ASDRP Fall 2021 Virtual Symposium & Expo
January 15, 2022
10:00am-1:00pm

ASDRP
Aspiring Scholars Directed Research Program

10:00-10:15am: Opening Session & Remarks
10:15am-12:30pm: Poster Presentations

Join Via Zoom: https://us06web.zoom.us/j/83634228724?pwd=Q0s1V1ptSzk1Ny9qM2dsZDhDa2lvdz09
Meeting ID: 836 3422 8724 Passcode: 719249

Presentation Time: 10:15-10:30am (1)	**Zoom Room:** Room 1
Research Group Njoo	**Authors/Researchers** Kuvam Bhatnagar, Natasha Gupta, Meher Jain, Andrew Chen, Rosie Chen, Pratyush Singh, Adrienne Ferguson, Srishti Venkatesan, Harrison Xu, Emily Dai
Title Comparison of Boc and Nitro Groups Based on Stereoelectronics in the Synthesis of Indole N-Benzoate Compounds, A Key Intermediate Towards the Synthesis of Psychrophilin E	
Abstract Cyclic peptides are a diverse class of bioactive molecules primarily derived from microbes. Specifically, Psychrophilin E is a cyclic tripeptide extracted from the marine-derived fungus Aspergillus Versicolor ZLN-60 with promising antiproliferative properties. The total synthesis of Psychrophilin E would allow for scalable alternatives to natural isolation as well as unnatural analogs. While a successful total synthesis of Psychrophilin E has been previously reported, our synthesis allows for other possible analogs, such as one with a 3-aminobenzoic acid. A key step of our total synthetic route is the indole n-acylation of N-Acetyl-L-Tryptophan Methyl Ester with Boc Anthranilic acid, which we are optimizing via the mechanistic study of the n-acylation of C3 substituted indoles with benzoic acids. This route also opens a gateway for novel analogs of Psychrophilin E with a potential for increased biological activity. In particular, one compound of interest is a glycine analog in which the pyrrolidine ring has been replaced with a glycine. The analog will have the potential to sample for increased conformational states as demonstrated by molecular mechanics search algorithms.	

Presentation Time: 10:15-10:30am (10)	**Zoom Room:** Room 2
Research Group Cunha	**Authors/Researchers** Aksithi Eswaran, Maya Poghosyan, Aparnaa Ananthakrishnan
Title Consensus Computational Drug Screening for DNMT Inhibitors using molecular docking and deep-learning approaches	
Abstract Deep-learning and algorithmic methods, such as MolTrans and AutoDock Vina, have been developed to discover potential treatments to diseases. We aim to utilize these search algorithms and neural networks in our research. We are looking for novel drugs to treat colon cancer by utilizing such computational methods. To treat colon cancer, the drug, or ligand, needs to bind to DNA methyltransferase 1, or DNMT1. Due to hypermethylation in CRC cancer, tumor suppressor genes are inactivated. So far, our research has confirmed results of previous studies using AutoDock Vina and MolTrans. Knowing that the tools work correctly, we can now look for and identify more potential DNMT1 inhibitors and test them in the wet lab.	

Presentation Time: 10:15-10:30am (11)	**Zoom Room:** Room 3
Research Group Downing	**Authors/Researchers** Shreya Gosavi, Rahul Prasannakumar, Aylin Salahifar
Title Deciphering the Voynich Manuscript: Tracking Missing Phonemes, Assessing Images, and Tracing Physical Components	
Abstract Having evaded intense efforts toward its translation for over 500 years, the Voynich Manuscript, a text dating back to the 15th century that is written in an unknown character set, remains a compelling mystery for researchers in the areas of linguistics, history, and cryptography. Within this study, the topic of inquiry relates to the Voynichese characters being a compilation from various cultures and their ancient languages, including an extensive basis in Vulgar Latin with additions from Middle Persian and Sanskrit. It is hypothesized that the Voynichese character set is an encoding based upon a source language of Vulgar Latin origin. When the author was unable to identify characters to match the phonemes found in Vulgar Latin-based languages, they likely borrowed characters that matched those particular sounds from other languages. Research methods performed to validate this hypothesis include character mapping, correlation with images within the text, and historical tracing of the origins of the manuscript. With regard to historical tracing, the Voynich manuscript's constituents bear many connections back to ancient Persia. Most, if not all of the inks and paints found in the manuscript were widely used in Persian manuscript painting. The ink was iron gall ink with traces of copper and zinc which were unusual for the time. It was inferred that those traces were from a brass inkwell, which had widespread use from the 12th-16th centuries in Persia. The constituents of the colors used in the manuscript were Azurite (for blue), Copper Chlorine resinate (green), Red Ochre (red), and Calcium Carbonate (white). Due to the timing and how all of the constituents of the manuscript originated in Persia, it is safe to infer that the manuscript had a chance of being influenced by Persian culture or written in the geographic region of ancient Persia. With regard to character mapping, the widely-accepted Extensive Voynich Alphabet was used to draw relevant connections between specific words in the manuscript and words utilized in Middle Persian and Sanskrit to describe concepts or images present in the diagrams in close proximity to the words in question. In addition, the history and origins of the Glagolitic script were studied in order to better understand how character sets may be created toward a specific purpose or created due to the rapid and concentrated exchange of cultural information. Posited theories toward explaining the origin of the manuscript include that it was created as a collection of medicinal, herbal, and astrological knowledge collected on the Silk Road, where European,	

Persian, Hindi, and Buddhist cultures were known to interact. As the scientific community continues on its journey toward revealing the secrets contained within the elusive Voynich Manuscript, further research avenues include investigating the frequencies of the decoded words presented in this study with their relation to depicted diagrams in the manuscript.

Presentation Time: 10:15-10:30am (24) **Zoom Room:** Room 4

Research Group	**Authors/Researchers**
Njoo	Charissa Luk, Xina Wang, Neha Mandava, Udbhav Avadhani, Emma Le, Julia Vu, Sarah Su, Jane Wu, Ananya Anand, Aashi Shah, Shloka Raghavan, Darshita Prathap, Aishi Rao, Jeslyn Wu, Anushka Peer, Suhani Babu

Title
In silico screen and kinetic studies towards the synthesis and optimization of a library of carmofur analogs as potential inhibitors of the SARS-CoV-2 main protease and its variants

Abstract
Carmofur, a 5-fluorouracil derivative, was initially developed as an antineoplastic agent that inhibits acid ceramidase and tested for its efficacy on colorectal cancer cell lines. More recently, through drug repurposing efforts, it has been identified as a covalent inhibitor of the main protease of SARS-CoV-2. This SARS-CoV-2 main protease (Mpro) plays an essential role in the processing of the polyproteins that are translated from the viral RNA, therefore making it an attractive drug target for the treatment of COVID-19.. Here, we present the in silico evaluation and synthesis of carmofur and a library of related 5-fluorouracil analogs with aliphatic, amino acid, and aromatic fragments against mutations in Mpro. Homology modeling was used to determine the interactions between carmofur analogs and Mpro as a result of the mutations and their effects on the binding affinity of our analogs, revealing potential hit compounds to further develop for combating COVID-19. Furthermore, using the 5-fluorinated position as a handle, benchtop 19F nuclear magnetic resonance spectroscopy (NMR) has enabled the real-time quantitative monitoring and scalable synthesis of novel 5-fluorouracil analogs as potentially more effective inhibitors.

Presentation Time: 10:15-10:30am (27) **Zoom Room:** Room 5

Research Group	**Authors/Researchers**
Benson	Advay Chatterji, Ankita Gadepalli, Olivia Ho, Mallika Saoji, Connie Yang

Title
Investigating the efficiency of the saltwater mussel Mytilus californianus's ability to filter microplastics from aquatic ecosystems

Abstract
The increase of microplastic pollution, otherwise known as plastics smaller than five millimeters, actively contributes to the threats faced by life in marine ecosystems. Microplastic pollution has the ability to adversely affect aquatic and human life by manipulating organisms' functions. However, novel research has demonstrated that as filter feeders who have been shown to intake and retain microplastics, mussels may have the ability to minimize such pollution. Therefore, we explored the potential that mussels may have in filtering and retaining microplastics and worked towards developing a method to extract, purify, clean, and quantify microplastics from mussels, as there currently is not a standardized method to do so. Given the rising trends of microplastic pollution, different-sized mussels collected from a local tidepool were exposed to varying levels of microplastics over a period of time. After exposure, the retained microplastics from the mussels were isolated and quantified using a mussel digestion process and vacuum filtration. In the future, we plan to analyze this digestion using a dissecting microscope, ultraviolet light, centrifuge technology, and FTIR spectroscopy. All microplastics used in the experiment were created using a power sander, including 1 PETE, 2 HDPE, 3 PVC, 4 LDPE, and 5 PP plastics. Elementary data suggests that mussels may be able to efficiently filter microplastics, illuminating the role mussels play in microplastic pollution. While we are still pursuing results, these findings may prove to be insightful for addressing an environmental issue presently affecting aquatic ecosystems and we hope to be able to implement our findings in a real water system.

Presentation Time: 10:30-10:45am (2) **Zoom Room:** Room 2

Research Group	**Authors/Researchers**
Jahanikia/Downing	Aniket Dey, Gia Oscherwitz, Medha Bhattacharya

Title
A Global Network Analysis of COVID-19 Vaccine Distribution to Predict Breakthrough Cases Among the Vaccinated Population

Abstract
The ongoing COVID-19 pandemic, also known as the coronavirus pandemic, is a global pandemic caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Multiple vaccines have been developed & underwent clinical trials to prove efficacy, such as the one produced by Pfizer & BioNTech. While these vaccines are currently being deployed, no vaccine is fully effective and thus, breakthrough infections, in which a fully vaccinated individual may contract the virus, occur, albeit infrequently. With the appearance of the Delta Variant, a more infectious & now most predominant strain of the SARS-CoV-2 variant that was first identified in India in December 2020, it is now being

questioned whether vaccinated individuals who are subject to a breakthrough infection may contract the Delta Variant as well.
This study aims to map the vaccination candidate connectome using network analysis with the Barabási-Albert model. This network science will provide scale-free networks that accurately model the powerful distribution of SARS-CoV-2 vaccines on a global scale. From there, the study will use R & Python, as well as Gephi to visually model these networks and predict the next pandemic among vaccinated candidates on a global scale.

Presentation Time: 10:30-10:45am (9) **Zoom Room:** Room 3

Research Group
Renganathan

Authors/Researchers
Sumayyah Ismail, Bridget Liu, Bhoomi Jain, Grace Hahn, Jay Subbiah

Title
Comparing the Efficacy of Different Polyphenols in Alzheimer's Disease Using Caenorhabditis Elegans as Model Organisms

Abstract
Alzheimer's Disease is caused by an aggregation of amyloid beta and tau proteins in the brain. Polyphenols, a broad class of naturally-existing compounds, have shown to inhibit the aggregation of those proteins. This project aims to focus on expressing different combinations of those proteins through a plasmid vector in bacteria and assaying those proteins for aggregation inhibition using polyphenols to determine which polyphenol is most effective in doing so. Molecular docking is also used after our assays to rank the polyphenols in terms of effectiveness and to eliminate less desired polyphenols or acquire new potentially better ones to use. Previous progress has been made through virtual screening to identify potential compounds that effectively inhibit protein aggregation, and those compounds will continue to be analyzed for bioactivity through more computational work and bioassays. However, we focused more on the biological aspect of it, such as conducting multiple assays such as Congo Red, Avoidance, and Chemotaxis, to receive tangible results.

Presentation Time: 10:30-10:45am (12) **Zoom Room:** Room 1

Research Group
Harman Brah

Authors/Researchers
Ayaan Khan, Gabrielle Macababbad, Nirupama Niranjan

Title
Design of novel benzimidazoles as K-RAS Inhibitors for Cancer Chemotherapy

Abstract
The KRAS gene, first identified as an oncogene in the Kirsten RAt Sarcoma virus, provides instruction towards the production of the K-Ras protein. The K-Ras protein is responsible for relaying various growth signals from outside of the cell to the cell's nucleus. When mutated, KRAS can fail to deactivate, leading to uncontrolled cell growth and signaling, causing cancerous growths. Mutations of KRAS proteins occur in approximately 25 percent of all human cancers, including more than 90 percent of pancreatic cancers and approximately 25 percent of lung cancers. Despite its prevalence as an oncogene, K-Ras's lack of clear binding sites has made K-Ras one of the most challenging and elusive targets as a cancer therapeutic.

Presentation Time: 10:30-10:45am (16) **Zoom Room:** Room 5

Research Group
Renganathan

Authors/Researchers
Meghana Iyer, Sophia Wang, Atul Thirumalai, Via Das

Title
Employing PGP and CYP Inhibitors to Increase Drug Bioavailability

Abstract
Bioenhancers, also known as PGP-inhibitors are substances that when administered with a drug, can increase its bio efficiency, allowing it to react in our bodies faster. In our study, we are researching different inhibitors such as those for PGP and CYP, trying to understand to what extent these inhibitors function in the body. A PGP inhibitor increases the bioavailability of the drug that is being induced while the CYP inhibitor is important for the drug metabolization. We are using cellular assays, in vivo assays with c elegans, and in silico software to study these bio-enhancers and their effects on PGP and CYP.
Our group has routinely been passaging cells and simultaneously using worms to test and record similar data. These two act as our model organisms. We chose a transgenic strain of worms since we needed them to express the PGP protein. As per our cells, we chose cells that most closely represented the cells of the intestinal epithelium, the location of PGP protein in humans. Like the worms, we needed our cells to express both PGP and CYP. Additionally, we wanted to choose a type of cell that would grow relatively quickly to increase the efficiency of our research. Currently, we are gathering different data and will soon use different assays such as a calcein assay and MTT assay to observe which one can reach the cells most efficiently.

Presentation Time: 10:30-10:45am (38) **Zoom Room:** Room 4

Research Group	**Authors/Researchers**
Renganathan	Emily Wang, Shikha Kathrani, Vivian Long, Yashas Shashidhara, Maddy Zhang, Anshi Arora

Title
Synthesis of Benfotiamine Prodrug Derivatives And Their Diabetic Neuropathy Activity in C. Elegans Model

Abstract
Diabetic neuropathy, a complication caused by both type 1 and 2 of diabetes, is a type of nerve damage experienced most commonly through pain and numbness in the legs. It affects over 200,000 diabetic patients in the US alone. This condition occurs through glycation: when free reducing sugars combine with amino groups or lipids, leading to the formation of irreversible advanced-glycation end products (AGEs). Accumulation of AGEs, especially in hyperglycemic environments, can lead to severe chronic complications. Benfotiamine (BFT), a synthetic S-acyl derivative of thiamine (vitamin B1), has been researched for its anti-glycative and anti-inflammatory properties, specifically in preventing the formation of AGEs and enhancing alternative pathways. However, BFT has a low bioavailability since it is sparingly soluble in water, octanol, and oils, ultimately decreasing its efficiency and absorbency in cells. While higher doses could serve as a potential solution, it may be dangerous due to the risk of adverse side effects and lack of research directed towards potential implications. Therefore, the purpose of this research is to synthesize prodrug derivatives of BFT to safely improve its bioavailability and effectiveness. In this presentation, we will focus on comparing the effectiveness of BFT and thiamine to the effectiveness of our synthesized azo and disulfide-based self-immolative linker (DSIL) prodrugs through in vivo pharyngeal pumping and anti-AGE assays on C. elegans.

Presentation Time: 10:45-11:00am (23) **Zoom Room:** Room 2

Research Group	**Authors/Researchers**
Renganathan	Aditi Adapala, Sahana Ravishankar, Shrimayi Chaganti, Shrinithi Sathiyaseelan, Amrita Guha, Aarya Morgaonkar, Tanvi Sri Sai Penugonda

Title
Hypoglycemic activity of Trigonella foenum-graecum in the C. elegans model

Abstract
Diabetes Mellitus is a high-risk chronic metabolic disease and is the seventh leading cause of death in the United States. There are several types of diabetes mellitus, including type 1 DM, type 2 DM, maturity-onset diabetes of the young, and gestational diabetes. Insulin is a key hormone that converts glucose to energy. Because of the lack of insulin production, cells are unable to use glucose in order to produce energy, resulting in hyperglycemia. Even though diabetes is one of the oldest diseases, no cure has been discovered; however, several drugs have been developed to manage it more effectively. Recently, natural products are becoming a major part of the pharmaceutical drug industry, and are widely used especially in the east. Trigonella foenum-graecum, or fenugreek, is one of these drugs. Fenugreek is a medicinal plant known to have antidiabetic properties which stem from its bioactive compounds like diosgenin, trigonelline, 4-hydroxyisoleucine, leucine, and L-lysine. Our research is focused on determining the most efficient method in which different phytoconstituents can be extracted, conduct total content assays and assess their anti-diabetic potential and chemical properties.

Presentation Time: 10:45-11:00am (30) **Zoom Room:** Room 4

Research Group	**Authors/Researchers**
Subramaniam	Yiran (Irene) Wang, Apoorva Kulshreshtha, Aditya Venkatraman, Aditi Ghosh

Title
Predict Next Word: Text Generation Using LSMT in a Professional Biomedical Context

Abstract
The use of machine intelligence to facilitate daily tasks has increased substantially, such as suggestions of what may be written next in text messages, emails, and more. However, sometimes the scope of the context may be too broad and the prediction fails to generate an appropriate term. The main goal of this project is to focus on the professional biomedical context and use bidirectional long short-term memory (bi-LSTM) for text prediction. To achieve this, the model is trained with Wikipedia documents related to this field, which narrows down the ranges of vocabularies fed into it, thus increasing the accuracy and specificity of the output. When given a starter string, our language model, using machine learning algorithms, is successful in predicting the next few words in a sentence with correct usage of biomedical terminology. Extending our research further can allow for the suggestions of nomenclatures in other professional contexts as well.

Presentation Time: 10:45-11:00am (34) **Zoom Room:** Room 5

Research Group	**Authors/Researchers**
Chen	Angie Tan, Kimberly Khow, Prisha Jain, Riya Patel, Sripradha Manikantan

Title
Stability Study with HPLC on Lovastatin and Simvastatin

Abstract
About 38% of American adults have high cholesterol so HMG-CoA reductase inhibitors like Lovastatin and Simvastatin are commonly-used medications for lowering cholesterol levels and preventing serious heart diseases. To determine the

suitable storage condition and the shelf life to ensure the safety of these drugs, our project aims to run a stability study using RP-HPLC to observe the amount of degradation at different temperatures during various storage times, as we predict that there will be higher amounts of drug impurities during higher temperatures and longer storage times. Our presentation will cover how we determined the RP-HPLC method most suited for Lovastatin and Simvastatin's stability study testing.

Presentation Time: 10:45-11:00am (35)	**Zoom Room:** Room 3

Research Group	**Authors/Researchers**
Jahanikia	Gia Oscherwitz, Hansika Daggolu, Neha Nabar, Sashvath Koyi, Sriya Gonuguntla, Anastasia Bubelich, Abhinav Satish,

Title
Steps towards developing a comprehensive resource to understand the Phases, Applications, and Exploring Real-Time Data from the Human Connectome Project (HCP)

Abstract
The Human Connectome Project is a large-scale initiative involving teams of researchers at institutions around the world. The main goal of the project is to create a completed map of the human brain through the use of various MRI scanners and digital software. The map will serve as a baseline for future studies of brain connectivity during physical development, aging, and neurodevelopment, as well as aiding in the study and classification of neuropsychiatric and neurological disorders. The end goal of connectomics is to understand how brain areas are connected and contribute to human behavior, and how complicated systems are altered or exhibit different functions in individuals with neurological and psychiatric diseases. Once completed, the human connectome will provide valuable insights into what makes humans human, and what accounts for diversity in the behavior of healthy adults. This review includes an overview of the history of the HCP, a comparison between the brain network and the connectome, a discussion of how the human connectome can allow for the creation of neural biomarkers, a discussion of imaging techniques used in the project, a look into the C. elegans connectome, which is the first and only organism with a completed brain map, and a discussion of future research in this field. Our project aims at creating a comprehensive book/textbook to disseminate the knowledge of the Human Connectome Project, which includes studying all aspects of the project from its phases, to its costs, to its modalities, to its assessments, fMRI techniques, applications and implementations to psycho degenerative diseases.

Presentation Time: 10:45-11:00am (37)	**Zoom Room:** Room 1

Research Group	**Authors/Researchers**
Renganathan	Sirivennela Gade, Siri Manthapuri, Avaneesh Warzarkar, Samir Kurudi, Shriya Sudini, Ananya Pinnamaneni

Title
Synergistic Studies of Sulforaphane and Cephalotaxine as an Agent

Abstract
Cancer is the abnormal cell growth of mutated cells with the capability spreading throughout the body. The disease is a major cause of deaths worldwide, causing about 10 million deaths per year. Thus, anticancer treatments, such as chemotherapy, are in demand. Paclitaxel, a chemotherapy drug mainly used to treat lung, ovarian, and breast cancer, is the main focus of our research. We focus on using a combination of two compounds linked to anticancer activity and apoptosis induction, Sulforaphane (SFN) and Cephalotaxine (CET), to achieve this. SFN is an organosulfur compound with a unique structure as it is classified in the isothiocyanate group. It can be obtained from cruciferous vegetables such as broccoli. SFN presents a unique approach to anticancer treatment. The compound is effective in reducing the size and limiting the variation of cancer cells. SFN releases antioxidant and detoxification enzymes to shield against carcinogens, one of the direct substances responsible for cancer cell growth. Our project aims to maximize the compound's activity by pairing it with another potent anticancer drug, CET. CET is a benzazepine alkaloid isolated from Cephalotaxus Harringtonia, a coniferous plant of the Taxaceae family. This drug has shown some anticancer activity as well. This project analyzes the anticancer effect of SFN and CET in combination treatments using assays on Caenorhabditis elegans (C. elegans) strains TJ 375 and JK1466 and molecular biology techniques. Thus far, our ongoing project consists of assays and investigation of background information on the drugs, as well as developing protocols for the various techniques that will be used.

Presentation Time: 11:00-11:15am (4)	**Zoom Room:** Room 4

Research Group	**Authors/Researchers**
Yamamoto	Harry Wang, Nathan Chiu, Paree Merchant, Anika Kulkarni

Title
A Stability Study of Torula Yeast RNA, with Applications in Drug Delivery

Abstract
In being an unstable, typically single-stranded molecule, RNA plays a variety of roles within the genome. Through its unique properties of binding and condensation and applications in gene interference and alteration, the nucleic acid has been considered to be a molecule with great clinical potential. In our research, we are investigating RNA stability and condensation with goals of improving clinical drug delivery via cytoplasmic transport, specifically in how its capabilities

for compaction can be leveraged as a delivery vehicle. RNase, or ribonuclease, a group of enzymes responsible for RNA degradation, is present in an abundance of environments and is the primary method of RNA degradation in our experiments, in the form of fetal bovine serum. These degradation assays serve to test the potential of calcium phosphate as a viable protective nanoparticle in which our susceptible RNA sample is enveloped. We bound our RNA to calcium phosphate to determine its degradation curve using RNase fetal bovine serum, which simulates in vivo environments with intense ribonuclease presence. We compared the degradation curves of RNA alone to RNA with calcium phosphate to determine its potential as a nucleic acid compaction agent. Depending on the results we receive, we plan to utilize the calcium phosphate nanoparticle to facilitate RNA compaction in order to encapsulate the nucleic acid within delivery vehicles, such as liposomes or lipid nanoparticles.

Presentation Time: 11:00-11:15am (17)	**Zoom Room:** Room 5
Research Group Renganathan	**Authors/Researchers** Meera Iyer, Aarya Morgaonkar, Simran Tawari, Rose Liu
Title Evaluation of EGCG and Ascorbic Acid Conjugated Nanoparticles	
Abstract In order to evade the pharmacokinetic challenges of anti-carcinogenic drugs, these drugs are often paired with more absorbable scaffolds. Our research aims to evaluate conjugated EGCG and ascorbic acid as potential nanoparticle for colon cancer.	

Presentation Time: 11:00-11:15am (19)	**Zoom Room:** Room 2
Research Group Jahanikia	**Authors/Researchers** Aditya Anantaraman, Anisha Grover, Brandon Brewer, Dhruv Bhargava, Julia Wind, Sruthi Sudarsan
Title fMRIusic: Understanding the Nature of Brain Imaging Data and Converting for Further Analysis of Musical Genre Perception	
Abstract Functional Magnetic Resonance Imaging, known as fMRI, is a non-invasive neuroimaging technique. It utilizes BOLD signals to construct high resolution images of brain activity from subjects instructed to perform tasks or respond to stimuli within an MRI machine. To do any time of neuroimaging analysis, we have to first investigate MRI raw data. By using neuroimaging tools and techniques, such as AFNI and Freesurfer, we will preprocess and analyze a fMRI dataset obtained from the Psychoinformatics Lab at the University of Magdeburg in Germany. The dataset comes from fMRI scans of 20 participants who were shown clips of the movie “Forrest Gump” with different genres of music featured in the movie, such as Country, Symphonic, and 50s Rock’n’Roll. The participants were asked to guess the genre of a piece of music with and without audio. The purpose of our project for this term was to understand the nature of the raw data. In order to preprocess this data, we first need to convert the raw data into the Brain Imaging Data Structure (BIDS), a standard way of organizing neuroimaging data. Due to the uniform file format that BIDS provides, many tools and resources for neuroimaging adopted the BIDS format as their input. With these tools, the aim of our research is to identify the networks of the brain associated with guessing a music genre correctly without audio. In previous studies, researchers have gathered a large amount of data regarding the auditory network and its relation to music. We aim to understand and explain the role of the auditory network in genre association.	

Presentation Time: 11:00-11:15am (28)	**Zoom Room:** Room 1
Research Group Brah	**Authors/Researchers** Rohinee, Shivani
Title Obesity, type-2 diabetes, and other cardiovascular related diseases	
Abstract The fat mass and obesity-related (FTO) gene, located on human chromosome 16, has been proven to increase the risk of obesity, type-2 diabetes, and other cardiovascular related diseases. The gene contains the code for the FTO protein. The FTO protein is a DNA/RNA demethylase, and is part of the AlkB family. The RNA demethylation caused by FTO is what links the FTO protein with cardiovascular diseases. The way the FTO protein interacts with molecules and compounds can provide a basis for design of FTO inhibitors.	

Presentation Time: 11:00-11:15am (40)	**Zoom Room:** Room 3
Research Group Downing	**Authors/Researchers** Hrithik Pai, Prachi Soni, Sanjay Ravishankar, Meha Selva, Alexander Lau, Vineet Rao, Christopher Lau, Vedant Gupta, Animan Patel, Alex Li, Stephen Park
Title The Analysis of Rocky Exoplanets to Determine Habitability	

Abstract
The search for habitable exoplanets is not a fruitless effort considering that there are thousands of exoplanets in the universe, and at least one must possess the characteristics needed to support basic life. Water, being the basis for life, leads to the main question regarding the habitability of an exoplanet: can the exoplanet support liquid, or molecular, water? Whether or not this is possible is dependent on a multitude of characteristics, including planetary radius, orbital period, stellar radius, and planetary mass, working together to create an environment capable of life. The purpose of our research was to unravel this "mystery" by looking at data values from the NASA Exoplanet Archive (Planetary Systems Dataset). We started with a deduplication Python program to weed out duplicate entries in the NASA Exoplanet Archives, and then analyzed multiple planetary and stellar data values, through Keplerian Mechanics and on their own to filter out a list for us to take a deeper dive into. Subsequently, we conducted statistical calculations for further analysis. Further efforts can be made by applying Albedo and Circumstellar Habitable Zone (CHZ) data to the analysis of the habitability of an exoplanet. In the end our group formulated a list of ten exoplanets that we believe to be capable of supporting life.

Presentation Time: 11:15-11:30am (5) **Zoom Room:** Room 5

Research Group	**Authors/Researchers**
Jahanikia/Downing	Jonathan Ma, Krishnaveni Parvataneni, Harsha Samavedam, Shashank Sastry, Deniz Yilmaz

Title
Aggregation of Computer-Based Cognitive-Training/Rehabilitation and Personalized Brain-Care Interventions into the CognoTrain App

Abstract
Methods of CBCT/CBCR (Computer-based Cognitive Training/Rehabilitation or Brain-Care) have shown effectiveness as a means of positive intervention for groups of early-stage Alzheimer's disease and Dementia patients, but their development and testing occurred independent of one another. CognoTrain will function as an aggregate of these therapies to provide a holistic means of rehabilitation. Implemented CBCT measures in the app such as an address reminder system have proven to minimize symptoms such as topographical disorientation. The combined power of these techniques would produce an unprecedented level of cognitive improvement, introducing the possibility of a better life for more than 50 million dementia patients worldwide.

Presentation Time: 11:15-11:30am (8) **Zoom Room:** Room 4

Research Group	**Authors/Researchers**
Njoo	Erika Yu, Shreya Anand, Shloka Raghavan, Harrison Xu, Julia Vu, Alivia Zhang, Niharika Nambiar, Suhani Babu, Elena Brierley-Green, Tvisha Nepanl, Anushka Peer, Alice Finkelstein, Adrienne Ferguson, Udbhav Avadhani

Title
Chemical synthesis and acetylcholinesterase inhibitory activity of novel rivastigmine carbamate analogs

Abstract
Rivastigmine is a synthetic, neuro-active compound that was FDA approved in 2000. Physostigmine is its naturally occurring counterpart, found in the Calabar bean plant (physostigma venenosum). We explored the relationship between synthetic and naturally occurring compounds with the example of rivastigmine and physostigmine. Additionally, our presentation discusses several novel rivastigmine carbamate analogs synthesized under various conditions to determine computationally and biologically which is the most favorable when inhibiting the enzyme Acetylcholinesterase. The results are justified using Lipinski's Rules of drug bioavailability.

Presentation Time: 11:15-11:30am (22) **Zoom Room:** Room 1

Research Group	**Authors/Researchers**
McMahan	Diptanshu Sikdar, Adelina Chau, Arjun Bhamra, Max Cui, Kanthi Makineedi, Joey Huang

Title
Hybrid Quantum-Classical Generative Adversarial Network for Generating Synthetic, Chemically Stable Molecules

Abstract
Current drug discovery pipelines take between five to ten years and cost billions of dollars. As a result, scientists are researching computational approaches to search for molecules from the chemical space. One solution is deep generative models, which learn from the nonlinear data by modeling the probability distribution of chemical structures. These generative models can extract salient features which characterize the molecules. One of the most well-known unsupervised learning algorithms—Generative Adversarial Networks (GANs)—can discover valid drug candidates that abide by the laws of physics and chemistry. However, GANs often suffer from problems, including vanishing gradient and increasing complexity, due to the exponential increase in the volume of data.
We need a generative model that can better learn the representation of molecules more efficiently than classical ML models by searching the exponentially large chemical space. Quantum computing is better than classical computing at processing high dimensional data because qubits can represent exponentially more states than bits at the same time. Because of the immense power of qubits and parallelization possible, which is necessary for searching the chemical space, we propose a Quantum Generative Adversarial Network with a hybrid architecture: a quantum generator and a

classical discriminator. The quantum generator, a variational quantum circuit, would automatically learn features and generate valid molecules. The discriminator is a classical neural network, which classifies the fake and real molecular structures. The QGAN would learn from more than 100,000 molecules represented by adjacency lists.

Presentation Time: 11:15-11:30am (25)	**Zoom Room:** Room 3
Research Group Njoo/ Downing	**Authors/Researchers** Shloka Raghavan, Niharika Nambiar, Elena Brierley-Green, Suhani Babu, Andrew Chen, Tvisha Nepani, Nathaniel Thomas, Jane Wu
Title In vivo and in silico spiroketal structure activity relationship of nematocidal activity of avermectin-related macrolides	
Abstract Since their initial discovery over 4 decades ago, the avermectin family of complex polyketide macrocyclic natural products has revolutionized treatment of parasitic infections and garnered the attention of chemists, biologists, and clinicians alike. Specifically, owing to its chemical complexity, different members of the avermectin family of macrocycles have demonstrated potent and selective nematocidal activity which has benefited both animal hosts and human patients who have been affected by otherwise potentially deadly parasitic infections. Changes in the spiroketal structure, in doramectin and ivermectin, can potentially alter the compound's binding affinity to the protein target and thus biological activity. Through dose dependent in vivo paralysis assay on Turbatrix aceti through pixel heat based image and computational modeling efforts, we were able to identify specific interactions between spiroketal functionalizations and protein targets.	

Presentation Time: 11:15-11:30am (36)	**Zoom Room:** Room 2
Research Group Renganathan	**Authors/Researchers** Amrita Guha, Shrimayi Chaganti, Sahana Ravishankar, Aarya Morgaonkar, Shrinithi Sathiyaseelan, Tanvi Penugonda
Title Studying the effects of Trigonella foenumgraceum on hyperglycemic Caenorhabditis Elegans	
Abstract Type 2 diabetes is an illness that causes a lack of insulin/insulin resistance which affects how the body processes sugar and creates high blood sugar levels and other associated health concerns. Trigonella foenum-graecum or Fenugreek, is a plant in which its phytoconstituents – including amino acids, phenolics, flavonoids, saponins, and alkaloids -- have been researched and shown to exhibit hypoglycemic, antioxidant and therapeutic effects. This study aims to find which of the aforementioned compounds has the greatest anti-diabetic effect through conducting a series of in-vivo assays, such as Nile Red staining and Pharyngeal Pumping assay, on the microscopic C. Elegans model; as well as studying the results of colorimetric assays measuring the antioxidant activity of each phytoconstituent. In- vivo assays like the Pharyngeal Pumping assay measure the effectivity of the individual phytoconstituents of Fenugreek through pharynx and reactionary determination. Our studies in this group span from the synthesis of Fenugreek extracts to their effectivity in combating hyperglycemia.	

Presentation Time: 11:30-11:45am (18)	**Zoom Room:** Room 3
Research Group Sangeneni	**Authors/Researchers** Aneri Sheth, Taran Govindu, Sachi Patel, Abhiram Hanumanchi, Shrey Raj
Title Finding a Cost-Effective and Green Process to Synthesize Graphene Nanoplatelets for Energy Storage	
Abstract Graphene is a single atom layer of carbon that is arranged in a hexagonal lattice and is highly conductive. It has many unique properties like conductivity, tensile strength, and the light weight. Additionally it is very easy to synthesize compared to other substances like carbon nanotubes. This material shows promise in many applications but most importantly in supercapacitors because of its high electrical conductivity. Currently we tested multiple methods of synthesis in order to find out which one has the highest cost efficiency and produces the highest quality yield. We would ideally want graphene that demonstrated high conductivity. We experimented with different sonication methods because of the differences in the graphene developed because of the dispersion, solutions used and the contact. Multiple characterization methods and tools were used in order to analyze the quality of the material especially to check if there is any oxidation. Once we find a way to synthesize graphene that is cost effective, we can start to research methods to apply it to future energy storage via supercapacitors.	

Presentation Time: 11:30-11:45am (32)	**Zoom Room:** Room 4

Research Group	**Authors/Researchers**
McMahan	Sweekrit Bhatnagar, Yue Cao, Joshua Li, Diya Hasteer

Title
Relating Socioeconomic Position (SEP) with Rates of Covid-19 and Vaccination in Select Populations

Abstract
COVID-19 has demonstrated the implications of economic and social interactions in our society, and how they are closely linked with the spread of disease. A negative relationship between socioeconomic position (SEP) and rates of disease have been observed in multiple studies concerning a variety of diseases, including dengue fever, malaria, rabies, hookworm, and tuberculosis. In our study, we observed the relationship between COVID-19 and economic factors such as per-capita GDP, net taxable assessed value, public assistance, and more. Our aim is to find a correlation between various economic factors and prevalence and vaccination rates for COVID-19, and work towards creating a model for it. In addition to that, a preliminary model representing probability-based spread of disease provides us with a baseline to compare the prevalence with. This presentation will cover the results and the relationships that we determined between certain economic factors and disease, and our reasoning behind this data.

Presentation Time: 11:30-11:45am (41)	**Zoom Room:** Room 1

Research Group	**Authors/Researchers**
Benson	Amber Lu, Arohi Chirputkar, Ian Chen, Rowan Campbell, Zoe Chu

Title
The Effect of COVID-19's Impact on Human Activity on non-Protected and Protected Rocky Intertidal Tide Pools in San Mateo County

Abstract
After watching the profound impacts the COVID-19 pandemic had on human activity – a reduction in large indoor events and an uptick in outdoor activities – our group sought to investigate the impact of the change in human activity on the Northern California rocky intertidal ecosystem. Our research centered around the question: How has the impact that COVID-19 has had on the amount of human interaction with rocky intertidal zones affected their ecosystem health, as well as species biodiversity and abundance, when compared between protected and non-protected marine areas?

During the COVID-19 pandemic, people began to look to outdoor recreational activities to stay within COVID-19 restrictions. One of these activities was visiting non-protected tide pools such as Maverick's Beach, which stayed open throughout the pandemic. Park rangers noted seeing a dramatic uptick in the number of visitors to the tide pools and the amount of species being taken. On the other hand, protected locations such as Fitzgerald Marine Reserve, shut down for a six month period during the peak of the pandemic. During this time, the tide pools were completely undisturbed as no one could enter the reserve or remove any species.

Due to humans being able to take species from non-protected sites including but not limited to: moon snails, shore crabs, rock crabs, limpets, turban snails, sea urchins, mussels, oysters, hermit crabs, and even octopuses, the ecosystems of the non-protected tidepools have been severely affected. For example, because of predator species (ex: sea urchins are a predator to algaes and plants, and they are now being taken) being removed by humans, many species of seagrass and other organisms have grown dramatically due to the uncompetitive environment. In addition, overfishing is largely unregulated and reduces the population count of organisms belonging to a particular species.
To support our hypothesis and the reality of the issue, we first went to Maverick's Beach, a non-protected area. There, we took quadrat data using random sampling and transect lines. After collecting data from Maverick's Beach through multiple trips, we obtained permits from the Fitzgerald Marine Reserve and began data collection for a protected area.

Presentation Time: 11:30-11:45am (42)	**Zoom Room:** Room 2

Research Group	**Authors/Researchers**
Benson	Devam Parekh, Harshini Vakkalagadda, Aruja Gupta, Smriti Jha, Delisha Doppa, Anish Jupudy

Title
The Effects of Ocean Acidification on Barnacle Feeding and Predator Avoidance Behaviors

Abstract
Oceans are a crucial part of the Earth's anatomy; it gives life to marine organisms, allows for transportation for ships, acts as a storage area for inorganic material, and prevents extreme heating of the Earth by absorbing excess CO2 from the Earth's atmosphere. Specifically, our experiment is geared towards understanding the effects of how an increase in ocean acidification affects its ability to maintain a sustainable environment for marine creatures.
In our experiment, we placed two types of barnacles(balanus aquila-acorn and tetraclita rubescens-volcano) into saltwater tanks of different pHs. The control tank was at 8.1 pH, and the other two were at levels of 7.8 pH(middle pH) and 7.5 pH(low pH). Barnacles were fed zooplankton per data collection, and their feeding activity was measured by counting the amount of cirri extensions at 10 minute intervals leading up to 30 minutes. We also tested predator avoidance response for barnacles by using a sponge to replicate its predator's effects, and our previous finding that a light brush to the

barnacle's surface by a sponge caused it to retract still holds true. Previous data presented itself as statistically significant, but current findings show possible changes, and further study is needed to make a more definitive statement.

Presentation Time: 11:30-11:45am (43) **Zoom Room:** Room 5

Research Group	**Authors/Researchers**
Cunha	Alfiya Raja, Sreshta Yelisetti, Hena Patel, Ojasvi Mudda, Anika Aeka, Samantha Wu

Title
The Effects of RG108, a human DNA methylation enzyme inhibitor, and its related analogs on HCT116 Colorectal Cancer Cells

Abstract
Colorectal cancer (CRC) is a type of cancer that starts in the colon or the rectum. CRC is the third most common cancer, and it is also the second most common cancer leading to death amongst men and women (American Cancer Society, 2019).
The cell line used in the following experimentation was the epithelial human colorectal carcinoma 116 (HCT-116) cell line derived from an adult male (Imanis Life Sciences, n.d.).
The project is focused on the use of analogs from the drug RG108 to test their efficacy against DNA methylation. RG108 is a DNA methyltransferase inhibitor (DNMT inhibitor), which reverses the effects of DNA methylation by reactivating the tumor suppressor genes. (Brueckner et al., 2005)
RG108 was specifically chosen because of its different structure and mechanism action, classifying it as a non-nucleoside inhibitor, contrasting to other frequently used DNMT inhibitors which are nucleoside analog inhibitors. (Kundakovic, 2014)
RG108 is not an FDA-approved treatment for colorectal cancer, so this research takes a step forward in that process. To conduct our research, MTT assays, qPCR, and gene expression analysis will be utilized.

Presentation Time: 11:45am-12:00pm (7) **Zoom Room:** Room 5

Research Group	**Authors/Researchers**
Harman Brah	Smriti Kallahalla, Chloe Poon, Kerem Cekic

Title
Analysis of Palmatine Based Ligands to Guanine Quadruplex Stabilization

Abstract
The G-quadruplex (G4) is formed in nucleic acids by guanine-rich DNA sequences and is commonly researched in the development of cancer treatments. Compounds such as Palmatine are a promising novel area of research in terms of G4 stabilization, providing a possible non-cytotoxic chemotherapy substitute by stunting cancer growth by inhibiting the reverse transcriptase hTERT. The large planar aromatic surface of the G4 is a promising rationale for the binding of cyclic, planar ligands with aromatic characteristics of berberine-based ligands. Our research suggests that contrary to previous research, intercalative binding plays a very small role in binding specificity. We developed palmatine-based ligands that effectively bind to and stabilize the G4's activity. Our research found that smaller drugs required binding to the phosphate backbones of the G4 for thermodynamic favorability, but that larger molecules were generally favorable with higher observed binding affinities. Smaller ligands pursued a different pathway of stabilization than more traditional ligands by binding to the formed grooves characterized in the G4's helical structure, making heavy use of polar interactions. The favorability of larger molecules was mostly attributed to pi-pi stacking with the endplate and interactions with the central cations; larger molecules needed to achieve a certain amount of curvature in order to successfully bind to the grooves in the G4.

Presentation Time: 11:45am-12:00pm (13) **Zoom Room:** Room 2

Research Group	**Authors/Researchers**
Downing	Ansh Gupta, Dominic Chang, Landon Stobaugh, Divit Purwar

Title
Developing a Framework for a Multi-Sensor Soil Data Collection & Analysis System

Abstract
For decades, many farmlands have had their productivity hampered by environmental pollutants from surrounding industrial infrastructure. However, the development of several physical sensors has allowed farmers to monitor the soil's health and prevent such loss. Here, we focus on developing a framework for collecting and analyzing soil data. Moisture and nitrogen/phosphorus/potassium (NPK) sensors will be integrated into an Arduino Uno. A client-server architecture will be built as the repository for a predictive, mathematical model to enable future data analysis. As environmental chemical changes alter the productivity of the soil, data collected by the proposed device will allow fluctuations [which impact soil health] to be identified and used as predictors for remediatiative treatment.

Presentation Time: 11:45am-12:00pm (14)	**Zoom Room:** Room 1
Research Group Kaur	**Authors/Researchers** Shreyan Phadke, Siddh Saxena, Shrinad Bangalore
Title Effects of Excess Arbuscular Mycorrhizae on Phosphorus Deprived Lactuca Sativa	
Abstract The associations between roots and fungi are called mycorrhizae. There is a mutualistic relationship between them fosters better water and nutrient absorption by plants, and can enable plants to share resources. The main nutrients required by plants for optimal growth are nitrogen, phosphorus and potassium (NPK). We hypothesised that when there is deficiency of any of these nutrients, arbuscular mycorrhizae may compensate by sharing the limited amount of the nutrient between various plants. We are studying the growth pattern of Lactuca Sativa (Buttercrunch Lettuce) in low and optimal phosphorus soil environments. We are testing the effect of low, natural and elevated levels of mycorrhizae in each of these soil environments. The growth of plants will be monitored based on leaf size, plant height, root depth and more. If the plants growing in phosphorus deficient soil compare or grow better than plants in optimal phosphorus soil, this will support our claim that mycorrhizae can replace soil nutrients.	

Presentation Time: 11:45am-12:00pm (20)	**Zoom Room:** Room 4
Research Group Brah	**Authors/Researchers** Rohinee Mattikalli, Shruthika Srinivasan, Shivani Ravindra
Title FTO inhibitor design through molecular docking	
Abstract The fat mass and obesity related (FTO) gene is located on human chromosome 16 and contains the codes for the FTO protein. The fto protein has been positively linked with an increased risk of obesity, diabetes, and other cardiovascular diseases. The protein is an RNA/DNA demethylase, which, according to studies, links the protein with the cardiovascular diseases. In our project, we used molecular docking to find and analyze interactions between ligands and the FTO protein to find a compound structure to inhibit the RNA demethylation.	

Presentation Time: 11:45am-12:00pm (44)	**Zoom Room:** Room 3
Research Group Jahanikia	**Authors/Researchers** Aaminah Mohammad, Abinaya Senthil, Ananya Ravi, Anika Mantripragada, Avi Uppalapati, Claire Wu, Destiny Pinto, Devan Melwani, Erin Yang, HeeJee Yoon, Matthew Kang
Title Understanding the Correlation Between COVID-19 Vaccines and Sleep Quality on Vaccinated versus Unvaccinated participants	
Abstract The COVID-19 pandemic has significantly impacted people's lives, including their sleep. The goal of this study is to track the correlation between sleep quality and COVID-19 vaccination status by assessing the sleep quality of both vaccinated and unvaccinated participants. In order to achieve this goal, an eligibility questionnaire, a demographic questionnaire, as well as a HIPAA-compliant digital questionnaire measuring sleep quality were constructed. As this study involves informed consent, the IRB has approved the study in relation to HIPAA compliance/IRB approval standards, which included the long and short consent forms for both adult and minor participants, as well as eligibility, demographic, and COVID-19 and sleep questionnaires. Dummy data is currently being collected in order to test Jotform, as real data collection is the next step for this study.	

Presentation Time: 12:00-12:15am (33)	**Zoom Room:** Room 5
Research Group Jahanikia	**Authors/Researchers** Shreya Udupa
Title Sentimental analysis using natural language processing	
Abstract Sentimental analysis using natural language processing	

Presentation Time: 12:00-12:15pm (6)	**Zoom Room:** Room 4
Research Group Sangeneni	**Authors/Researchers** Aneri Sheth, Sahand Adibnia, Caton Zhu, Masroor Uddin, Aaron Hsi

Title
Analysis of Microsilicon and Nanosilicon for Lithium-Ion Battery Anodes

Abstract
Silicon anodes are currently being researched as a more energy-dense alternative to graphite anodes in lithium-ion batteries. However, silicon anodes exhibit volume expansion, a property not observed with nano-silicon. The application of nano-silicon is currently limited due to greater surface area compared to normal silicon resulting from smaller particle sizes which uses more electrolyte in a battery. The goal of our research is to find the optimal particle size of nano-silicon that will minimize surface area to use less electrolyte without causing significant volume expansion. We have begun characterizing micro- and nano-silicon of particle size ranges of 50 µm, 150-200 nm, and 20-30 nm. We utilized Fourier-Transform Infrared Spectroscopy (FTIR) to evaluate the presence of impurities in these nano-silicon samples, X-Ray Diffraction Spectroscopy (XRD) to determine the crystal structure of our nano-silicon samples, UV-Visible spectroscopy to evaluate absorbance trends with particle size, and cyclic voltammetry (CV) to determine the energy density of different nano-silicon-based inks. Our FTIR analysis showed that nano-silicon of particle sizes ranging from 20-30 nm was more prone to oxygen-related impurity formation due to an FTIR peak at 1071 cm-1 that corresponds to asymmetric vibration of Si-O bonds.

Presentation Time: 12:00-12:15pm (21)	**Zoom Room:** Room 3
Research Group Brah	**Authors/Researchers** Sankrith Ramani, Isha Tailor, Chloe Poon, Smriti Kallahalla, Stephanie Cheung, Vivek Parashar, Aashita Krupadanam

Title
G-Quadruplex Stabilization

Abstract
In order to understand how the G-Quad can form, it is important to understand more about DNA. The scientific community has known about the 2-stranded B-DNA structure since the 1950s, but over the years, scientists have discovered that DNA can fold into structures that deviate from this. The G-Quadruplex is a DNA secondary structure that deviates from this. At one point, the G-Quadruplex was thought to only form in-vitro, but research in bioinformatics has shown that sequences capable of forming into a G-Quadruplex have been conserved throughout evolution, implying that these structures may have physiological importance and can assemble in physiological conditions.

Presentation Time: 12:00-12:15pm (29)	**Zoom Room:** Room 2
Research Group Jahanikia	**Authors/Researchers** Aanika Bedi, Amulya Harish, Heejee Yoon, Lale Kurtulush, Mano Tatapudi, Myra Malik, Rohan Kondapalli, Rujuta Jambe, Tanisha Mehta, Tanvi Vidyala, Tanya Naveen

Title
Overview of Cognitive Dissonance Theory With Associated Neuroimaging Modalities

Abstract
Cognitive dissonance theory is a theory stating that when there exists a discrepancy between someone's external actions (behaviour) and their internal values (attitude), in most people this discrepancy will cause dissonance, and, to justify this dissonance, cognitive rationalization. Cognitive dissonance has been studied and measured using neuroimaging modalities, namely EEG and fMRI. Certain event-related potentials, measured by EEG, and areas of the brain, detected by fMRI, are involved primarily in cognitive dissonance and cognitive rationalization. This information can be utilized to analyse cognitive dissonance and its applications in aspects of everyday life by contrasting a positive behavior with a negative/biased attitude, as opposed to the typical model of a negative behavior and a positive/morally 'just' attitude, as well as to develop a psychological assessment to measure someone's individual level or experience of cognitive dissonance.

Presentation Time: 12:00-12:15pm (45)	**Zoom Room:** Room 1
Research Group Jahanikia	**Authors/Researchers** Aditya Anantaraman, Anisha Grover, Brandon Brewer, Dhruv Bhargava, Julia Wind, Sruthi Sudarsan, Leo Sun

Title
Understanding the Nature of Brain Imaging Data and Converting for Further Analysis of Musical Genre Perception

Abstract
FMRI is a non-invasive neuroimaging technique that uses BOLD signals to construct high-resolution images of brain activity in response to stimuli. By using various neuroimaging tools and techniques, we will preprocess and analyze a fMRI dataset obtained from the University of Magdeburg Psycho- informatics Lab which contains scans of participants

guessing the genre of music featured in clips from a movie both with and without audio. In order to preprocess the data, we first need to convert the raw data into the Brain Imaging Data Structure (BIDS), a standard way of organizing neuroimaging data. In our research, we aim to identify networks of the brain associated with guessing a music genre without audio and understand and explain the role of the auditory network in genre association.

Presentation Time: 12:15-12:30pm (3) **Zoom Room:** Room 5

Research Group	**Authors/Researchers**
Jahanikia	Alissa Doemling, Amritha Srinivasan, Angeline Yeh, Maaya Selva, Megan Pau, Rucha Kulkarni, Meenakshi Yarlagadda

Title
A process towards collecting data to validate the novel psychological assessment to measuring Creativity of Social Media Influencers (MCSMI)

Abstract
Creativity assessments are used to determine how creative an individual is; some assess to what degree of achievement someone has attained in a certain skill whereas other assessments ask individuals to think of ways to repurpose or create something in a certain amount of time. The Creative Achievement Questionnaire (CAQ) currently assesses achievement in categories like music, art, dance, design, and scientific discovery, among other topics. Another assessment, the Inventory of Creative Activities and Achievements (ICAA), assesses the frequency of actions alongside the degree of achievement attained. One category not currently present in the CAQ or ICAA is creative influencers — people who use social media to promote their creative skill and influence others to learn what they do or get endorsements from companies to help promote their skill. We aim to create an assessment that will determine whether an individual is a creative influencer and possibly add this assessment to the CAQ or ICAA. The modern age has changed the traditional definition and view of creativity due to the presence of social media, so determining the difference between creative social media influencers versus just social media influencers is crucial. This term we started to streamline the data collection process, learning the proper protocol to collect human behavioral data and continuing the effort from last term to shortlist creative influencers as well as beginning with initial steps of getting IRB approval through consent forms for HIPAA compliance and PHI protection. We created the online questionnaires on a secure platform and figured out the logistics for collecting and analyzing the data.

Presentation Time: 12:15-12:30pm (15) **Zoom Room:** Room 1

Research Group	**Authors/Researchers**
Renganathan	Archana Satish, Harshita Bathina, Shreya Gulati, Sameeksha Ramesh, Julianna Chang, Srinidhi Sampath, Shikha K

Title
Emerging Potential of Thymoquinone and Piperine Nanostructured Lipid Carriers for Cancer Treatment

Abstract
Nanostructured lipid carriers (NLCs) are drug delivery systems that can improve oral administration of drugs that have poor aqueous solubility and poor metabolic stability, while also reducing toxicity and increasing the dosage of drugs delivered to the body. Thymoquinone (TQ), a flavonoid, is obtained from black cumin (Nigella sativa) and possesses anti-inflammatory and antioxidant qualities that prevent damage to cells and induce apoptosis in cancer cells. However, thymoquinone has poor aqueous solubility leading to limited bioavailability, the dose of drugs that reach the treatment site. To combat this, we chose piperine (PP), an alkaloid responsible for the pungency of black pepper (Piper nigrum), to increase the bioavailability and absorption of drugs such as curcumin, making it a likely component in increasing thymoquinone's solubility and anticancer effects via NLCs. We report that the NLCs are viable delivery systems with a constant release rate and high entrapment efficiency of 99.64% and 99.74% average entrapment of TQ-loaded and TQ and PP-loaded NLCs. With the NLCs, we investigated TQ's anticancer mechanism that targets copper located in cancer cells to induce oxidative damage. Post-gel electrophoresis assay, the DNA damage and elongation of HCT116 cells exposed to TQ and PP loaded NLCs averaged out to be greater than that of the cells exposed to unloaded NLCs and TQ loaded NLCs, respectively. Our findings indicate that the NLCs are optimal for drug delivery, and based on the cell morphology and quantitative results, piperine is a favorable candidate in enhancing thymoquinone's anticancer abilities.

Presentation Time: 12:15-12:30pm (26) **Zoom Room:** Room 4

Research Group	**Authors/Researchers**
Benson	Rachel Jiang, Aryel Zhang, Anusha Sainarayanan, Nitya Sharma, Pranav Prakash

Title
Investigating the Ecological Impacts of Invasive Mud Snail Species, Ilyanassa obsoleta, on Native San Francisco Bay Mudflat Inhabitants

Abstract
Ilyanassa obsoleta, native to the Atlantic coast, is a foreign yet abundant mollusk in the San Francisco Bay mudflats. It is a well-established invasive species noted for displacing the native mud snail, Cerithidea californica (Race, 1982). The objective of this study was to analyze the impact of I. obsoleta's presence on the biodiversity, species abundance, and size distribution of native mudflat species. Using random sampling and biodiversity hotspot methods, our team collected

samples from four different locations: Berkeley Marina (North and South), Point Emery, and Crab Cove. We processed samples based on specimen wet weights and sizes and compared data from sites with a presence to sites with an absence of I. obsoleta. We plan to extend our project by acquiring more field data, especially in sites observed to have an abundance of I. obsoleta, and diversifying our means of processing and analysis.

Presentation Time: 12:15-12:30pm (31)	**Zoom Room:** Room 2
Research Group Njoo	**Authors/Researchers** Samyukta Athreya, Srishti Venkatesan, Harrison Xu, Pratyush Singh, Andrew Chen, Kara Tran, Aishi Rao, Modakar Kurma

Title
Reactivity-informed design and synthesis of novel andrographolide analogs, therapeutic leads for cancer & neurodegenerative disease

Abstract
Andrographolide is a natural product extracted from the plant Andrographis paniculata, and has been shown to be incredibly versatile in biological activity. Andrographolide demonstrates anticancer, antiviral, antioxidant, and more properties, while also being relatively nontoxic. The compound has an α, β unsaturated lactone, which serves as a Michael acceptor, irreversibly alkylating its protein targets. Numerous studies have been reported attempting to create novel analogs of andrographolide in order to increase efficacy, but the complexity of the compound proves to be an issue in development. We aim to build on current approaches to improving andrographolide as a drug, as well as experimenting with chemoselective modification of both the A/B trans-decalin core, which we postulate is important for target binding, and the C-ring butenolide warhead.

Presentation Time: 12:15-12:30pm (39)	**Zoom Room:** Room 3
Research Group Kaur	**Authors/Researchers** Sylvia Lyu, Antone Jung, Navya Gupta

Title
Testing relative abundance and diversity of Rhizobium in urban gardens

Abstract
Rhizobium bacteria, while characteristically living in the root nodules of mutualistic legumes, exist independently in soil as motile bacteroides. They are of great ecological and agricultural importance, for their ability of nitrogen fixation. In this study, we investigate the diversity and abundance of Rhizobium in differently developed soil types. Samples were collected in triplicate from the LEAF Urban garden in Fremont from three sublocations. qPCR with genus-specific nifH primers quantified the relative abundance of Rhizobium populations. Preliminary data suggests significant differences between groups. DNA extracted from group 1 (undeveloped with nearby vegetation) had an average Ct value of 15.22, group 2 (cultivated for 7 years) had an average Ct value of 30.60, and group 3 (undeveloped) did not reach the threshold position. Downstream RFLP analysis of amplified DNA can determine Rhizobium species diversity. In this presentation we will present the results of our research.