanogaster*, these mechanisms of immunosenescence are observed and driven by the expression of certain genes like *Cofilin2*. *Cofilin2* is a tissue-specific gene that can either be expressed or knocked-down, and a previous study by Felix et al (2014) found that high *Cofilin2* expression was correlated with increased clearance of infection in the blood cells of older flies. This raises a compelling question with regards to whether *Cofilin2* expression promotes increased bacterial clearance ability in flies. If *Cofilin2* expression is involved in bacterial clearance, we hypothesize that by down-regulating its expression, there should be a reduction in the ability for older flies to clear an infection. The approach is to knock-down *Cofilin2* expression in hemocytes from both young (1 week old) and old (5 weeks old) F1 flies, and then infect them with an E. coli solution. This will help us determine whether the absence of *Cofilin2* expression will result in lower clearance ability. To achieve this knock-down, we have established genotypic crosses that will use the Gal4/UAS system, which contains a hemocyte-specific hemolectin driver and RNA interference. If the outcome of this experiment affirms the hypothesis, another trial will be conducted for validation. Essentially, if the knock-down of *Cofilin2* expression shows an age-specific decline in bacterial clearance ability, we will confirm this finding by setting crosses with young and old flies of two other lines (65055/*Cofilin2* & attp2/control). If this result is identical to the former, we can conclude that *Cofilin2* expression knock-down reduces bacterial clearance ability. If our results do not support our hypothesis, we could infer that another gene may be a more suitable target than *Cofilin2*.

This research was partially funded by the USM LSAMP program, supported by the NSF LSAMP Award #1619676.

THE AGE-SPECIFIC EFFECT OF *COFILIN2* GENE EXPRESSION ON BACTERIAL CLEARANCE ABILITY IN *DROSOPHILA MELANOGASTER.*

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This research was partially funded by the USM LSAMP program, supported by the NSF LSAMP Award #1619676.

INVESTIGATING MECHANISTIC DETAILS OF SACCHAROMYCES CEREVISIAE ARGINYL-TRNA TRANSFERASE 1 (SCATE1) ACTIVE AND REGULATORY SITES USING SITE-DIRECTED MUTAGENESIS

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Arginyl-tRNA transferase 1 (ATE1), a eukaryotic enzyme that arginylates cellular proteins, is an essential regulator of eukaryotic homeostasis and is involved in processes such as embryogenesis, aging, cell migration, muscle contraction, and stress. Despite its importance, the structure, mechanism of action, and even the regulation of ATE1 have yet to be elucidated. The objective of this work is to determine essential conserved residues that are involved in substrate recognition and enzymatic regulation. To search for highly conserved residues in ATE1, we performed a multiple sequence alignment (MSA) of over 1500 ATE1s across the eukaryotic domain. Our analyses revealed two elements of ATE1s that may be important in its function. First, our MSAs revealed highly conserved CC and CxxC motifs that may be essential for coordinating an [Fe-S] cluster, which we have recently demonstrated to be oxygen sensitive and to regulate arginylation efficacy. Additionally, our alignment revealed a highly conserved His residue that may be involved in recognition of negatively charged substrates; we have mapped the location of this conserved residue to a structural homologous site present in functional analogs that are present in bacteria. To test the importance of these residues, we have performed site-directed mutagenesis to generate Cys and His variants of *Saccharomyces cerevisiae* ATE1 (*Sc*ATE1) in order to test how these residues regulate [Fe-S] cluster binding and substrate recognition, respectively. This work thus sheds light onto the regulatory and active sites of this essential post-translational modifier, which could be leveraged to develop therapeutics to target this enzyme.

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DIVIDING TIGHT FRAMES

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A frame is a spanning set of N vectors in dimension $\mathbf{C}^d$ where N≥d. A tight frame is a type of frame that is similar to an orthonormal basis, but without linear independence. If every vector in a tight frame is a unit vector, we call that a Finite Unit Norm Tight Frame (FUN-TF). This project focuses on dividing FUNTFs obtained from the DFT matrix into smaller FUNTFs in dimension d = 3. The NxN Discrete Fourier Transform (DFT) matrix is the unitary matrix whose entries are powers of the Nth root of unity. FUNTFs are created by taking d rows in the DFT matrix and putting the renormalized column vectors into a new matrix U. The columns of the matrix U form a FUN-TF of N vectors in d dimension. Our goal is to classify which FUNTF's for $\mathbf{C}^3$ formed from the DFT can be divided into smaller FUNTFs for $\mathbf{C}^3$, then expanding that concept for other scenarios.

My project focused on the 6x6 matrix and the N=2p matrix where p is prime. First, we determined the potential size possible for the new FUN-TF to be. Then we wrote code that tested every combination of rows and columns that form a matrix of that size. In the 6x6 case, the only size option was 3x3. I found there are only 5 prime tight frames that can be formed in the 6x6 matrix. We also explore the applications to Fuglede's Conjecture, and the general N=2p case.

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CHARACTERIZING OF THE PROTEIN-PROTEIN, PROTEIN-RNA, AND PROTEIN-MEMBRANE, INTERACTIONS THAT NUCLEATE HIV-1 VIRAL ASSEMBLY

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Human immunodeficiency virus type 1 (HIV-1) is the causative agent of acquired immunodeficiency syndrome (AIDS), leading to one million deaths annually. Although antiretroviral therapies are available, drug resistance prompts the development of novel therapeutic strategies. Our research focuses on studying the molecular mechanisms that direct the assembly of HIV-1 virions, which may facilitate the discovery of new drug targets.

The key player of HIV-1 assembly is its major structural protein Gag, which consists of multiple domains including matrix (MA), capsid (CA), and nucleocapsid (NC). The NC domain recognizes the RNA packaging signals (Ψ) located at the viral genomic RNA (gRNA); the MA domain directs the Gag/gRNA complex to the assembly site at the plasma membrane, while the CA domain mediates Gag-Gag interactions and facilitates the formation of the spherical Gag shell, which encapsidates the gRNA and eventually buds off the plasma membrane. Although the individual NC-Ψ, CA-CA, and MA-membrane interactions have been extensively studied, how does the full-length Gag exerts these interactions and their affects on each other remain poorly understood. It has been proposed that binding to Ψ promotes the self-association of Gag, and Gag oligomerization further facilitates membrane targeting, which in turn stabilizes the Gag/gRNA complex and thus contributes to the selective packaging of gRNA. We seek to test these hypotheses using a system containing a Gag variant (MA through NC), in-vitro transcribed Ψ RNA, and liposome (as the mimetic of plasma membrane). The protein-RNA, protein-membrane, and protein-protein interactions that nucleate HIV-1 assembly will be characterized using Electrophoretic Mobility Shift Assay (EMSA), solution nuclear magnetic resonance (NMR), and chemical crosslinking experiments. This study will help further our understanding of the mechanisms in which protein, RNA, and membrane interact and contribute to HIV-1 assembly, which may lead to the development of novel therapeutic targets.

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MODIFYING A GENOME SCALE MODEL TO SIMULATE VIRAL INFECTION OF HEK-293 CELLS

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The rise in popularity and interest in the use of Adeno-Associated Viruses(AAV) for Gene-Therapy applications has made clear a need for an efficient host cell and environment that facilitates easy and scalable production of AAV vectors. Previous studies identified HEK-293 cells as an effective and practical host for AAV cultivation. In this paper we will improve an existing AAV model to explore optimization strategies for viral production in HEK-293 cells. We used a previously developed genome scale model called Recon 2.2 which was constrained to reflect the HEK-293 cell and added reactions for viral production. Using flux balance analysis (FBA), we are able to determine AAV capsid protein and GFP DNA production under constraints of the helper proteins, GFP protein, and the rep proteins. As the objective of the cell shifts from cell growth to virus production, expectedly there is viral flux increases. However, with the current constraints, at about 60% growth optimization the cell changes metabolic pathways; below 60% while virus production still increases it does so at a much slower rate. This is due to a shift in metabolic priority, as more of the cell's energy and resources are being focused to increase viral production rather than to grow and reproduce; this is known as resource reallocation. Our present model can be used as a tool for other research to examine metabolic pathways given a set of observed constraints. This will allow a team to get more out of their results by analyzing the impact of their observations. With the help of our research, we will be able to enhance viral production within HEK-293 cells that will further research in the field of gene therapy.

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EXAMINING THE POTENTIAL FOR CHLAMYDOMONAS REINHARDTII AS AN ALTERNATIVE PLATFORM TO EXPRESS INSULIN

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Insulin is a high-demand therapeutic that is vital for those who struggle with type 1 diabetes. Its main function is to permit cells to take up glucose from the bloodstream. The purpose of this study is to explore the potential of the green alga *Chlamydomonas reinhardtti* as an alternative platform to produce insulin, and eventually other proteins of value to the medical and scientific communities. *C. reinhardtii* could be a cost-effective production organism for insulin because it can be grown without external carbon sources. To test this idea, we used Gibson Assembly to generate *C. reinhardtii* expression plasmids for secreted and non-secreted versions of insulin. The plasmids contain a synthetic gene insert of human pro-insulin, connected by a self-cleaving peptide sequence (FMDVA 2A). We are in the process of transforming these plasmids into *C. reinhardtti* cells by electroporation, and we will perform western blot analysis to determine insulin levels in transformants. If we succeed and find detectable protein expression we will then explore improving expression and scaling up our production and applying these expression methods to other proteins and algae. One ogttpotential algal production organism would be *Chlorella vulgaris,* which is better suited for large-scale production.

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INVESTIGATING SUGAR CONCENTRATION AND CONSUMPTION IN THE FUNGAL SPECIES RHODOTORULA GLUTINIS

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Rhodotorula glutinis has become a topic of interest in the scientific community because of its ability to produce lipids and carotenoids, which have many agricultural, medical, and industrial uses. Therefore, scientists have been looking at ways to optimize the production of lipids and carotenoids including sugar consumption. However, several sugars have not been thoroughly studied and there is insufficient research comparing different sugar substrates. In order to investigate the sugar consumption of R. glutinis, MATLAB and COBRA Toolbox were used to model the consumption of different D-Glucose, D-Xylose, L-Arabinose, Sucrose, D-Galactose, Maltose, D-Trehalose, and D-Fructose concentrations. D-Trehalose had the best sugar growth rate, closely followed by Sucrose and Maltose. D-Xylose and L-Arabinose had the worst growth rate with D-Glucose, D-Galactose, and D-Fructose better by a minor margin.

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IDENTIFYING NOVEL DEUBIQUITINATING ENZYMES THAT REGULATE MUTANT p53 LEVELS IN OVARIAN CANCER CELLS

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Ovarian cancer is the most lethal gynecologic cancer and the 5th leading cause of cancer-associated deaths among women in the United States. Lack of early-stage biomarkers and ineffective therapeutics have resulted in the disappointing 5-year survival rate (~30%) among patients. These data highlight the urgent need to identify new therapeutic targets and develop more effective ovarian cancer treatment options.

The tumor suppressor gene *p53* is mutated in over 90% of ovarian cancers. Mutant *p53* (mutp53) promotes tumor progression, drug resistance, and suppresses anti-tumor immune response. Interestingly, mutp53 depletion results in cancer cell death and tumor regression. Therefore, strategies that achieve selective mutp53 depletion have immense therapeutic potential. Previous studies revealed that deubiquitinating enzymes (DUBs), specifically USP15, play a role in mediating mutp53 turnover. We hypothesize that other DUBs will also regulate mutp53 and serve as potential therapeutic targets. My goal is to identify novel DUBs that regulate mutp53 levels in ovarian cancer cells, through two aims.

In Aim 1, I will establish a library of plasmids expressing each DUB. The ~100 human DUBs will be cloned with a N-terminal 6xHis tag into pcDNA3.1-IRES-GFP. Primers will be designed, and polymerase chain reaction (PCR) amplification conditions will be optimized. Clean PCR products will be inserted into the vector using a modified Gibson Assembly protocol. In aim 2, these constructs will be transfected into ovarian cancer cells expressing either wildtype or mutp53. Transfected cells will be processed and analyzed by Western Blot to determine the effect of each DUB on mutant and wild-type p53 levels. The blot is probed sequentially using a 6xHis and p53 antibody to determine the success of transfection and the impact on p53 levels respectively. Overall, my work will identify novel selective regulators of mutp53 in ovarian cancer cells that can serve as potential therapeutic targets.

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FABRICATION OF A GLUCOSE SENSING LASER-INDUCED GRAPHENE BIOSENSOR

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Laser direct writing techniques have been demonstrated as a facile alternative approach for the development of graphene-based electronics. Here this facile, chemical-free, and direct patterning of graphene was used to fabricate a wearable glucose biosensor. The LIG was patterned on polyimide film on glass substrate using CO2 and exhibited three-dimensional macroporous flake-like structures. The LIG electrode material was functionalized with gold and platinum nanoparticles to detect sweat glucose non-invasively. Electrochemical characterization was used to analyze the performance of LIG-based glucose biosensor. This robust wearable biosensor showed good sensitivity and selectivity towards glucose. The performance of this LIG biosensor was enhanced by the synergistic electrocatalytic activity between graphene and the nanoparticles. The morphological characterization was conducted via scanning electron microscopy. The LIG electrode upon surface modification, the graphene flakes were masked with the nanoparticles. The LIG wearable glucose biosensor has the potential for the development point-of-care clinical tool to diagnose diseases.

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MODERN RESPONSIVE WEB APPLICATION

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Software engineering is the process of developing software for use, such as web applications, mobile applications, and games, with the main objectives being to design, develop, maintain, and improve the software. Designing and developing a web application that will work across different form factors is one of the key roles in making what will be useful and interactive for clients.

The goal of this research is to build a modern, responsive web application. In order to accomplish this, an understanding of the software engineering process, scientific knowledge, and web application pipeline and tooling process was required. The approach taken in this research was to design, develop and iterate web application prototypes using modern web development technologies. To do so, research was conducted to research existing web applications for software engineering (e.g.,https://thesoftwaredesignlab.github.io/) research labs to derive site requirements and architecture. Finally, an understanding of how software development teams utilize software repositories was necessary.

The outcome of this research resulted in an application of the software engineering development lifecycle to design, develop and deploy a prototype web application. Furthermore, while the research did result in a responsive website, a strong understanding of the use of Git from the command line, software development IDE for web applications, use of modern UI/UX design styles to a web application, and the understanding of web application development using HTML, CSS, and JavaScript was achieved. These factors also play a consistent role in what makes a web application functional.

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ASSESSING THE FUNCTION OF HUMAN AMYLOID PRECURSOR PROTEIN AND ITS FLY HOMOLOG APP-LIKE IN DROSOPHILA

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Alzheimer's disease (AD) is a neurodegenerative disease that eventually leads to a loss of basic human brain function. The disease manifests itself through the destruction of nerve cells. The amyloid beta fragment (Aβ42) that results from the cleavage of the amyloid precursor protein (APP), forms plaques in the brain which causes cell death. The fruit fly Drosophila melanogaster has a protein APP-like (APPL) that shares a high degree of conservation to human APP. Therefore, we plan to use powerful genetic tools and tractable neuroanatomy available in Drosophila to study human APP and its homolog APPL. We will test APPL mutants, as well as flies expressing transgenes of different variants of APPL and human APP. A flight behavioral assay will be used to analyze the effects of the expression of the different transgenes in flies that are 2 days (2d), 10 days (10d), and 30 days old (30d). To test the flies, a drop test will be conducted which consists of dropping flies in a graduated cylinder and recording their landing distance. The measured flight performance will be a reading of the function of the motor network including identified flight motoneurons. The observations that will be recorded will help provide better understanding of the function of APP and APPL.

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MULTI-DOMAIN VULNERABILITY ASSESMENT

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The development of the network of systems and applications brings many advantages to the world but also carries risk. One of the biggest risks is the presence of vulnerabilities in software and hardware components due to an application weakness, which could be a design defect or an implementation error. This opens a window to third parties that could take advantage of this weakness and attack the system's core functionalities and often cause irreversible damage.

Due to the presence of many vulnerabilities, it is often hard to process them manually and also identify potential relationships between vulnerabilities. To address this problem, we propose an approach that has the ability to process thousands of vulnerabilities from different reporting platforms to associate and connect them. To start this association process, the description of vulnerabilities is preprocessed to include the terminologies of different system components. This allows us to evaluate the importance of each word through TF (Term Frequency) and TF- IDF (Term Frequency - Inverse Document Frequency). We use these matrices to elaborate association rules and show how certain vulnerabilities are connected to each other.

Our results are depicted through precision, maximum lift and the number of rules obtained from the dataset. In order to conclude whether or not the rules are related to each other, we use Likert scales (1-5) by a domain expert to signify if the relationship is high or low. Furthermore, when the program was tested on a large number of vulnerabilities using the RSS feed from the National Vulnerability Database (NVD), one day 200 were found and the other day 400 were found. This result verifies that the program, each time it is run, updates the information efficiently through the RSS feed.

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VQA FOR POST-DISASTER DAMAGE ASSESSMENT

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In the wake of the recent Surfside condominium collapse and deadly flooding in Western Europe in addition to the growing threat of natural disasters from climate change, the need for post-disaster analysis tools has been exemplified. Unmanned aerial vehicles (UAVs) have the ability to safely survey the aftermath of disasters and when combined with Visual Question Answering (VQA) systems can return real-time answers to image-related questions that can assist in cleanup and analysis.

The creation of such a VQA system requires training a neural network on images of disaster aftermath. Our current dataset uses high resolution (4000 x 3000) photos taken by a UAV of wreckage after Hurricane Harvey, specifically at Fort Bend County, TX and other impacted areas. The dataset also consists of some footage taken by emergency responders, which makes it effective for training the model in real-world situations. This project builds off the previous work performed by the Bina Lab researchers on VQA models for both Hurricane Michael and Harvey, specifically the three baselines for feature combination.

Questions for the VQA model can be categorized as either *Simple Counting* (e.g. How many buildings are in the image?), *Complex Counting* (e.g. How many buildings are *non-flooded* in this image?), *Condition* (e.g. What is the condition of the image?) which returns either flooded or non-flooded, or *Yes/No* (e.g. Is the entire road flooded?).

The VQA model is made accessible to test via a published site. Users can enter any questions and either select from a sample of existing disaster photos or upload their own which the model will evaluate and output the most likely responses.

THE CORRELATION BETWEEN HOLIN PROTEINS AND THE PHAGE MORPHOLOGICAL TYPE

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Holins are proteins that are used in the breakdown of a cell membrane, also known as lysis. They are programmed to start the process of lysis, during the last step of the lytic cycle, where newly made phages are released. One way to classify a holin gene is by the number of times that it crosses the cell membrane. Based on this number, the holin proteins are then put into specific classes such as class I or class III, with three and one transmembrane domains (TMDs), respectively.

In this study we are investigating the correlation between the structure of the holin gene and the phage morphotype. We hypothesized that the structure of the holin protein strongly correlates with the phage morphotype.

Phages were selected from both the UMBC archived class data (2014 - 2019) and Phamerator. Phamerator maps were used to determine the presence of holin genes and obtain the protein sequences on each selected phage. The TOPCONS program was used to analyze the holin protein sequences from the selected phages to identify the number of TMD's. The data collected allowed us to look at how many times the holin protein passed through the bacterial membrane.

This data showed that from the 18 phages investigated, approximately 83% were classified as Class II holins, while the remainder were Class III. Surprisingly, all the phages with holins with two TMDs were classified as myoviruses while the phages with one TMD were classified as podoviruses in the UMBC archived class data (2014-2019).

In the future, we would like to repeat the analysis with a larger sample size and investigate other types of proteins such as the endolysin in a phage, to analyze its purpose and how the structure correlates with the structure of the holin gene.

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SpecTextor: Dense Automated Text Generator for Sports News Articles

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A dense text generator learns the semantic knowledge and visual features of each frame of a video and maps them to describe the video's most relevant subjects and events. Although dense text generation has been widely explored for untrimmed videos to generate associated texts across various domains, generating dense captions in the sports domain to supplement journalistic works without relying on commentators and experts still needs much investigation.

This paper proposes an end-to-end automated text-generator that learns the semantic features from untrimmed videos of sports games and generates associated descriptive texts. The proposed approach considers the video as a sequence of frames and uses a sequential generation of words to develop detailed textual descriptions. After splitting videos into frames, we use a pre-trained VGG-16 model for feature extraction and encoding the video frames. With these encoded frames, we posit an LSTM based attention-decoder architecture that leverages self-attention mechanisms to map the semantic features with relevant textual descriptions to generate the explanation of the game. Because developing a comprehensive description of the game warrants training on a set of dense time-stamped captions, we leverage the ActivityNet Captions dataset. In addition, we evaluate the proposed framework on both the ActivityNet Captions dataset and the Microsoft Video Description Dataset (MSVD), a dataset of shorter generalized video-caption pairs, to showcase the generalizability and scalability of ***SpecTextor***.

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INVESTIGATING THE DIFFERENCE BETWEEN TWO ENDOLYSINS ENCODED BY PHAGES IN CLUSTER BF

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Endolysins are enzymes that are used in the lytic cycle to break down a bacterial cell wall from the inside. They can also be used to treat bacterial infections by acting as antibacterial agents. While investigating phages, we found that two different endolysins were encoded by cluster BF phages. When using Phamerator, one endolysin was found only in cluster BF (Endolysin 1) while another was found in multiple clusters (Endolysin 2). We then created phylogenetic trees using the protein sequences of Endolysin 1, Endolysin 2, and both combined using the program VICTOR. The purpose of our research was to investigate the relationship between Endolysin 1 and Endolysin 2 found in cluster BF.

Our original hypothesis predicted that the reason for this was due to the endolysin genes evolving in different ways. Therefore, we investigated the difference between the clusters present that could be identified through phylogenetic trees. The tree indicated that the two proteins shared many similarities. To further evaluate this, we performed an alignment of both endolysin proteins using the HHpred program. From this we noticed that while Endolysins 1 and 2 appeared to be similar from the beginning of the sequence, they began to present more differences at the end of the sequence.

Additionally, the phylogenetic tree also suggested that Endolysin 2 is older than Endolysin 1 as it is present in multiple clusters unlike Endolysin 1, which is only found in some cluster BF phages. From this we can infer that Endolysin 1 likely diverged from the older Endolysin 2. For future studies, we would like to investigate the differences in the two genes and the reason why Endolysin 1 only appears in cluster BF while Endolysin 2 appears in multiple clusters.

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THE EFFECT OF CaMKI ON THE SOCIABILITY OF DROSOPHILA

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Autism Spectrum Disorder (ASD) is a debilitating neurobehavioral syndrome resulting from neurological dysfunction of the central nervous system, and in the process of synaptic refinement, leading to disordered development. Unfortunately, its exact cause is poorly understood.

In a preliminary genetic screen of genes that are suspected of being involved in Autism, there is evidence that CaMK1, a gene directly involved in developmental synaptic refinement, is involved in the onset of ASD. It is known that abalated CaMK1 results in brain mutations in fruit flies. This study analyzes if these mutations cause physical social behavioral abnormalities, a hallmark of human ASD, by studying the gene in Drosophila melanogaster.

The method used in this study involved repeat trials of exposing either CaMK1 mutated flies or wildtype flies to a Sylgard plate that was either empty, or had a false social setup of ten flies that were glued to a single corner. The location of the experimental flies relative to the false flies were tracked by an imaging system that imaged the plates in regular intervals over a total of two hours. The images were then analyzed in the ImageJ software to determine the relationship found between wildtype and CaMK1 mutated flies. The results showed that there was a weak, yet present, evidence of impairment of social behavior in CaMK1 mutated flies.

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ELUCIDATING INTERACTIONS BETWEEN THE HIV-1 RRE AND THE VIRAL PROTEINS REV AND GAG

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The human immunodeficiency virus (HIV) is a retrovirus that can cause acquired immunodeficiency syndrome (AIDS). Although multiple pharmaceutical options exist to control HIV and maintain undetectable viral load, medication compliance, feasibility of medicine acquisition, and rapid viral mutations present ongoing issues in treating HIV. Thus, future drug targets require an increased biochemical and structural understanding of viral components and processes. To help facilitate the export of the viral genome from a host cell's nucleus to the cytoplasm, the HIV-1 genome codes for Rev, an RNA-binding protein translated in the early phases of viral replication. Later, Rev re-enters the nucleus mediated by its nuclear localization sequence and binds to the Rev Response Element (RRE) found on unspliced viral RNAs. This complex is then exported into the cytoplasm where the RNA is available for packaging and translation, which is essential for viral replication. The RRE has also been shown to interact with the nucleocapsid domain of the larger structural viral protein Gag. However, the binding sites for Rev and Gag on the RRE have only been partially determined, and the biological importance of the Gag interaction is unclear. Therefore, this project seeks to provide a detailed characterization of the interactions between the RRE, Rev, and Gag. We have initially focused on an RRE fragment from Stem I, a peptide containing the RNA-binding arginine rich motif (ARM) of Rev, and the nucleocapsid domain of Gag. We will describe construct design, sample preparation, and characterization by isothermal titration calorimetry and electrophoretic mobility shift assays. The full-length molecules form oligomeric complexes which will not be recapitulated by the fragments used here. Therefore we are also developing protocols to express and purify Rev and Gag constructs to enable future research into the native complexes, providing greater insight into their role in the HIV life cycle.

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REVERSING METABOLIC ARREST: DOWNREGULATION AND RETURN OF Na+-K+ ATPase (NKA)

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Oxygen plays a critical role in ATP synthesis during oxidative phosphorylation; thus it is not surprising that ischemic damage (i.e. stroke due to lack of oxygen) is a leading cause of death in the United States. By contrast, zebrafish embryos can survive up to fifty hours in a zero-oxygen (anoxic) environment, as they are hypoxia-tolerant. The embryos can withstand these harsh conditions by entering into a state of hypometabolism characterized by reversible metabolic arrest of ATP-demanding processes, such as Na^+-K^+ ATPase (NKA). The Brewster Lab has previously shown that the N-myc Downstream Regulated Gene (NDRG) mediates this transition, although exact molecular mechanisms remain unknown. My project specifically addresses the reversibility of zebrafish NKA downregulation to preserve cellular energy in anoxia. I hypothesize that if downregulation is an adaptive process, then normoxic (normal oxygen) NKA levels should be restored upon re-oxygenation, possibly via recycling of NKA stored in intracellular vesicles and/or via *de novo* protein synthesis. I tested this hypothesis by exposing 24-hour old zebrafish embryos to eighteen hours of anoxia (a duration of anoxia sufficient to cause severe downregulation of NKA), gradually reoxygenating them, then immunolabeling at five timepoints post-anoxia to observe if and when NKA levels in the plasma membrane return to their normoxic value. After three rounds of experiment and analysis, there appears to be a significant increase in NKA levels in the hours following anoxia. In the future, I plan on performing a proximity ligation assay to investigate whether NDRG1 and NKA interact during this reversal process, which would suggest that NDRG1 mediates both the down- and up-regulation of NKA in response to environmental fluctuations in oxygen. We anticipate that these studies will further our understanding of hypometabolism as a protective adaptation with great human therapeutic potential.

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A RESOURCE EFFICIENT QUANTIZED FEDERATED LEARNING MODEL FOR BRAIN TUMOR SEGMENTATION

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The proliferation of smart computing devices paves the way of applying artificial intelligence in almost all sectors of digital civilization but raises issues like personal data breaches. Preserving privacy of the data has become a crucial aspect especially in the medical domain, where sensitive information about the patients and even the institutions should be kept confidential. Federated learning is being investigated as a promising solution to this challenge but has some drawbacks itself. One of them is the issue of higher communication and computation cost when the model becomes large and complex because the model must be sent back and forth between sever and clients while training. The combination of model compression techniques with federated learning algorithms can be a viable approach to subdue this problem. Considering this research scope, in this work, we present a resource-efficient federated learning scheme implemented considering medical domain application. We have chosen 'Brain Tumor Segmentation (BraTS)' dataset published in 2020 for our experiments because of its comprehensiveness, and its well-suited for our motivation. We utilize U-net as our base deep model and develop a ternary quantized version of it to reduce computation complexity. We also present a benchmark study while running our proposed model at the client-side based on required power, memory, and inference time as a measurement of computation efficiency.

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DEVELOPING *CHLAMYDOMONAS REINHARDTII* AS A PRODUCTION PLATFORM FOR THE ENZYME CHITINASE

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The enzyme chitinase has remarkable potential for biotechnological applications in fields ranging from medicine to biofuels. To make chitinase more industrially available, it is necessary to develop efficient platforms for producing the enzyme. The goal of this project is to develop the green alga *Chlamydomonas reinhardtii* (Chlamydomonas) as a production platform for chitinase by genetically engineering it to over-express the enzyme. To achieve this, we are using basic gene-cloning methods to generate two expression vectors. One vector will result in chitinase production in the cytoplasm; the second vector will result in the production of the enzyme with a secretion tag that triggers export out of the cell. We are attempting to express a family 18 chitinase gene coding sequence from the bacterium *Vibrio alginolyticus*. Via PCR, we amplified the chitinase gene to contain terminal restriction sites, and we then subcloned the fragments into the vector pBluescript to facilitate excision and ligation into the final expression vectors. We sequenced several candidate ligation products to identify one secretion and one non-secretion vector that contain the correct chitinase sequence. We are now subcloning the chitinase gene fragments into the final expression vectors. Once both expression vectors are assembled they will be transformed into Chlamydomonas. Western blot analysis will be used to determine how much chitinase the transformants produce and chitinase enzyme assays will be done to determine the activity of the recombinant protein. Additional tests will determine the efficiencies of the non-secretion and secretion chitinase vectors for the further development of Chlamydomonas as an industrial platform for producing chitinase.

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COMPARISON OF THE PRESENCE OF NG2 EXPRESSING PERICYTES IN BREAST TUMOR TISSUE VS NON-TUMOR TISSUE

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Pericytes are a type of perivascular cell that line the walls of capillaries. Their previous function was thought to only be blood vessel stabilization, but new studies have identified that pericytes can act as stem cells, regulate other stem cells such as hematopoietic stem cells, display immune functions, are present in tumor microenvironment (TME) and play a role in tumor angiogenesis. As part of the TME, pericytes may contribute to tumor growth and metastasis. The role of pericytes in breast cancer is of growing research interest. Our research question is focused on determining if there is a higher presence of pericytes in tissue extracted from mouse models of breast cancer compared to tissue from a non-cancerous model.

Pericytes are identified by their anatomical location and specific molecular markers. Although no molecular cell surface marker exclusively for pericytes has been discovered, there are a few that are commonly present on pericytes and are used for their detection. We will be using Neuron-glial 2 (NG2), a chondroitin sulfate proteoglycan as our cell surface marker for pericyte detection. NG2 is encoded by the Chondroitin Sulfate Proteoglycan 4 (CSPG4) gene. We hypothesize that NG2 expressing pericytes play a tumorigenic role in the breast tumor microenvironment.

To test our hypothesis, we used tissue sections from four different mouse models. Using direct immunofluorescence staining and confocal microscopy, we captured images of the tissue slides and confirmed the presence of the target antigen, NG2. The digital fluorescence intensity of the cells was measured using an image processing software called Fiji and average intensity was calculated in excel. Increased NG2 expression suggests that pericytes may aid in tumor development and future steps include targeting pericytes in the TME. Targeting pericytes in the TME could give us insight into what factors secreted by pericytes support tumor growth.

SEMANTIC SEGMENTATION OF HEAD AND NECK TUMORS IN PET/CT IMAGES

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Cancer is the second leading cause of death in the United States. Within this category, head and neck cancers comprise approximately 4% of malignancies annually. Although the statistic may seem somewhat insignificant, it has only a 32% 5-year survival rate for brain tumors**.** For treatments pertaining to tumors in the brain, there is limited room for error which ultimately presents the challenge of accurately identifying where exactly the tumor exists. Thus, recent work has explored the use of medical imaging such as Positron Emission Tomography (PET) and Computed Tomography (CT) scans for non-invasive detection of brain tumors. The goal of this research project is to segment the location of the head and neck tumors in the PET and CT scans by developing deep learning based semantic segmentation methods. Recent segmentation approaches are designed to work with one modality while our goal is to use both PET and CT scans for accurate tumor image segmentation. We are conducting our experiments on a dataset provided by the MICCAI HECKTOR 2021 challenge which consists of CT, PET scans, clinical data for 224 patients across 5 different centers. Our exploratory data analysis on this dataset has shown that slice and data distribution varies across centers. Empirical results by using Otsu's algorithm, a threshold based segmentation approach, on CT scan segmentation achieves a Dice Similarity Coefficient (DSC) score of 0.20. We are now developing 2D and 3D UNet based deep learning models for achieving accurate segmentation from both CT and PET scan images. We are also building a Docker image pipeline for end-to-end training and testing of various segmentation models. The semantic segmentation results of this project will be used for prediction of progression free survival time.

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4D METABOLIC NETWORKS IN LIVING CELLS

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In this research project, the long-term goal is to understand how metabolic pathways are orchestrated within live mammalian cells; specifically, glucose metabolism within the cytoplasm. It is known that enzymes in glycolysis and gluconeogenesis assemble multi-enzyme compartments, which were discovered and named "glucosomes" in prior studies. To elucidate how glucosomes play a role in 4-dimensional metabolic networks, their quantitative characterizations in living cells are essential.

In this research conducted under the BUILD program, we focused on determining how specific metabolic enzymes/networks are visualized in living cells and how 3-dimensional cellular images can be analyzed to extract quantitative data. For live cell visualization, we researched how fluorescent proteins are used to achieve highest specificity among various ways of labeling enzymes in living cells, and fluorescence microscopic techniques provide great sensitivity. Next, we tested multiple methodologies for quantitative image analysis. Images captured under a fluorescent microscope were segmented and quantitative data was extracted. We tested three tools in the program ImageJ on images of intracellular mitochondria labeled with TOM20 proteins, skeletal muscles labeled with TNN1 proteins, and yeast cells labeled with RAD5 proteins from the Allen Institute for Cell Science. For TNN1, Weka Segmentation and Probability Map were the best methods applied. We next used the Threshold method, which was used for RAD5. TOM20 was segmented by Weka Segmentation Probability Map and Edge-Based segmentation. Each method made the image analyses more manageable, allowing "hidden patterns" to become viewable, such as the localization trends of these multienzyme pathways in relation to other cellular processes.

Quantitative image analysis helps researchers understand how complicated metabolic pathways are dynamically interconnected in live cells. By assessing available tools and interpolating them, this research provides a selection of segmentation solutions to reveal quantitative 3D characteristics of glucosomes.

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CONNECTIONS BETWEEN MOTOR ACTIVATED BRAIN REGIONS IN THE TELENCEPHALON OF MALE ZEBRA FINCH

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Vocal learning is the ability to imitate heard sounds, a behavior which forms a core module of spoken language in humans. This complex learned behavior has independently evolved in 8 non- human vertebrate lineages, the most widely studied being the oscine songbirds such as the Australian zebra finch (*Taeniopygia guttata*) used here. Within the brains of zebra finch, vocal learning is produced by a series of interconnected telencephalic song nuclei including the robust nucleus of the arcopallium (RA) which projects to the motor neurons controlling the vocal organ, and HVC (proper name) which projects to RA. Recent work from our group has shown that the brain regions immediately surrounding these song structures are active during general locomotion, specifically hopping on a wheel, similar to activity in the song system during singing. These motor activated regions are the lateral intermediate arcopallium surrounding RA and the dorsolateral and posterolateral nidopallium (DLN, PLN) surrounding HVC. These motor activated surroundings have strikingly similar gene expression profiles to their respective song system components, leading us to believe this motor system is the evolutionary precursor to the song system. Here we replicated these motor activation patterns by measuring protein expression of the immediate early gene c-Fos using immunohistochemistry following either song or locomotor behavior. We went on to partially resolve the connections between these motor activated brain regions by injecting dextran amine based neuronal tracers into DLN which provide both retrograde and anterograde labeling. Our results indicate that PLN sends axons into DLN projects into the lateral intermediate arcopallium (LAI) immediately adjacent to RA. These results mirror the connectivity of the song system, where HVC receives inputs from several smaller nidopallial regions and sends a robust projection to RA.

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DIFFERENTIATING GENETIC MANIPULATIONS IN DROSOPHILA TO INVESTIGATE SYNAPTIC REFINEMENT

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Drosophila have developed nociceptive (pain sensing) neurons that are located in the ventral nerve cord (VNC). They are associated with other sensory neurons such as the mechanosensory neurons (pressure sensors). The nociceptive neurons are connected to interneurons called basins 2 and 4 which help build a stereotypic axon ladder structure in the central nervous system present in wildtype larvae. Meanwhile, the mechanosensory neurons are connected to basins 1 through 4. The concept in question revolves around the mechanism of synapse refinement. Synapse refinement is the reorganization of synaptic partners during early stages of nervous system development. It determines which neuron connections are vital for optimal anatomical and behavioral function. The known connections between nociceptive cells and basin interneurons will be manipulated to be used as an anatomical model to study synaptic refinement. We hypothesize that nociceptive neurons would make connections with basins 1 and 3 as well as 2 and 4 in early development stages, to test whether synaptic refinement mechanism regulates the precise connectivity with basins 2 and 4. We will utilize genetic tools and mutations in molecules that are involved in the mechanism of synapse refinement. Furthermore, the anatomical views of the nociceptive ladder-like structure will change depending on the genetic mutation used. The main method to conduct the experiment is micro-dissection of larvae to expose the nervous system and image their neuroanatomy using a confocal microscope. The larvae have been introduced to a genetic tool called the green fluorescent protein (GFP) to highlight the ladder-like structure of the VNC. The analysis can be constructed by comparing the control and mutated anatomical structures of the VNC. To conclude, the anatomical model being used is a good way to represent this experiment. In the future this model will be utilized to test a variety of mutations and their possible involvement in autism. To confirm such a relation, social behavior experiments can be done to strengthen the connection between the identified genes, synapse refinement and autism.

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UNSEEN TRAVEL MODE IDENTIFICATION USING TRANSFER LEARNING

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Travel mode detection has been targeted in few literatures in the past. Several geometrical and machine learning based algorithms have been designed to detect the mode of transportation. However, existing models require significant amounts of labeled trajectory data. of different transportation modes. From the perspective of transportation, some trajectory features can be similar for a set of transportation modes while it differs from other types of transportation modes. For example, the rate of changing direction for walking and biking is not as straightforward as for car, bus, or taxi. According to our study in this area, there is not much research found exploring the use of transfer learning in this regard. In this project, we are experimenting on the feasibility of using pretrained models on GPS trajectory data to predict unseen transportation modes of trajectories collected from smartphone GPS applications. We use Microsoft Geolife dataset, and we focus on a subset of the data which comprises 73 users with labeled data. We also collected trajectory data from different locations using a smartphone application named 'Strava' which provides similar data variables as of Geo-life dataset, but with different frequency. We incorporated all the features mentioned in the previous literature and tested several shallow learning algorithms (i.e. Random Forest, SVM, Decision Tree) on the labeled geo-life dataset where Random Forest (96.9% accuracy) outperforms other algorithms. We also implemented a supervised CNN-based network to detect the transportation modes.

We plan to use initial layers of the model to extract general features from our collected dataset with strava and detect the unseen travel modes (i.e. segway) that are not present in the geo-life dataset.

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STUDY OF DOMAIN ADAPTATION OPPORTUNITIES IN RESPIRATORY SYMPTOM DETECTION USING EARABLES

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Machine learning algorithms allow for the rapid detection and classification of physiological health signals. In this project, we study the ability of earables to detect and classify respiratory symptoms with established models and to test the models' scalability with unseen data. Earable devices like Bluetooth earpieces are commonplace and offer a convenient platform to detect respiratory sounds for health monitoring. However, there is often a lack of labeled data for various contexts to train these models. This motivates us to investigate and incorporate domain adaptation techniques within our respiratory symptom detection models to take advantage of large datasets available in similar domains.

We tested four traditional machine learning models: Random Forest, Decision Trees, SVM, and MLP, as well as our own deep learning model for respiratory symptoms detection from in-house audio data collected from four participants using Esense Earables and public datasets. The machine learning models were trained and tested on the collected dataset and were adjusted to achieve optimal performance to establish a baseline. Then, they were tested on the public datasets to determine the models' performance on unseen data. Comparing the performances allows us to study the potential opportunities for domain adaptation.

Our deep learning model takes in sound spectrograms and processes them through a CNN utilizing Pytorch. The model was trained and tested on the collected dataset to determine its performance. Moreover, the model was adapted to include a domain adaptation component and the resulting testing performance was compared to the previous results. This allows us to see if domain adaptation provides any benefits.

In conclusion, our experiments allow us to study domain adaptation opportunities in respiratory symptom detection using earables. This could ease the developments of human vital signs detection models and could allow for greater ease in medical analysis using convenient earables.

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CORRELATION BETWEEN MYOVIRUS TAIL CONTRACTION & INFECTION OF *BACILLUS ANTHRACIS* DELTA-STERNE

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Anthrax is a deadly disease caused by the bacterium *Bacillus anthracis*. It can spread through inhalation, creating infectious spores on livestock and humans. It is treated with antibiotics, but this treatment is becoming less effective due to its inability to evolve with the bacteria. An alternative approach is the use of bacteriophages (phages), which are viruses able to infect and kill bacteria while adapting to the bacteria's growing resistance.

Phages exist in different morphotypes, including myoviruses which are characterized by a contractile tail that is inserted into the bacterial host. We investigated the relationship between the amount of contraction in the tail observed and its ability to infect the host *B. anthracis* delta-Sterne. We hypothesized that the higher contraction percentage in the tail of the phage, the more likely it is to infect *B. anthracis*.

To test this, we analyzed archived wet-lab data collected by UMBC phage hunters from 2015-2017. The percentage of contraction was determined for 72 phages using the measurements of their uncontracted and contracted tails. A histogram was created to compare the distributions of contraction percentage among phages infecting *B. anthracis* delta-Sterne and those that cannot.

We found the tails of myoviruses able to infect *B. anthracis* delta-Sterne contracted an average (±SD) of 41.16% ± 13.15 from their original tail length while myoviruses unable to infect *B. anthracis* delta-Sterne contracted an average of 38.53% ± 10.59. Contrary to our hypothesis, analysis by t-test showed there is no significant difference between the tail contraction of phages that infected *B. anthracis* delta-Sterne and those that did not. In the future, we could strengthen our conclusion by increasing the sample size of bacteriophages as well as investigating the correlation between phage clustering and infection of *B. anthracis* delta-Sterne.

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THE EFFECTS OF MODIFIED CARBON CONCENTRATING MECHANISM GENES ON CHLAMYDOMONAS GROWTH RATE

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There is a substantial need for sustainable alternatives to crude oil. One possible alternative is biofuels, in particular algal biofuels. However, algal biofuel is currently very expensive to produce, with a cost of about $33 per gallon. The purpose of our study is to increase the growth rate of algae to decrease production costs. We are attempting to increase growth by overexpressing enzymes of the carbon concentrating mechanism (CCM) in the model green alga C. reinhardtii (Chlamydomonas). We are focusing on carbonic anhydrases CAH 1 and CAH 3 and carbonate transporters LCI 1 and NAR 1.2. Our strategy involves coupling expression of these genes to that of the Ble antibiotic resistance protein via a viral self-cleaving 2a peptide gene sequence. Our vectors were constructed using Gibson assembly to combine gene-synthesized fragments with a preexisting Chlamydomonas expression vector. We are currently transforming these vectors into Chlamydomonas, and antibiotic resistant lines will be tested by western blot for expression of the CCM genes. A growth analysis will be performed to determine whether any transformants have an increased growth rate. If successful, this strategy could be applied to production algae and lead to a decrease in production costs of algal biofuel, making it a viable option as a sustainable fuel source.

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ANALYSIS OF FRACTIONAL DATA WITH CLUSTERING METHODS

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K means clustering is a way to make inferences about data by partitioning a set of observations into a cluster. Using these clustering methods, we can figure out why there is group success which leads to better insight for diagnostic interventions. Our goal in this project is to use k-means clustering, incorporate restricted class models to improve diagnostic methods of studying the types of addition and subtraction of fractions with varying usages of whole numbers, proper and improper fractions. The methods we used in this project were k-means clustering of "items fractions" dataset to analyze various clusters and centroids, restricted latent class model, and generating simulated data from the latent class model. Lastly, we used Monte Carlo simulation to evaluate k-means in the context of latent class models. What we learned is that using k-means clustering we can figure out why a cluster has the problems that they have. For future work doing a simulation study on the accuracy of different methods in selecting the ideal number of clusters.

DETERMINING CLOTTING STRENGTH OF HEMOSTATIC NANOPARTICLE THROUGH A COAGULATION ASSAY

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Trauma and injury that lead to severe bleeding are among the leading causes of death globally if the bleeding in particular goes untreated, or at the very least, unclotted. The rate at which blood clots can be an imperative factor in the aid of patients receiving first aid care, though at the moment there are not many methods to increase clotting rate for internally bleeding patients. Fortunately, hemostatic nanoparticles are quickly developing into an effective therapeutic and drug delivery system for these clinically-imposed blood clotting scenarios. As of now, this material still requires additional fine-tuning and understanding to ensure they are as reliable as conceivably possible, especially concerning the characteristics of the polymeric vehicle transporting them, the reliability of the on-demand release of encapsulated materials, and the consequential hemostatic strength. The general nanocapsule structure is constructed of a polyurethane core covered with PEG corona arms on the surface. This is later conjugated with peptide GRGDS, which is well known for displaying coagulant factors due to the presence of the RGD moiety. A coagulation assay was performed using a polyurethane-based capsule conjugated with hemostatic peptide GRGDS and PEG peptide in order to test the hemostatic effect observed in a polyurethane model through both a quantitative and qualitative lens. Platelets were forced into an anticoagulant state via heparin until the time of clotting analysis where ADP was introduced to activate the platelets, which is when hemostatic nanoparticles can properly attach to platelets for coagulation. Beyond seeing hemostatic reactions occurring during the assay readings, our objectives are to ultimately test the feasibility of anticoagulants being used in the assay to determine if clotting will dissipate when reactively triggered.

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RECREATING THE NEUROVASCULAR NICHE USING HYDROGELS

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The neurovascular niche (NVN) is a region of the brain linked to multiple developmental disorders including autism spectrum disorder. The NVN plays a crucial role in maintaining neural stem cells and regulating neurogenesis. Currently, our knowledge of the human NVN is limited to the interpretation of data from non-human mammals. Recreating the human neural niche in vitro is an important step forward in elucidating the mechanisms involved in a number of neurological disorders. In pursuit of developing the NVN we have developed a partially degradable library of poly(ethylene glycol) (PEG) based hydrogels combined with poly-l-lysine (PLL) and poly-allylamine (PAA) that are biocompatible and have been proven to support the maturation -of rat endothelial cells, an important component of our NVN. To start this experiment, varied gel ratios have been made to test cell viability. We tested 75% PLL vs PAA by free amines with 1:4 PEG to amines and 75% PLL vs PAA by amines with 1:8 PEG to amines. The data indicates that the rat endothelial cells were alive and forming networks in the hydrogels, an indication of maturing endothelial cells. This will mean that we are able to move into the next phase of recreating the neural niche. This will involve replicating this study with human endothelial cells and screen printing patterned hydrogels with the endothelial cells. .

Funded by USM LSAMP Program

POPULATION SURVEY OF INVASIVE NEST PREDATORS IN THE ANDROS ISLAND COMPLEX IN THE BAHAMAS

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Rats are invasive introduced species on many tropical islands, and they are known to be nest predators. The black rat (*Rattus rattus*) is a documented threat for many songbirds in the Caribbean. The Bahama Oriole, *Icterus northropi*, is a critically endangered songbird species endemic to the Andros Island complex in the Bahamas. In the 1990s, the oriole went locally extinct on the island of Abaco. Currently very little is known about predators of this species, but nest predation may be a factor that is attributing to the decline of the Bahama Oriole. This survey will use peanut butter wax baits called WaxTags to evaluate whether rats are present in different habitats on Andros. Preliminary studies found little evidence of a rat population in native pine forest, which would be very good news for the conservation of the Bahama Oriole.

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CHARACTERIZING THE ACTIVITY OF THE UAS-roGFP-GRX1 SENSOR IN *DROSOPHILA MELANOGASTER*

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In most biochemical pathways, oxygen is the final electron acceptor. In some cases, the electrons that are transferred to oxygen are unpaired, making them very reactive. This produces reactive oxidative species (ROS) which can damage DNA and other components of the cell.
Cells can produce antioxidants which can clear ROS to reduce the potential destruction it can cause. The gene expression system GAL4/UAS encodes GAL4, which is a transcription factor that binds directly to the UAS (upstream activator sequence) to activate gene expression of the chosen sequence. For this project, The UAS/GAL4 system has been utilized to introduce a fluorescent roGFP sensor that indicates levels of redox activity in the model organism *Drosophila melanogaster*. At this point in time, the purpose of these experiments is to characterize the behavior of the roGFP sensor in Drosophila by examining its response to oxidants and reductants. Diathiothreitol (DTT) is a reducing agent that will donate electrons and diamide (DA) is an oxidizing agent that accepts electrons. Therefore, it is hypothesized that administering these chemicals separately on different groups of brains should have an opposite effect on the fluorescence of the roGFP probe. It is thought that these groups of brains will also show a different level of fluorescence compared to control brains as well. Imaging will be conducted using a 405- and 488-mm probe for fluorescent activity in Drosophila brains. It will confirm the functionality of the roGFP sensor as well as its response to oxidative stress via added oxidants and reductants in the form of DTT and DA. In future experiments, we would also like to determine if the expression of appl protein correlates with changes in the roGFP sensor. We would also like to explore potential therapeutics for Alzheimer's disease induced by oxidative stress.

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COMPARISON OF SELECTION PRESSURES IN THE ARDA GENE WITH GENOME IN BF PHAGES

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ArdA antirestriction proteins are found in various prokaryotes and bacteriophages and function as protectors of DNA. During an infection event, these proteins protect phage DNA by disabling endonucleases in the host. The purpose of this investigation is to examine the evolution of the *ard*A gene compared to the entire genome of the BF phages.

The *ard*A gene was only found in bacteriophages within the cluster BF. The program OneClick was used to produce a phylogenetic tree depicting how the *ard*A gene sequences from cluster BF are related. A genome based phylogeny was produced using the web program VICTOR to analyze how the phage genomes are related. The two trees produced were compared to analyze differences in selection pressures in both the gene and genome. We hypothesized that if the two trees were different then that would mean the gene is being selected for under different pressures than the phages themselves leading to the conclusion that the gene does not hold an important role within this cluster of phages.

Contrary to what was expected, we found that there was no significant selection occurring. Based on phylogenetic analysis, it is evident that if there is any selection occurring for the *ardA* gene, it was under the same pressures present for the genome. It should be noted that the bootstrap values for the genome based phylogenetic analysis were marginal. Additional methods of examining the genomic relationship of these phages would be appropriate. Nevertheless, it can still be reasonably assumed that the *ard*A gene is well conserved in comparison to the phages within cluster BF likely indicating it plays an important role in these phages. Future investigations would include analyzing different antirestriction proteins found in other phage clusters to determine if there is any significance in how they experience selection.

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OPTIMIZING IN-VITRO CAPPING REACTION TO UNDERSTAND THE INTERACTIONS BETWEEN eIF4E AND THE HIV-1 RNA GENOME

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The human immunodeficiency virus (HIV) affects approximately 38 million individuals worldwide and is the determinant for the acquired immunodeficiency syndrome (AIDS). Patients with HIV type-1 (HIV-1) are treated with a drug cocktail to target various steps of the viral replication cycle, but high mutation rates lead to drug resistance. Therefore, we study highly conserved regions of the viral life cycle to ultimately develop better treatments for patients. Specifically, we study the 5′-Leader of the viral RNA genome, which exists as a monomer and dimer. Our group investigates how the cellular cap binding protein, eIF4E, interacts with the monomeric and dimeric conformations as eIF4E interacts with 5′-cap-RNAs to initiate translation. Recently, our laboratory determined eIF4E interacts to the exposed 5′-cap of the monomer; whereas in the dimer, the 5′-cap is sequestered between the TAR and polyA hairpins, contributing to the dimer being packaged and not translated.

To study the interaction between eIF4E and 5′-cap-RNAs, we perform in-vitro capping reactions. Currently, our in-vitro capping reaction produces 70% capped RNAs, while the remaining 30% exists as monophosphate RNAs that are unable to be capped. It is difficult to purify capped RNAs due impurities in our enzyme purification and the presence of exonucleases that degrade RNAs. This contributes to the challenges of capping larger RNA constructs. To improve capping efficiency, we tested different concentrations of GTP and S-adenosylmethionine (SAM). We also explored the use of additional $MgCl_2$ and performed time-dependent capping experiments. By altering the $MgCl_2$ concentration and introducing incubation periods between reagents, we obtained 100% capping for small RNA constructs. Through gel mobility shift assays, we confirm our RNAs are 100% capped by testing their binding interactions with eIF4E. Given these findings, we aim to purify larger constructs of the 5′-leader to ultimately understand the structural interactions between eIF4E and the HIV-1 5′-leader.

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PACKAGING VIRAL RNA TO FORM THE HIV-1 VIRION: THE COMPLEX INTERACTION BETWEEN THE GAG PROTEIN AND THE CORE ENCAPSIDATION SIGNAL

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HIV-1 is a reverse transcriptase retrovirus that binds to receptors on CD4 cells of the immune system. After fusion to the host cell membrane, two single stranded RNAs along with several viral proteins are released into the cell. By reverse transcription and integration of viral genome into the host cell genome, the cell machinery becomes hijacked to produce components needed for viral replication. Over time, this can leave the body with low white blood cell count leading to Acquired Immunodeficiency Syndrome (AIDs).

Essential to the replication of HIV-1 is binding between the genomic RNA (gRNA) and the group specific antigen (gag) polyprotein. Gag consists of four structured domains: the matrix (MA), the N-terminal (CA_{ntd}) and C-terminal capsid (CA_{ctd}), and the nucleocapsid domain (NC). The latter domain is responsible for interaction with the core encapsidation signal (CES) of the gRNA, facilitated by two high affinity RNA-binding zinc-finger motifs. Selective binding of the zinc fingers to the viral RNA is crucial for the assembly of the immature virion.

Our research focuses on the structural determination of the Gag-RNA complex, specifically the interaction and assembly of the gag NC domain with the core encapsidation signal (CES), the minimal necessary sequence in the 5' UTR of the viral RNA, that is needed for efficient packaging. To gain structural information, we aim to use a hybrid approach of crystallography, electron microscopy, and Nuclear Magnetic Resonance Spectroscopy, coupled with biochemical assays like Isothermal Calorimetry and gel shift interaction studies. By determining the structure of the Gag-RNA binding complex, the synthesis of drugs that disrupt this interaction can be employed to assist in stopping replication of HIV-1.

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CHARACTERIZING THE ROLE OF A PATIENT DERIVED MUTATION ON HIV-1 PACKAGING

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After decades of research, antiretroviral therapies (ARTs) exist to treat HIV, yet there is still no cure. This is largely because cells latently infected with the virus remain in patients despite adherence to treatment. Our collaborators at Johns Hopkins identified a patient with a detectable viral load in spite of treatment, which was linked to a single clone that is replication incompetent. This residual viremia only increases through clonal expansion of infected T cells. Understanding viral replication in this patient will help us characterize viral dynamics in latently infected cells. The viral clone was found to contain a 22-nucleotide deletion in the 5' leader (5'- L), the untranslated region of HIV RNA that regulates processes such as packaging and translation. We hypothesized that this 22-nucleotide deletion remodels 5'-L structure, leading to a packaging defect. To study packaging, we must characterize the dimeric structure for this mutant. The wildtype dimeric 5'-L contains a stacking interaction between two hairpins, sequestering the 5'-guanosine methyl cap. Recent work has shown that when stacking is disrupted, packaging is inhibited and molecules involved in translational machinery, such as eIF4E, can bind to the exposed 5'-guanosine methyl cap. To investigate the effect of the 22-nt deletion on stacking, we required capped RNA. Capping large RNAs *in vitro* is non-trivial; therefore, we began with a small RNA (~35 nucleotides) with increased magnesium to produce 100% capped RNA. We mimicked these conditions to cap larger RNAs (>300 nucleotides). To evaluate capping efficiency, we are optimizing a novel method where DNA is annealed to the 5'L, disrupting stacking and exposing the 5'-guanosine cap. A gel shift assay using eIF4E will then be used to assess capping efficiency. 100% capped RNA can then be evaluated for the stacking interaction, comparing the mutant and our wildtype 5'-L.

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THE EFFECT DIFFERENT LIGHT HAS ON THE PRODUCTION OF SUCROSE

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The rising demand for food, fossil fuel, and other products by humans is an increasing concern in countries all around the globe. This is where our project comes in. The purpose of this study is to investigate various lights and the roles they play in the growth and production of sugar (sucrose). Using Flux balance Analysis, MATLAB, and CobraToolbox, this study analyzed the 11 different

light conditions of the *Anabaena* genome-scale model iDN1004 and measured the results that were found against a similar study found in a sample code that was used. The light composition of the 11 different lights was used, to determine which lights were to be used for faster Sucrose production and which lights were to be used for a slower and more efficient Sucrose production. This study definitely answers the question regarding the roles lights play in the growth and production of sugar(sucrose). Further studies are needed to determine the wavelengths within each light and how they are used for every plant's growth and production.

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ELUCIDATING THE 3D STRUCTURE OF THE HIV-1 5' LEADER

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The Human Immunodeficiency Virus (HIV) is a retrovirus that infects helper T cells and suppresses the activity of the human immune system. Currently, some treatments can aid in managing HIV, however, there is no cure. Due to the high mutation rate of HIV-1, current therapies have the potential to become ineffective. The 5' leader is a site in HIV-1's RNA genome, including the untranslated region, that has a low mutation rate which plays a critical role in mRNA packaging and transcription. Thus, characterizing the 5' leader will be significant toward developing new HIV-1 therapeutics. Our group uses paramagnetic labeled M8-DOTA- SPy tagged U1A protein, to induce long-range pseudocontact shifts (PCS) within the 5' leader to elucidate its 3D structure. The 5' leader can exist in two distinct conformations, either as a dimer or a monomer. These structures can be distinguished by the number of guanosines following the initial methylated guanosine. The $^{cap3G}_{5'}$ leader structure acts as a monomer and plays a role in viral host machinery translation. The $^{cap1G}_{5'}$ leader structure acts as a dimer and is selectively packaged in an assembling virion. Currently, we are focusing on determining the orientation of a three-way junction, 2G-TPUA, which mimics the dimeric structure of the 5' leader. Within this junction, there may be possible stacking interactions occurring between the TAR and polyA regions of the 5' leader. This interaction can potentially aid in RNA protection by sequestering the 5' cap which prevents RNA decapping and splicing. We will then show binding of the spliceosomal U1A protein to our TPUA construct. From there, we will then show PCS within TPUA which will be used to elucidate a 3D structure.

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DESIGNING A CONTACT TRACING ONTOLOGY TO HELP CONTAIN INFECTIOUS DISEASES

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The rapid evolution of the COVID-19 pandemic has shown that the ability to identify and control the spread of infectious disease is an essential part of public health infrastructure. One of the primary methods of controlling the spread of highly infectious diseases is contact tracing. Contact tracing is the process of identifying who an infected individual may have exposed while contagious. Manual contact tracing is often conducted through interviews with infected individuals, their contacts, and the places the infected individual has visited, but this can be slow and logistically challenging. App-based contact tracing often identifies contacts using either the location data or Bluetooth proximity data, but this has been shown to have substantial privacy and security concerns and is ineffective for individuals without the app.

Effective contact tracing requires efficiency, clear communication, flexibility, and a level of trust that allows for the rapid exchange of data between all parties. To this end we propose a novel contact tracing ontology to facilitate situation-aware access control and automation of parts of the contact tracing process using semantic web technologies. The ontology is designed to allow the implementation of situation-aware access control using query rewriting to allow authorized system users to query an institution's relevant data directly to ensure efficiency while maintaining security. Additionally, queries built leveraging semantic web technologies would allow automation of parts of the contact tracing process, including but not limited to identifying contacts, prioritizing investigations, and delegating responsibilities among available contact tracers and case investigators. Development of this ontology required carefully considering the existing contact tracing process, ontology structure and functionality, and potential access control and automation rules.

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MODIFICATION AND SENSITIVITY OF OLFACTORY-GUIDED BEHAVIOR BY SECOND HAND EXPOSURE TO E-CIGARETTE AEROSOL

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Electronic cigarettes have been used by millions of young people in recent years, creating concerns about unknown long-term adverse health effects. Due to the increased popularity of e-cigarettes, the effects of vaping exposure and second-hand vaping are incompletely understood. E-cigarette use is promoted by nicotine and a plethora of other dangerous chemicals that could potentially affect the sensitive neurons in the olfactory system. This project presents two olfactory-guided behavioral protocols that offer an analysis of second-hand vaping exposure in an animal model. The two methods we used were the buried food and the t-maze test. The buried food test used a small piece of Oreo cookie to test how exposing mice to e-liquid aerosol affects time taken for mice to find food after starvation. The t-maze test used a petri dish of water and the urine of the opposite sex on opposing ends of the maze to test whether e-cigarette exposure alters the mouse's odor preference. We found that the ability for mice to perform simple behaviors, such as locating buried food after starvation and detecting sexually relevant odors after their bedding was exposed to e-cigarette aerosol, was altered by e-liquid aerosol exposure. The time it took the mice to locate the cookie in the buried food test, after being second-handedly exposed, increased. Additionally, second-handedly exposed mice had no clear preference for sexually relevant odors. Our results demonstrated that second-hand vaping exposure to e-liquid aerosol results in decreased olfactory sensitivity, and as a result, behavioral alteration.

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TRAINING AND EVALUATING CLASSIFIERS OF MENTAL WORKLOAD USING FNIRS: THE IMPACT OF WINDOW SIZE AND FEATURE CHOICE

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Functional near-infrared spectroscopy (fNIRS) is a noninvasive imaging technique that bounces near-infrared light off a subject's brain to measure hemodynamic activity as a proxy for cognitive workload. Short windows of fNIRS data can be provided as an input to a machine learning model which can classify a subject's cognitive workload in near real-time, enabling next-generation brain-computer interfaces. Two key design decisions impact the performance of such classifiers: the feature representations that summarize short windows of multivariate fNIRS data as well as window size. We present a novel analysis, where we utilize the open-access TU-Berlin dataset of 26 subjects (Shin et al. 2018), that evaluates how the accuracy of a sliding window feature extractor then logistic regression classifier pipeline depends on window sizes and feature choice. Our preliminary results suggest that window sizes between 45-55 seconds are recommended, with further insight into the importance of cross-correlation features suggested by past work we can also gain more perspective. We anticipate these results will make fNIRS-based cognitive workload classification easier for future researchers to explore.

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REFOCUSING ANALOG ELECTRONIC PEDAGOGY TO EMPHASIZE PRACTICAL SKILL DEVELOPMENT WITHIN A PSOC ENVIRONMENT

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Electrical circuits stand at the center of design for providing functionality to many modern products. In order for Electrical Engineers in training to be as innovative and creative as possible when designing an electronic solution to a problem, hands-on experience is a critical part of undergraduate and graduate education. The complexity of modern products and components makes it harder to keep practical hardware examples in front of students. We seek to address these challenges by tailoring an analog electronics curriculum solely around efficient, practical implementations of electrical signal theory within the voltage, current, and other signal limiting constraints of a modern embedded system called the PSoC, or Programmable System On-Chip. The curriculum is a handbook full of concise, optimized hands-on labs with the goal of familiarizing students with a real-world environment in a microcontroller and helping them internalize effective electronics techniques. We have worked to isolate the overarching characteristics of specific signal processing / analog circuitry concepts and interfacing them with peripherals on-board a PCB was a pedagogically valuable delivery mechanism for helping students understand both the theoretical and practical. Our plan is to launch the finished product for students to use during their undergraduate career, not only invoking a problem-solving thought process within them, but giving them the tools they need to become mature, seasoned, Electrical Engineers with the ability to confidently approach electronic projects.

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MANIPULATING MIX DESIGN AND SURFACE TEXTURE FOR ECO-FRIENDLY CONCRETE BIO-TILES

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Creating the cement used in concrete is a highly energy intensive process, therefore supplementary materials can be used to reduce CO2 pollution associated with concrete production. In addition to this, concrete is generally not recycled when it reaches its end of life, but its life expectancy can be increased through processes such as bio-cementation and reactions with seawater as is the case in traditional Roman concrete. This project aims to create a more eco-friendly concrete mix by 1) reducing CO2 pollution associated with the production of concrete, 2) promoting growth of microorganisms (creating a microhabitat) on the concrete surface, and 3) entraining materials that are not easily recycled as aggregates in the concrete. Mix designs were identified that had the potential to fulfill one or more of these objectives, and each mix was tested for compressive strength to ensure it had sufficient strength for use in pavement or Riprap. Once this was complete, these mixes were also cast into tiles with varying mix designs and surface textures to determine their potential for attracting microorganisms and promoting biodiversity in the surrounding environment. It was discovered that using volcanic ash and olivine as supplementary materials produces concrete viable for use in pavement and Riprap. This mix reduces cement content by 17%, and can potentially capture additional carbon from the atmosphere due to the presence of olivine, a mineral capable of CO2 sequestration, in the mix. The concrete tiles with varying surface texture must be deployed in the field for at least one year before their efficacy at promoting biodiversity can be determined.

FROM BENCH TO BIOSOCIAL RESEARCH: APPROACHING SCIENCE AS AN EMBODIED RESEARCHER

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The causes of health disparities are complex and requires a multipronged approach with diverse stakeholders to create effective solutions. Historically within the research community, the focus on biological factors as opposed to nonbiological factors (e.g. socioeconomics, discrimination, environment) has slowed progress in closing the health disparities gap. This project reports insights of an undergraduate to a novel biosocial research training that sought to educate and build capacity for biomedical students to address health disparities from a "cells to communities" lens.

Community Based Participatory Research, or CBPR, is an approach that involves collective, reflective, and systematic inquiry where researchers and community stakeholders engage in collaborative work. As an undergraduate researcher within the Baltimore community, I am in a unique position where I understand the biology of disease and can participate in CBPR projects that reflect on the power relationships to co-create solutions to address health disparities and epistemic injustices.

Through examining the literature based on CBPR power dynamics, discovering embodied research, and my experience as a scientist we have identified three key steps of biosocial research training: (1) Identifying the right mentors, (2) Familiarizing yourself with the literature and (3) Aligning yourself with like-minded community partners, e.g. International Collaboration for Participatory Health Research (ICPHR). Participating in social science research has been beneficial in understanding the social implications of health and broadened my perspective of experimental design. Even though I am not currently impacted from the health injustices of Black women, I still belong to this group in society. My perspective gives me insight when formulating research questions and methods. This viewpoint can be defined as embodied research. The combination of CBPR and embodied research can be used to pave a new way of public health research where the transition from theory to practice is more seamless and occurs more often.

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THE RELATIONSHIP BETWEEN LENGTH OF TAPE MEASURE PROTEIN AND HOST RANGE

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The tape measure protein (TMP) determines tail length in bacteriophages and facilitates the infection process with the transfer of DNA into the host's (bacterial) cytoplasm. The goal of our work was to identify the relationship between TMP length and a bacteriophage host range, defined as the diversity of hosts a phage can successfully infect. Our hypothesis is that *Streptomyces* phages with a longer TMP will have broader host range ability.

Phamerator was utilized to locate and measure the TMP of 15 Siphovirus morphotypes belonging to *Streptomyces* phages. We also located 5 Podovirus and Tectivirus phages, but these were not measured due to lack of a TMP. Host range data from selected phages was obtained from the UMBC archived lab data (2014-2019). Google sheets were used to compare TMP length versus host ranges.

We found the majority of our phages had a Siphovirus morphotype. This type of phage has a long tail length and includes a TMP in their genome. Within the Siphovirus morphotype, the phage MindFlayer had the longest TMP of 6.30 kbp but only had an infection rate of 50% of their hosts while the phage RavenPuff, with TMP length of 5.20 kbp had the highest infection rate of 75%. It is important to notice that the TMP is not the only factor influencing the infection rates as phages without a TMP are also able to infect *Streptomyces.* Podovirus and Tectivirus morphotypes (n=5) were also able to infect hosts with an average infection rate of 29.85%, demonstrating the TMP protein is not the only protein associated with infection. As a result, our hypothesis is not supported by the data. For future research, we can study the relationships of other morphotypes, like Myovirus, to see if there is a correlation among other families.

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SYNTHESIS AND BIOCHEMICAL STUDIES OF HUMAN IMMUNODEFICIENCY VIRUS TYPE-1 SPLICED RNA

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Human Immunodeficiency Virus Type 1 (HIV-1) infects human $CD4^+$ cells by integrating its RNA genome into the host genome; therefore, it utilizes the cellular machinery to reproduce new virions. The highly conserved 5′ leader of the viral full-length RNA is crucial for a functional viral replication cycle. Previous studies have shown that the structure of the 5′ leader regulates viral activities. It adopts either a monomeric conformation for translation and splicing or a dimeric conformation for genome dimerization and packaging. Through alternative splicing, more than 40 species of viral spliced RNAs are generated from full-length RNA. Similar to the monomeric conformation of full-length RNA, spliced RNAs can code for various viral proteins and are not packaged efficiently. All spliced RNAs contain a majority of the 5′ leader sequence, which is named the common exon, and its structure has not been investigated yet. Therefore, we are interested in the structure of the common exon within the 5′ leader of spliced RNAs and how it impacts the function of spliced RNAs.

Here, in vitro transcription and ultra-filtration is performed for large scale RNA synthesis and purification for structural studies. Gel electrophoresis has been carried out which indicates that the spliced RNA 5′ leader is monomeric under physiological conditions. This result is consistent with the fact that dimerization is required for viral genome RNA encapsidation. Selective 2′-hydroxyl acylation analyzed by primer extension (SHAPE) and Nuclear magnetic resonance (NMR) will be used for further structural study.

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IN PURSUIT OF PLEIOTROPY

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Pleiotropy occurs when one gene is responsible for the expression of various phenotypic traits. The pervasiveness of pleiotropy is unknown and research has not yet determined what traits are interconnected by specific genes. The goal of this project is to identify pleiotropic genes influencing phenotypes that are important to the fitness of organisms to understand their potential influence on evolution. Discovering pleiotropic genes and their associated phenotypes can have practical implications for the design of medical treatments, as it can decrease the likelihood of malignant side effects. We intend to identify traits that are connected through pleiotropy and hypothesize the genetic pathways associated with these traits. *Drosophila melanogaster* was used as a model organism to investigate pleiotropy and the genetic basis of natural variation. We searched for literature that used the *Drosophila* Genetic Reference Panel (DGRP) to conduct Genome-wide association studies to identify genes associated with different phenotypic traits studied in this panel of flies. We used the Web of Sciences database and identified 74 articles that used the DGRP lines. We compiled a gene list containing genes associated with each trait from the articles. All the differently formatted genes were converted into the FBGN format. An algorithm was used to find genes controlling more than one phenotypic trait. It showed genes ranging from no pleiotropic effect to various pleiotropic candidates that controlled multiple phenotypic traits. We discovered a total of 11,057 pleiotropic genes out of 17,873 genes. The most pleiotropic gene connected a total of 11 phenotypic traits. Furthermore, we theorize that these traits are associated with neurodevelopmental pathways based on what is known about the pleiotropic gene's function. Future studies will focus on validating the effects of highly pleiotropic genes on focal traits and test the hypothesis that interconnected traits are influenced by common neurodevelopmental pathways.

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DEVELOPING SYNTHETIC ANTIBODY PROBES FOR RNA ANALYSIS INSIDE CELLS

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Antibodies are proteins that bind to their corresponding antigens with high specificity and selectivity through complementarity-determining regions (CDRs). Antibody derivatives such as single-chain variable fragments (scFvs) are often used as probes to visualize and analyze a variety of proteins inside cells. However, there is a lack of such an antibody-based toolbox for RNA visualization. In this project, we worked on developing synthetic scFv probes against RNA molecules that will allow RNA visualization intracellularly. We used CDRs of anti-RNA antigen-binding fragments (Fabs), Fab BRG and Fab HAVx specifically, to replace the CDRs of previously reported scFv scaffolds that are proven to fold and function in living cells. This will produce the chimeric scFvs that retain the stability of the scaffolds while acquiring the target specificity from the grafted CDRs. First, we generated a scFv scaffold database using different resources such as literature and online databases. The DNA sequences of these scFvs were translated into protein sequences using the ExPASy tool. The purpose of translating the sequences was to ensure that all scFvs were in the same protein format to facilitate the identification of the CDRs. Second, we used Ofran Lab and Clustal Omega to identify the CDRs of the scFv scaffolds semi-automatically. Based on the Clustal Omega alignment, we found one scFv scaffold with similar lengths of CDRs as in Fab BRG and Fab HAVx, which was then used as the scaffold to graft the donor CDRs and develop one chimeric scFv per Fab. The proposed chimeric scFvs will undergo further work and tests in the laboratory to see if they can be expressed as expected and can bind the corresponding RNA targets. We anticipate that these scFv probes will be beneficial to advance RNA visualization in cells when fused with genetically encoded fluorophores such as green fluorescent protein.

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COMPARING SOIL BACTERIOPHAGE BIODIVERSITY CHARACTERIZED BY MORPHOLOGY IN *BACILLUS* AND *STREPTOMYCES* HOSTS

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Bacteriophage therapy is becoming an important alternative to antibiotics in the treatment of multidrug-resistant bacterial infections. Research in this field will benefit from increased knowledge of bacteriophage biodiversity and taxonomy. Current studies have focused on a metagenomic approach to characterize biodiversity; however, morphological diversity can also indicate underlying genetic or functional variation.

Tailed bacteriophages exhibit three morphotypes (groups with distinct physical structures) distinguished mainly by their tail features and referred to as siphovirus, myovirus and podovirus. Within each morphotype there is immense diversity in capsid (head) size, capsid shape, and tail length. The purpose of this investigation was to examine the biodiversity in soil of tailed bacteriophages infecting *Bacillus* and *Streptomyces* bacterial hosts using morphology.

We analyzed electron microscopy images of bacteriophages that were isolated by students in the UMBC Genetics laboratory course from 2014-2019. Measurements of capsid length/width and tail length were performed in Fiji/ImageJ. Using morphological characteristics of capsid size/shape and tail length, we performed cluster analyses in SPSS to assign individual bacteriophages to "sub-morphotypes" within a given morphotype. To compare morphological diversity between hosts, we calculated the Simpson's index, which takes into account both the numbers of sub-morphotypes present and the abundance of each sub-morphotype in relation to one another.

A total of 12 distinct sub-morphotypes were found across five hosts. *Bacillus* bacteriophages were primarily myovirus while conversely *Streptomyces* bacteriophages were almost exclusively siphovirus. Phages infecting *B. thuringiensis* DSM 350 had the highest morphological diversity between the two *Bacillus* species and *Streptomyces mirabili*s of the three *Streptomyces* species examined.

For future studies, we would like to further investigate host morphotype specificity and why some hosts display more morphological diversity. Furthermore, we would like to examine the ability of sub-morphotypes to infect clinical strains of bacteria.

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IN SILICO ANALYSIS OF VOLVOX TRANSCRIPTION FACTORS AND THEIR DEVELOPMENTAL EXPRESSION

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The multicellular green alga *Volvox carteri* (Volvox) and its unicellular cousin *Chlamydomonas reinhardtii* (Chlamydomonas) comprise an excellent model for investigating how multicellularity evolved. Volvox possesses just two cell types: large reproductive gonidia and small motile somatic cells. Since differential expression of transcription factors (TFs) often determines cell fate, we set out to determine how TF families differ in Volvox vs Chlamydomonas and which TF genes are differentially expressed in gonidia vs somatic cells. We first used BLAST searches of the public databases Phytozyme and NCBI to identify Volvox homologs of previously identified Chlamydomonas TF genes, then used previously published RNAseq data to determine differential expression. We found 234 non-orphan Volvox TF genes, slightly more than the 225 non-orphan TF genes previously identified in Chlamydomonas, and of these, 99 (~42%) are differentially expressed (gonidial vs somatic specific). The sizes of TF gene families in the two species are similar, but some transcription factor families are larger or smaller in Volvox by as many as 27 or 6 genes, respectively. Of the 61 TF genes that are differentially expressed by 2x-4x, 34 are gonidial-specific and 27 are somatic-specific. Moreover, of the 38 TF genes that are differentially expressed by >4x, 18 are gonidial-specific and 20 are somatic-specific. By comparison, ~48% of all genes in Volvox are differentially expressed, and ~⅔ of these are more highly expressed in gonidia than somatic cells. Therefore a smaller fraction of TF genes are differentially expressed than of the genome as a whole, and differentially expressed TF genes are skewed more toward somatic specificity than the genome is. Next steps in this project will be to include orphan TF genes in the analysis, and eventually to target TF genes that are gonidial- or somatic-specific for CRISPR knockout to test their possible roles in cellular differentiation.

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NDRG1 PROTECTS THE KIDNEY FROM HYPOXIC INJURY

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Low oxygen disrupts homeostasis in human cells and can fatally damage vital organs. Numerous studies show that hypoxia impairs kidney function and contributes to the development of kidney disease. Interestingly, zebrafish can withstand hypoxia by entering a reversible hypometabolic state to maintain homeostasis. Subsequently, the function of organs with high metabolic demand, including the kidney, declines. Because the pronephros (embryonic kidney) is functionally and structurally similar to the human nephron, the zebrafish is a valuable model to study human kidney disease. Our lab has identified a nine-fold upregulation of *n-myc downstream gene 1a* (*ndrg1a)* transcript in zebrafish exposed to prolonged hypoxia, suggesting that this gene is crucial to the organism's survival and recovery from low oxygen. Furthermore, our lab found that neither the presence nor lack of Ndrg1a affects kidney development or function under normoxic conditions, suggesting that Ndrg1a does not regulate physiological processes under normoxia. However, it remains unclear whether Ndrg1a is required to maintain kidney homeostasis under hypoxia. Given that *ndrg1a* transcript is upregulated under hypoxia, we hypothesized that it may play an adaptive role in kidney function and survival. Here, we investigate the protective role of Ndrg1a in maintaining kidney function after exposure to prolonged anoxia (zero oxygen) followed by a period of re-oxygenation, using a kidney clearance assay. Preliminary results from the assay revealed that in *ndrg1a* -/- mutants, the filtering capability of the kidney is approximately 1.5x lower than that of WT embryos when exposed to 12 hours of anoxia. Furthermore, we found that embryos with the most severe kidney malfunction had the lowest survival rate post-anoxia. Together, these observations suggest that Ndrg1a protects the kidney from hypoxic damage. These findings are significant, given that NDRG1 function is likely to be conserved in humans and modulation of its function could be exploited for therapeutic benefit.

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3D PRINTING IODIXANOL-INFUSED BIORESORBABLE VASCULAR STENTS FOR ENHANCED IN-VIVO CONTRAST PROPERTIES

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Atherosclerotic coronary artery disease contributes a significant amount to the considerably high cardiovascular disease related deaths in the United States. Current clinical treatment of such vascular diseases typically involves the use of balloon angioplasty followed by deployment of a metallic stent. Though beneficial in the prevention of restenosis, metallic stents may introduce new complications such as late-stent thrombosis, neointimal cell proliferation, or other unwanted immune responses. Fortunately, previous studies have led to the development of a bioresorbable vascular stent (BVS) with drug-eluting properties as a safer alternative. However, due to its radiolucent nature, the proposed polymer-based stent has shown low visibility under standard x-ray imaging devices. Through this study, we propose the incorporation of Iodixanol– an iodine-containing radiodense contrast agent– into BVS 3D-printing ink to increase stent contrasting capabilities while examining the effects of varying Iodixanol concentrations on radiopacity, crimping and deployment, and mechanical strength.

A BVS ink sample that did not contain any contrast medium was set as the control and compared to ink samples containing various concentrations of Iodixanol (4%, 5%, 6%, and 7%). Mechanical tensile testing, CT imaging, and stent crimping and deployment testing were performed on each printed stent and the resulting data was analyzed. Our findings have shown that the addition of iodixanol as a contrast medium in 3D printing BVS ink increases stent radiopacity. Concentrations of four and five percent have proven to be optimal in maintaining mechanical elasticity while providing for better visibility.

Though further testing must be done to examine the previously studied properties in vivo, as well as examining the drug degradation rate and cytotoxicity, we believe that the use of an iodixanol-infused bioresorbable vascular stent could provide for better stent visibility and tracking in angioplasty patients following deployment.

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