SUMMER UNDERGRADUATE

RESEARCH CONFERENCE

2020

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NSERC USRA:
UNDERGRADUATE STUDENT RESEARCH AWARD

RAMAN ABBASPOUR

BIOLOGY

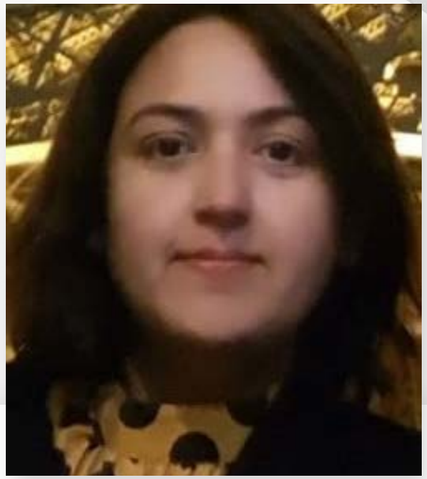
PROJECT

Probing sex differences in neuromodulation of LTP

SUPERVISOR

Steven Connor

Specialized zones of communication between neurons known as synapses serve as "weight stations" for information processing throughout the brain. Synapses accomplish this through an intrinsic ability to be modified in response to ongoing experience, a process known as synaptic plasticity. A central mechanism through which synapses undergo enduring changes is through activation of neuromodulatory receptors, which engage a diverse array of molecular signaling events. Of the neuromodulators linked to memory formation, perhaps none is more powerful than noradrenaline (NA). Activation of NA receptors initiates bidirectional changes in synaptic strength that can promote or prevent memory formation, dependent upon the type of receptor and brain cell in which it is expressed. A major gap in our understanding of how NA regulates synapses is due to the lack of investigation into the sex-dependent shifts in plasticity responses that remain virtually unexplored in female subjects. Understanding the cellular and molecular events associated with NA receptor activation that are sexually dimorphic in nature is key for understanding the fundamental properties of synapses. My project uses electrophysiology techniques combined with pharmacological tools to probe for sex-based mechanistic differences in NA receptors mediated synaptic plasticity.



AISHA ADIL

BIOLOGY

PROJECT

Persistent phosphorylated state maintains elasticity of tethers during anaphase cell division

SUPERVISOR

Arthur Forer

My research is on understanding the dynamics of chromosome movements during cell division, which involves partner chromosomes being pulled apart by spindle fibers towards their corresponding poles. Dr. Arthur has discovered elastic tethers which connect partner chromosome arms; these tethers behave like elastic bungee cords and exert a force on the separating partner arms directed towards each other and opposite to spindle fiber force directed towards the pole.

My work provides evidence supporting elastic tether dynamics during cell division; we cut chromosomal arms at different stages of chromosomal separation and measure cut arm velocity, distance and direction moved by cut arm, cut arm behavior at end of its motion, and behavior when both partner arms are cut. These parameters are measured in control cells and in experimental cells treated with phosphatase inhibitor, so as to test the theory that elasticity of tethers is preserved as long as they remain phosphorylated during the course of chromosomal segregation.

This project is exciting for me because it can pave the path to better understanding of chromosomal segregation anomalies; the possible cause (and treatment) of chromosomes failing to separate properly during gametic cell division leading to diseases, like Down's syndrome, in the resultant fetus.

JULYANA AL-HUSSAIN

BIOLOGY

PROJECT

Synthesis of copper nanoparticles with antimicrobial properties

SUPERVISOR

Jennifer Chen

Nanoparticle technology is a captivating branch of science, where nanoparticle properties can be used in a variety of fields. They have many applications in biomedical sensing, electronics and medicine, to name a few. This is due to their unique properties, such as distinctive quantum properties, that differ from their bulk metal counterparts due to their shapes and sizes. Specifically, copper nanoparticles display unique properties, are abundant, relatively inexpensive, and can be prepared using straightforward techniques. This allows for their incorporation in the production of materials.

Julyana's project involves the synthesis of stable copper nanoparticles from copper (II) sulfate and various stabilizing agents, such as Polyvinylpyrrolidone, and reducing agents, such as sodium borohydride and citrate. UV-vis spectroscopy is used for optical characterization of the size, shape, and amount of nanoparticles. The project also involves developing methods to coat fabric and non-woven materials and testing the microbial capabilities of the nanoparticle-coated material. Copper oxide has displayed potential antiviral and antibacterial properties that would be useful in implementing this technology into coatings, such as gowns and respiratory masks, to serve as an extra layer of protection from droplets containing the microbes. This would reduce disease transmission between individuals. With the emergence of COVID-19, which has impacted the lives of many, the implementation of nanoparticle technology could potentially mitigate the spread of the virus in the hospital and community setting.

EMILY ANACLETO

BIOCHEMISTRY

PROJECT

Conformational dynamics of the anti-ppoptotic BCL-2 / BID protein complex

SUPERVISOR

Derek Wilson

A protein's function does not solely depend on its ground state structure, but also on the motions it undergoes when carrying out its function, i.e., conformational dynamics. By modelling the dynamics of a protein, active regions can be identified and used to better understand the underlying mechanisms essential for function.

The BCL-2 family of proteins regulate programmed cell death through binding interactions that affect the mitochondrial outer membrane permeabilization (MOMP), leading to the release of intermembrane space proteins, caspase activation and apoptosis. BH3 interacting-domain death agonist (BID), is a BCL-2 family protein that is pro-apoptotic, and its pro-apoptotic ability can be inhibited by anti-apoptotic proteins like the BCL-2 protein. The BCL-2 protein can sequester BID and prevent it from binding to and activating BAX, which can form pores in the mitochondrial outer membrane and release cytochrome c and other pro-apoptotic factors.

Through the use of molecular dynamics (MD) simulations, we will develop virtual models of the two proteins BID and BCL-2 that will allow us to observe how binding changes the way that the proteins move and fold. The dynamics of the human BCL-2 protein and a peptide fragment of the protein BID will be analyzed independently and when the two proteins bind to each other. The dynamics of a protein when not bound will be compared to the dynamics of the protein when it is bound. The aim of my project is to understand how conformational dynamics allows proteins that have highly similar structures to have significantly different binding specificities.

DYUMAN BHATTACHARYA

PHYSICS & ASTRONOMY

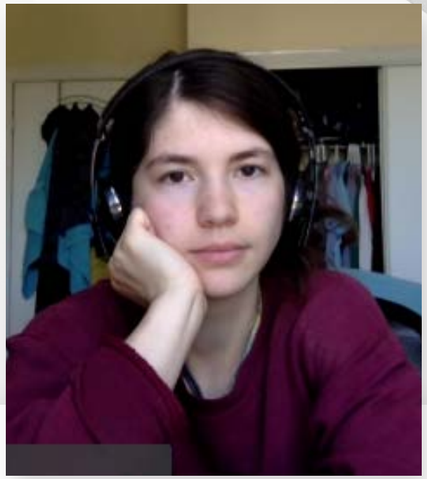
PROJECT

Modelling and analysis of quasar spectra

SUPERVISOR

Patrick Hall

Quasars are highly luminous active galactic nuclei in which gas forms an accretion disk around a central supermassive black hole. As gas falls into the gravitational well of the black hole, gravitational potential energy is converted into radiation energy. Ultraviolet photons ionize gas that is farther away from the quasar, and the destruction or creation of photons by this gas gives rise to broad absorption or emission lines. Studying these broad absorption and emission features in the spectra of quasars tells us about the properties of their central black holes, such as their masses and spins. This in turn improves our understanding of the evolution of galaxies. Professor Hall and his team model existing complex quasar spectra as a combination of a comparatively small number of components using a technique called Heteroscedastic Matrix Factorization (HMF) to construct a basis set for quasars. Modifications were made so that extinction (radiation being reddened due to scattering off interstellar dust) was taken account in the analysis of the quasar spectra. This project will advance our understanding of quasars and black holes through the use of machine learning to "build up" reconstructed spectra, which are then compared to real spectra.



SOPHIA BUGARIJA

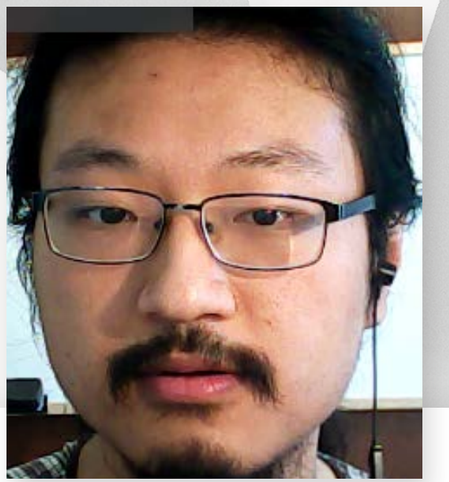
MATH & PHYSICS

PROJECT

Hyperbolic geometry and acoustic Imaging of layered media

SUPERVISOR

Peter Gibson



MATTHEW TSANG

MATH & PHYSICS

The interaction of sound with physical materials is governed by mathematical equations, aspects of which are only partially understood. The familiar fact that bats and porpoises are able to navigate in total darkness by listening to the echoes of clicks they emit shows that it is possible to use recorded echoes to construct a picture of ones surroundings. However current technologies such as ultrasonic imaging are severely limited by our incomplete understanding of the mathematics underlying this process. Indeed the search for a better understanding is the focus of an international research effort. This USRA project centres on a recent mathematical discovery linking hyperbolic geometry (famously illustrated by MC Escher) to the mathematics of acoustic imaging, drawing on pure mathematical results to analyze acoustic imaging of a special class of physical media having a laminated structure—known as layered media. Layered media include biological tissues such as skin or the retina, stratified geological structures such as sedimentary rock, and laminated materials in the built environment. The work spans pure mathematics, computational algorithms and real world data. It offers the possibility of new methods to image layered media using ultrasound, for example, with the goal of transcending the limitations of current technologies.

BARTOLOMEO CANDELMA

CHEMISTRY

PROJECT

Study of the microstructure and corrosion properties of a Ni-SiO_2 nano-composite Coating

SUPERVISOR

Sylvie Morin
Mehry Fattah

Corrosion has been an ongoing problem that causes a waste of valuable resources, loss of money and release of contamination products in our environment. Nickel coatings are commonly used as protective coating on plane gears and gas pipes; if these were to corrode rapidly it would be very dangerous. Electro-codepostion further improves corrosion resistance by depositing metals and nanoparticles simultaneously onto a surface. In electro-codespostion, metal ions are reduced while dispersed fine powders, like nanoparticles, are trapped in the deposited coating. The nanoparticles are used to improve the coating hardness and corrosion resistance. My research focuses on the preparation of nickel/silicon dioxide (SiO_2) coatings onto a carbon steel surface using different preparation parameters. The goal is to find out if the nanoparticles improve the coating properties and under which preparation conditions. To find out, I prepare polished carbon steel samples that are then electro-codeposited with nickel and SiO_2. High resolution microscopy is used to see if the nanocomposite surfaces are uniform and their structure is characterized using X-ray diffraction. The samples are then tested for their corrosion resistance and hardness in order to quantify how the presence of nanoparticles affect the properties of the nickel coatings.

KATRINA CARVER

PHYSICS

PROJECT

Modeling electric field uniformity for the EDMcubed collaboration

SUPERVISOR

Eric Hessels

Katrina's research involves modelling electromagnetic fields for the EDMcubed Collaboration under the supervision of Dr. Eric Hessels. Specifically, Katrina is investigating the uniformity of the electric field over the volume surrounding the rare-gas argon matrix. This matrix holds the polar molecules which will be studied to measure the electron's electric dipole moment (eEDM). By trapping the polar molecules, the EDMcubed experiment has the ability to reduce the uncertainty in the measurement of the eEDM by up to five orders of magnitude compared to other leading experiments. This more precise eEDM value could guide extensions to the Standard Model, aiding in the understanding of dark matter or matter-antimatter asymmetry, for example.

Determining the uniformity of the electric field is vital, as it will be essential that all molecules embedded in the solid argon have the same environment for a measurement at this precision. Employing numerical techniques such as the Successive Overrelaxation Method, Katrina uses FORTRAN to write programs that compute the steady-state electric field at any point in the system, subject to increasingly complex boundary conditions. Furthermore, Katrina is learning to use Comsol Multiphysics, a physics modelling software, which will allow her to represent and study various other systems within the experiment.

DAYANA DAVOUDI

KINESIOLOGY & HEALTH SCIENCE

PROJECT

Bioinformatic analysis of a signaling pathway in *Tetrahymena thermophila*

SUPERVISOR

Ronald E. Pearlman

The eukaryotic ciliate protozoan, *Tetrahymena thermophila*, is a useful model organism for the study of biological processes conserved in many eukaryotes. The unique genetic features of this organism have been used to answer fundamental questions in the field of biology, and have led to the Nobel Prize-winning discoveries of catalytic RNAs and telomeres. The fully sequenced genome of *T. thermophila* along with extensive genomic and proteomic databases available for this organism, allow for the bioinformatic analysis of its proteins and molecular pathways.

Using these collections of data, Dayana is investigating the cellular signaling pathways that use protein kinase enzymes to carry out the post-translational addition of a phosphate group to specific amino acid residues of proteins. The focus is on tyrosine phosphorylation pathways that are involved in many important biological processes. Dayana is analyzing the cyclin-dependent kinase annotated as Cdk13, which is thought to be dual-specific in nature and involved in the stress response and sexual reproduction of *T. thermophila*. Through this bioinformatic analysis, it is hoped to gain a better understanding of the nature of dual specific kinase enzymes that are capable of phosphorylating serine, threonine, and tyrosine amino acids, and find critical information about the function and evolution of cellular communication systems.

KEVIN DU

HEALTH SCIENCE

PROJECT

MiRNAs in ovarian cancer metastasis

SUPERVISOR

Chun Peng

Ovarian cancer is the sixth deadliest form of cancer in females, with a 5-year survival rate under 50%. Although outcomes at early stages are relatively favorable, patients are often diagnosed at advanced stages with metastasis. Symptoms are often unnoticed or nonexistent and there is a lack of effective screening and early detection. Ovarian cancer most commonly metastasizes through transcoloemic spread- the occurrence of epithelial-mesenchymal transition allows for dispersal into the peritoneal space and invasion of surrounding structures. MicroRNAs are short, non-coding RNA molecules which regulate gene expression by pairing to mRNAs. With a considerable sum of targets, miRNAs are involved in many cellular processes. Deviations in tissue and serum levels of specific miRNAs correlate with and may promote the progression of ovarian cancer. Kevin Du will work towards a review of microRNA in ovarian cancer metastasis. The review will identify, consolidate, and assess current literature while evaluating future paths of research to develop the understanding of miRNAs in ovarian cancer and their potential as diagnostic and treatment targets.

NAZANIN GHELICHI

MATHEMATICS

PROJECT

An attempt to a deep understanding of the Strong Goldbach's conjecture

SUPERVISOR

Alexy Kuznetsov

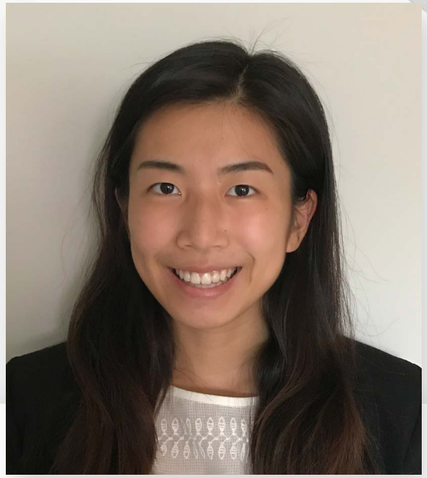
We are working on the strong Goldbach's Conjecture, one of the oldest and most famous unsolved problems in mathematics. It asserts that every even integer greater than or equal to four can be expressed as a sum of two prime numbers. This conjecture was first posed in 1742 by the German mathematician Christian Goldbach.

The conjecture is easy to express, yet it is tough to prove assuming there exist a proof. Case in point, as the name "conjecture" suggests, the proof of the query remained a mystery for almost three hundred years.

The significance of the strong Goldbach's Conjecture can be traced back to numerous precincts of Number Theory, such as Additive Number Theory, Sieve Methods, Analytic Number Theory. Moreover it has connections to many other branches of Mathematics and understanding other transcendent enigmas such as Generalized Riemann Hypothesis (GRH).

We plan to look at Schnirelman's approach, which reached to one of the first significant results on Goldbach's Conjecture. We also plan to study the Goldbach's Conjecture from the numerical point of view.

Our main aim is to understand Schnirelman's method and its extensions while trying to study the strong Goldbach's Conjecture's applicability to other problems in Additive Number Theory.



MUZI LI

BIOMEDICAL SCIENCE

PROJECT

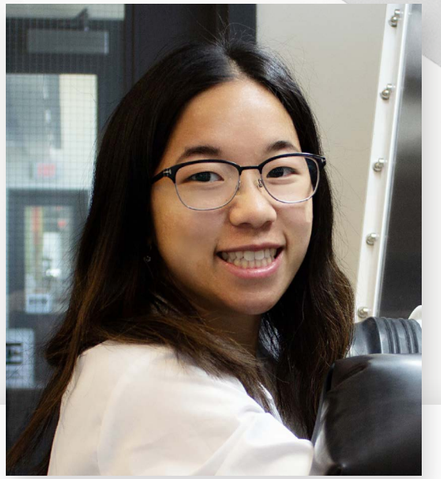
Synthesis of symmetric biphospholes for systematic structure-property studies

SUPERVISOR

Thomas Baumgartner

There is currently a global energy crisis that calls for scientists to seek out environmentally friendly, sustainable energy sources. Carbon-based optoelectronic devices such as organic field-effect transistors (OFETs), organic photovoltaics (OPVs), and organic light-emitting diodes (OLEDs) are developed to replace traditional, non-sustainable energy devices. As a result, this calls for the development of materials with good conductive and photovoltaic properties for incorporation in these devices. There are already numerous established p-type semiconducting materials, but the instability of n-type materials demands for further scientific exploration.

My project focuses on utilizing dithieno[*3,2-b:2′,3′-d*]phospholes to create unique building blocks for n-type materials as they are capable of electron conduction. Seeing that the majority of the work performed on these molecules are electronic modifications to the phosphorus center and the main scaffold, my project takes a different approach and seeks dimerization through P-P bridging. The P-P bridged dimers expand the effect of conjugation into three dimensions, and they further exhibit improved electron-accepting properties. These symmetric dimers show unique packing structure and allow for the delocalization of electrons through 3D step conjugation. I specifically focus on modifying the main scaffold of these symmetric dimers with electron-donating and electron-withdrawing substituents to study their effect on photophysical, electronic, and redox properties.



STEPHANIE LO

BIOLOGY

PROJECT

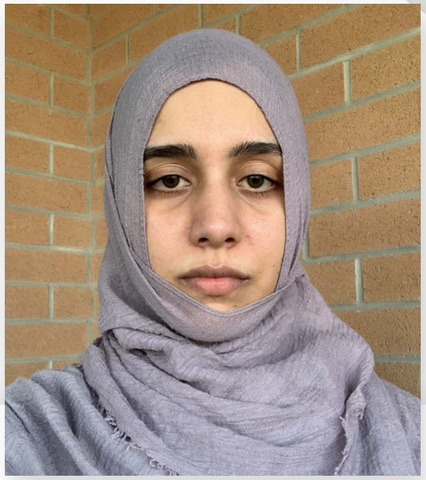
Designing viologen-based electrode materials for rechargeable batteries

SUPERVISOR

Thomas Baumgartner

The global demand for energy, which spurs our use of fossil fuels, continues to increase despite the resulting pollution and rapidly changing climate. This has initiated a strong demand for storing energy produced from intermittent renewable sources like wind and solar and to integrate them into city grids. However, present large-scale energy storage practices can only store a fraction of the renewable energy being generated. Further, state-of-the-art rechargeable battery materials contain elements that are toxic, costly and not abundant making them unsuitable to scale up to power cities and factories worldwide. Using organic materials as battery electrodes is beneficial as they are non-toxic, use abundant elements, and materials can obtain unique properties from synthesis techniques and the diversity of organic molecules.

Stephanie's focus is on creating organic polymers as electrode materials for rechargeable batteries. Viologen is an attractive organic molecule for rechargeable electrode materials due to its highly reversible electrochemical properties. She is incorporating viologen into polymers with varying amounts of molecular structures designed to improve ion conductivity, electron conductivity, and decrease solubility to optimize battery performance. Specifically, she is looking at how the final composition of the viologen polymer can be tuned to maximize how quickly the electrode can be charged and discharged, while minimizing electrode degradation with repeated use. This will increase the power output and reliability of organic electrodes, allowing this technology to be translated into grid-scale energy storage systems that are cheap, sustainable, and non-toxic. Organic electrodes are promising technology that is necessary to achieve a fully sustainable energy economy.



MARIA MEHMOOD

MATH & PHYSICS

PROJECT

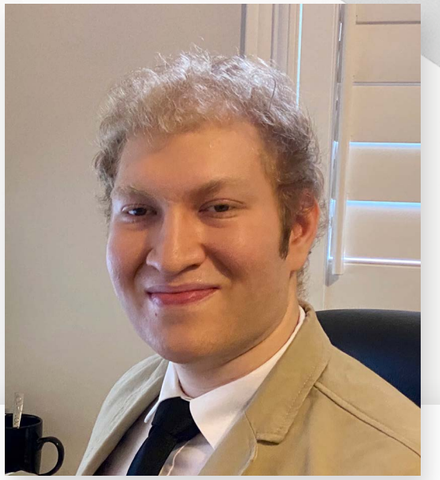
Analyzing neutrino data obtained from the MINERvA experiment at Fermilab

SUPERVISOR

Deborah Harris

The MINERvA experiment at Fermilab uses a high intensity beam of neutrinos obtained by crashing 120 GeV protons on a carbon target and focusing the positively or negatively charged particles that get produced using a magnetic horn. Most of the focused particles then decay to neutrinos. The interactions of the neutrinos on three different nuclei: Carbon, Iron, and Lead, are being studied in order to determine how the environment of the nucleus might change those interactions. This can tell us about the nucleus itself. Different targets of the same nuclei appear in different locations in the detector.

My study focuses on analyzing how different the flux is for different locations of the detector. The study compares a simple program which only predicts the average flux over the entire detector with the fluxes obtained using a more first principles prediction. I want to understand the flux as a function of neutrino energy because to measure the cross section as a function of neutrino energy you need to divide by that flux. For the current cross section measurement, the flux is assumed to be the same at different locations. Hence, this flux study will allow the experiment to do the cross check on the cross-section measurements because there should be agreement between the cross sections in different areas of the detector for the same nucleus.



WALLY MIR

BIOLOGY

PROJECT

Examining the correlation between the frequency of mating events and the genetic diversity of a colony by categorizing worker bees

SUPERVISOR

Amro Zayed

Bees exhibit unique genetic makeup whereby females have two sets of each chromosome and males have one set (diploid and haploid, respectively). This in turn results in males transferring all their genetic information to their children, whereas females will transfer only half. The queen is often the only bee that mates within a colony, meaning every male bee (drones) born will be genetically identical to the queen or their dad. Female bees (worker bees) will have all the genetic information of their father, and half of the queen's. Using this knowledge, this research project aims to examine the relationship between colony diversity and how often the queen mates. This will be determined by analyzing and categorizing worker bees in each colony, based on their genetic makeup at various genes (also known as microsatellite loci), to determine their siblingship to one another. This siblingship will also discern how many distinct "families" (patrilines) exist in a particular colony (one unique drone per family). Colonies with higher genetic diversity can influence resistance to pathogens and overall benefit a colony's health, thereby making it beneficial to mate more and produce unique offspring. If this hypothesis holds, it would be a remarkable finding with applications to bee conservation and preventing inbreeding within colonies necessary for agriculture.

DIEGO MONTALVO

PHYSICS

PROJECT

Light attenuation from OCT measurements

SUPERVISOR

Ozzy Mermut

My research interest lies on mathematical models for light interactions with matter. Specifically, I'm interested in how light may behave when it reflects, scatters, and diffracts off tissues on OCT scans. Optical Coherence Tomography (OCT) is a non-invasive imaging technique that allows us to visualize inner structures in biological matter with a remarkable resolution on small depths (1-2 millimeters). OCT has found clinical applications in the fields of ophthalmology, optometry, and quite recently, it has received attention in cardiology and dermatology.

OCT works similarly in principle to a Michelson Interferometer. A light beam is split in two, one beam acts as a reference and the other will interact with tissues. Eventually, both will converge at a detector where information on the sample may be inferred from how these two interfere with each other. OCT scans produce raw images that need to be processed to account for noise and artifacts that occur from chaotic light behaviour. Furthermore, applying mathematical models to these images allows us to quantify and differentiate various types of tissues and structures. The implications that arise from this yield promise in tissue characterization, where our main focus is identification of oral lesions and early detection of cancerous tissue.

SARAH POWELL

PHYSICS

PROJECT

Error mitigation for physics on a quantum computer

SUPERVISOR

Randy Lewis

Quantum computing relies on the principles of quantum mechanics to perform calculations more effectively. Quantum bits, called qubits, differ from classical bits because they can also exist in a superposition state between 0 and 1. As a result, the amount of information contained in a quantum system grows exponentially with each additional qubit. Using this vast potential, we want to calculate properties of subatomic particles that are incalculable using conventional computers.

We have remote access to IBM's quantum computer labs in New York and I have been running code on their quantum computers. I have run different versions of a variational quantum eigensolver (VQE) algorithm that uses either one or two qubits. The VQE is a quantum computer algorithm that uses the variational method to find the ground state of a quantum system. Finding the ground state is one of the most important applications for quantum computing, not only for physics, but also for areas such as chemistry and biology. We are expecting that the VQE will have valuable applications for our lattice gauge theories of subatomic particle physics.

Currently, quantum computers are very sensitive and error prone. Thus, a main goal is to implement useful algorithms that identify and mitigate errors made by the quantum computer hardware and this is what I will be focusing on for the remainder of the project.

BIBISOMAIA REZAEE

CHEMISTRY

PROJECT

Investigation of the properties of amorphous metal oxides as electrocatalysts for comparison to that of crystalline materials

SUPERVISOR

Sylvie Morin

Bibisomaia Rezaee is studying the properties of transition metal oxides. These materials have received renewed attention with their demonstrated usefulness as efficient electrodes in dye-sensitized solar cells and in fuel cell applications, both devices are cleaner alternative of portable sources of energy. But the efficiency of these devices needs to be further improved in order to be competitive with existing fossil fuel-based technologies.

In this project, various metal spinel oxides have been prepared and tested for their structural and electrochemical properties. The films were analyzed, using several structural, chemical and electrochemical methods such as X-ray diffraction, scanning electron microscopy, energy dispersive X-ray spectroscopy, cyclic voltammetry and X-ray photoelectron spectroscopy (XPS). The oxygen evolution reaction was used to determine the electrocatalytic activity of the electrodes. It is known that in catalysis the surface of the material plays a crucial role and that the surface composition may differ from that of the bulk of the material as demonstrated by the Morin group using XPS. I am researching the properties of amorphous metal oxides with the aim of comparing their compositions and their performance as electrocatalysts to the surface composition of the materials previously prepared.

MARIAM SHAMEKH

BIOLOGY

PROJECT

Epigenetic mechanisms of maternal care

SUPERVISOR

Sandra Rehan

The Rehan lab studies maternal care and social behaviour in bees. Little is known about the molecular mechanisms underlying care behaviour and the lasting effects on offspring. Seminal studies on rodents have shown that prolonged maternal care results in developmental changes in offspring, further supported by genetic data that revealed associated differential gene expression and DNA methylation patterns centered on neurodevelopment and metabolic pathways responsible for fear and anxiety responses. Dr. Rehan has proposed this to be a foundational mechanism for the mutual tolerance and cohabitation observed in insect societies. I will test if the loss of maternal care alters brood development, yielding pronounced behavioural and gene expression differences in young adults. Further, I will experimentally observe bees reared in the absence of maternal care to determine their likelihood to engage in maternal care towards their own offspring.

I believe this is important to understand not only social insects, but cooperation and conflict in general. These data can be used to inform early childhood development, maternal care, stress and anxiety response across insect and human societies.

CHENYANG YUE

BIOMEDICAL SCIENCE

PROJECT

Role of anti-metastatic microRNAs in ovarian cancer

SUPERVISOR

Chun Peng

Chenyang is reviewing published articles on the roles of anti-metastatic microRNAs in ovarian cancer. Ovarian cancer (OC) is the most lethal gynecological malignancy due to the silent nature of its onset and the lack of effective treatment for advanced metastatic disease. As most cancer mortality is associated with metastasis rather than the primary tumor, metastasis is the most significant process affecting the clinical management of OC patients.

As research concerning metastasis continues to grow, the mechanisms that underlie cancer cell metastasis are beginning to come into view. Recent studies have described the involvement of a class of non-coding regulatory RNA, termed microRNA (miRNA), in the regulation of OC metastasis. A large number of miRNAs have been shown to inhibit critical steps in metastasis, such as epithelial-mesenchymal transition (EMT), apoptosis, and angiogenesis. This explosion of papers describing miRNAs and their metastasis-inhibiting effects compelled us to summarize the advances in this field. Understanding how these anti-metastatic miRNAs are involved in metastasis will help identify possible biomarkers and targets for the diagnosis and treatment of the metastatic OC.

DURA: DEAN'S UNDERGRADUATE RESEARCH AWARD

JABAVU ADAMS

BIOPHYSICS

PROJECT

Integrated information in deep neural networks

SUPERVISOR

Joel Zylberberg

Integrated information has been proposed as a testable and computable measure that correlates with consciousness. It can be computed from recordings of brain signals in humans and fruit flies, for example. It goes up when the subject is conscious, and decreases when the subject is unconscious. It can also be computed for engineered mechanisms, such as artificial neural networks.

We are estimating integrated information in neural networks before and after they have been trained to perform a task. Our hypothesis is that integrated information should go up during training, as information processing becomes more coordinated between different parts of the networks.

We will repeat the analysis on different network architectures, to ask which architectures lead to higher integrated information after training, and (separately) which architectures lead to higher task performance. This could give us clues as to why consciousness might be a selected-for adaptation in animals like us.

FAHAD HANNAN

PHYSICS & ASTRONOMY

PROJECT

Modulation-free scheme for laser frequency stabilization and Faraday isolator optimization

SUPERVISOR

Anantharaman Kumarakrishnan

A variety of atomic physics experiments in my group require the use of homebuilt diode lasers that are frequency stabilized using lock-in detection. The underlying principle is the detection of frequency modulated laser light and use of a feedback loop to correct the laser's frequency excursions. However, in sensitive experiments involving ultracold atoms, frequency modulation is undesirable since it causes the laser linewidth to be broadened and contributes to a heating mechanism for atoms. One of my goals is to setup a feedback loop without modulating the laser frequency. This scheme will utilize the Zeeman effect to shift energy levels of atoms in a vapor cell using a uniform magnetic field such that absorption signals produce a dispersion shaped signal to correct the laser frequency. In another project, I am optimizing the design of Faraday isolators. An isolator allows laser light to travel only in one direction by completely blocking any reflected light, which can potentially damage the laser diode. I have developed a simulation package to calculate the strong magnetic field produced by the isolator's magnet stack to optimize device performance so that high quality isolators can be constructed for a small fraction of the commercial cost.

ARDALAN HOSSEINI-MANSOB

BIOMEDICAL SCIENCE

PROJECT

The role of La protein in the dynamics of phase-separated condensates

SUPERVISOR

Mark Bayfield

La antigen is an indispensable RNA binding protein in higher eukaryotes that binds to RNA polymerase III transcripts and plays an important role in processing them through its RNA chaperone activity. Additionally, previous work in our lab demonstrated that La binds to poly(A) tail of mRNAs in length dependant manner. Under stress, La is associated with stress-linked mRNAs that are expressed through non-canonical translation initiation mechanisms. During translation, multiple elongating ribosomes bind to mRNAs, forming structures called polysomes. Stressed cells adapt to inhibit cap-dependant translation initiation, often resulting in the formation of cytosolic non-membrane clusters of ribonucleoproteins, called stress granules (SGs), where mRNAs are temporarily stored. Our lab found La associated with both SGs and polysomes in sodium arsenite treated cells. We aim to study the mechanism(s) by which La interacts with SGs and its possible role in the formation or dissociation of liquid-liquid phase-separated condensates *in vitro*. Defective SG dynamics are linked to the pathogenesis of neurodegenerative and autoimmune disease, cancer, and viral infections. Moreover, La promotes translation of both cellular and viral mRNAs containing internal ribosome entry sites (IRESs) by acting as an IRES *trans*-acting factor, therefore studying the interactions between La and SG have important clinical implications.

MAHBOUBEH KOROUZHDEHI

CHEMISTRY

PROJECT

Purification and crystallization of TrhF from the R27 plasmid

SUPERVISOR

Gerald Audette

TrhF is a protein which is encoded by plasmid R27 in Salmonella typhimurium, an enteric bacterium causes typhoid fever. TrhF is a homolog of TraF, which is a protein encoded by plasmid F in *E. coli* important in the formation of a conjugative pilus and DNA transfer from donor to recipient. The R27 plasmid is a temperature sensitive conjugative plasmid that is implicated in multiple drug resistance of *S. typhimurium*. R27 is a plasmid that is transferable between all gram-negative and enterobacteria making it of significant concern for human health. Similar to TraF from the F plasmid, TrhF from the R27 plasmid is predicted to be a soluble periplasmic protein that contains a thioredoxin like fold at the C-terminal end of the protein. Thioredoxins are a large family of proteins that catalyze the formation and isomerization of disulfide bonds; they contain an active site C-X-X-C motif in some, but not all TraF homologs.

For this project, we were targeting the expression and purification of TrhF for analysis by X-ray crystallography. However, at this time we are taking a bioinformatics approach to focus on it's amino acid sequence to model the structure and figure out the functions of different residues and the thioredoxin fold/C-X-X-C motif in assembling of pilus and transferring DNA during the conjugation process. This project aims to figure out how these two homologous proteins (TraF and TrhF) are connected and similar in structure and function within each particular plasmid.

PARTH PATEL

BIOLOGY

PROJECT

Decision-theoretic approaches to understanding free movement in 3D space

SUPERVISOR

Nikolaus Troje

Biological organisms are frequently confronted with movement planning tasks. These movements require the organisms to know the rewards and penalties associated with outcomes of planned movements as well as any motor uncertainty associated with the movement. To better understand motor planning in humans, I will be developing software for accurately tracking movements of subjects in virtual reality using motion tracking devices. We will place participants in an immersive virtual world with their individualized self-avatars and engage them in a variety of motor tasks to test their decision making abilities under various different conditions. Thereafter, we will compare the performance of participants with an ideal performance using a framework that is frequently used to model human perceptual and motor performance. Through these experiments, we seek to understand whether the visuo-motor system in humans can take into account its own visual and motor limitations in planning actions. This will help us better understand how well an organism knows itself.

SIBEI QIN

BIOCHEMISTRY

PROJECT

Determining molecule dynamic difference of Sso-Acp at medium and high temperature by using MD simulation

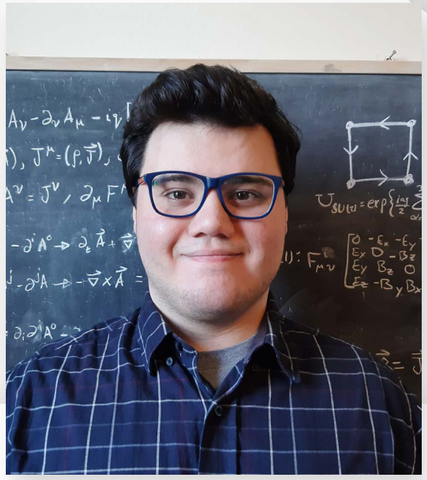
SUPERVISOR

Derek Wilson

Sso-Acp stands for the acylphosphatase from hyperthermophilic archaea, Sulfurous solfataricus. The enzymic activity of Sso-Acp is peaked at about 80oC (353K) and is reduced at room temperature (300K). This feature may closely relate to the kinetics and thermodynamics behaviour of Sso-Acp. According to previous studies, the structured part of Sso-Acp displays the same topology as the other acylphosphatase from mesophilic sources. Therefore, the folding behaviour of unstructured polypeptide tail might be critical for the hyperthermophilic feature of Sso-Acp.

In order to determine the molecule dynamic process of Sso-Acp, Sibei is trying to compare the difference of the molecule dynamic of Sso-Acp at medium and high temperatures. He uses Groningen machine for chemical simulations (GROMACS) to find the local energy minimum state of Sso-Acp in an aqueous system and simulate its molecule dynamic process. He loads the results of both temperatures in Visual molecule dynamic (VMD), calculates and compares the root-mean-square deviation (RMSD) of both results to acquire visible and intuitionistic data.

The comparative analysis of the molecule dynamic of Sso-Acp at two temperatures provides opportunities to receive an insight into the molecular reason for enzymic activity. In terms of future studies, the aggregation process of Sso-Acp can also be a determinant for its enzyme catalysis reactions under a high-temperature environment.



SARMED A RAHMAN

PHYSICS

PROJECT

Lattice gauge theories on a quantum computer

SUPERVISOR

Randy Lewis

The Standard Model of elementary particle physics is a quantum field theory that describes the fundamental forces in the universe, including the electromagnetic force, which describes charged particles, and the strong force that describes the quarks inside hadrons. When forces are large, quantum field theories can only be solved by computer simulations using a method called lattice gauge theory. On classical computers, this computational method accurately describes the properties of motionless particles, but unfortunately cannot provide access to the dynamics of the particles through time. However, quantum computers should make that possible.

Over the past couple of years, quantum computing has allowed us to reformulate some of the fundamental forces into a spin representation that can be encoded into quantum bits, called qubits. This allows us to take advantage of quantum superposition and quantum entanglement to study the time evolution and other properties of the fundamental forces and particles.

I started my project by exploring electromagnetism (U(1) gauge theory) on lattices of various geometries and boundary conditions, studying their energies at different coupling constants as well as the time evolution of the fields in free space. I am now doing the same for SU(2) gauge theory, which is closely related to the Standard Model's strong force.

ALI REZAEISHAHREZA

BIOLOGY

PROJECT

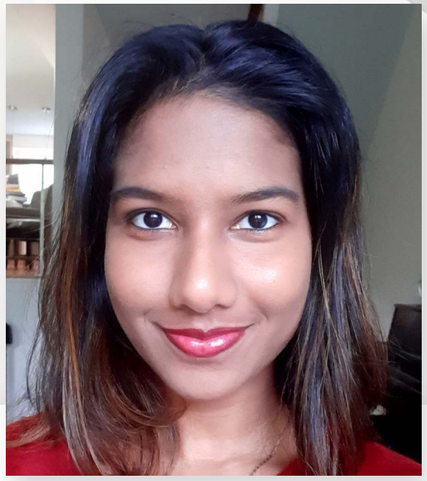
MEKK2 regulation by 14-3-3 binding to a novel phosphorylation site

SUPERVISOR

Michael Scheid

Mitogen-activated protein kinases (MAPK) are signaling molecules that regulate multiple cellular functions including cell survival, differentiation, gene expression, and cell migration. MAP kinases are being highly regulated by the activity of MAP3K. Two of the most important MAP3K class of protein are MEKK2 and MEKK3. We will be focusing on MEKK2 for our purposes.

In the previous study that took place in the lab, we showed that adaptor protein,14-3-3, can regulate MEKK2 by its association MEKK2 at phosphorylated residue (T283). However, it is known that 14-3-3 normally binds to two phosphorylated residues. Studies have shown another adaptor protein, paxillin, plays an important role to induce autophosphorylation in MEKK2 at T283 and T263 in a loop shape. Given the autophosphorylation at T283 and T263, we believe that T263 should be the other residue that associated with 14-3-3. Alternatively, some evidence shows 14-3-3 and paxillin might make a ternary complex with MEKK2 but no reports have confirmed that yet. Our goal is to fully understand the mechanism of the regulation of MEKK2. As MEKK2 is a kinase and targeting kinases is not possible for a lot of drug companies, Upstream regulation of MEKK2 will make the production of drugs possible for many cardiac and cancer diseases.



VENITA SITAHAL

BIOCHEMISTRY

PROJECT

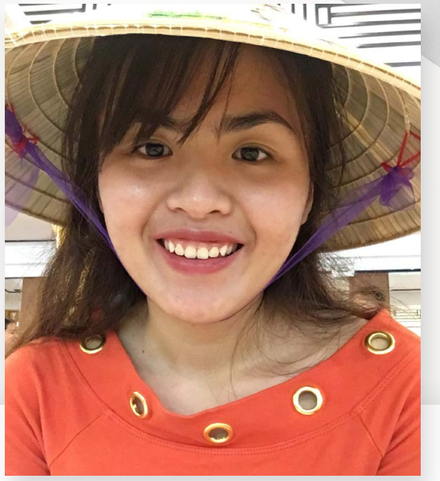
An investigation into the correlation between the sources of PFCAs and PFASs.

SUPERVISOR

Cora Young

Perfluoroalkyl substances, or PFAS, are synthetic organic compounds that are used in a myriad of everyday items due to their stability. However, it is precisely this innate stability that presents PFAS as an environmental pollutant. PFAS have been proven to bioaccumulate and biomagnify to toxic quantities and have been found in multiple wildlife and human blood samples globally, including in remote areas such as the Arctic. Consequently, the CJY group is interested in determining the methods by which PFAS are transported across long distances to be deposited in whale environments.

Wastewater treatment plants (WWTPs) are an important bridge between humans and the environment since a large proportion of human waste is processed by these plants before being released into rivers. Although WWTPs are intended to remove pollutants like PFAS from treated water, research has shown that effluent from WWTPs have greater concentrations of PFASs than the influent. Venita, who followed the guidance of Jessica Clouthier, a graduate student in the CJY group, sought to determine if there is a correlation between PFCAs and PFSAs and their sources. This was done by conducting correlations between the different homologues of the two types of compounds derived from data taken in WWTPs across Canada.



QUYNH PHUONG VU

STATISTICS

PROJECT

Application of Monte Carlo Markov chain algorithms in search of pattern-avoiding affine permutations

SUPERVISOR

Neal Madras

Pattern-avoiding affine permutation represents an interface between combinatorics and group theory, which has been a topic of research interest for decades. Following the attainments made previously, this project, under the supervision of Professor Neal Madras, focuses on assessing various conjectures on the features of a permutation of a given size that avoids a certain pattern. Specifically, the 4231-avoiding permutation is at the center of this project.

As my primary objective, I automate Monte Carlo simulations, which aim at randomly generating many permutations avoiding the pattern of interest, by preceding academic programming training. This swift and precise approach initially offers insightful observations into the relationships between random points, which graphically assists with inspecting patterns within the geometric space. Once the desired Markov chain is at hand, mathematical and other probabilistic methods will be employed to examine the properties of pattern-avoiding permutations.

The study is important and timely since, if accomplished, it will provide an intuitive sense and thorough guidance for further research in combinatorics and probability theory.

BENJAMEN ZONDAG

CHEMISTRY

PROJECT

Computational study of new ligands and zinc complexes for the controlled synthesis of biodegradable polymers

SUPERVISOR

Gino Lavoie

Over the Summer term, I am studying bidentate ligands that contain a guanidine fragment and their coordination to transition metals. Our group has demonstrated that the resulting complexes are active titanium and zirconium catalysts for the polymerization of fossil fuel-based olefins. However, these ligands, when coordinated to other metals, have the potential to also polymerize lactide, a renewable resource-based building block, into a biodegradable polylactide. The modularity of the guanidine fragment offers the opportunity to vary the electronic and steric parameters of both the ligands and catalysts. With the mandated closure of all laboratories due to the COVID-19 pandemic, I am currently performing computational studies of this system at the density functional theory level using parallel computing facilities accessible remotely. The objectives of this research are to design a library of ligands and complexes, to calculate their properties, and to identify trends and correlations. The ab initio data will predict the most stable molecular conformations and configurations, the electrostatic charges of all atoms, the bond lengths, bond orders, and stretching frequencies. The Lavoie research team will utilize this database to identify the best candidates for catalysts and focus their synthetic efforts upon their return to the laboratory to prepare and test the performance of these catalysts.

YSSA: YORK SCIENCE SCHOLAR'S AWARD

ALEX AKHUNDOV

BIOCHEMISTRY

PROJECT

Developing chemical tools for quantitative sequencing of N^6-methyladenosine

SUPERVISOR

Ryan Hili

Methylated nucleobases are common modifications of RNA that have important effects towards the *in vivo* structure and biological function of RNA. m^6A is one such methylated RNA nucleobase, which is regulated in organisms by a dynamic system of cellular proteins that write, read, and erase this modification. m^6A plays a role in epitranscriptomic genetic regulation, and to better understand the effects of m^6A, its abundance and expression in RNA must first be quantified through high-throughput sequencing.

Recently in the Hili Group, work has been done to develop a chemical process to chemoselectively modify m^6A in the presence of normal adenosine, which allows for single-nucleotide resolution mapping of m^6A sites throughout RNA using high-throughput sequencing technologies. The next step in the project is to carefully optimize the chemical process using high-performance liquid chromatography and mass spectrometry analysis to ensure selective and quantitative labelling of m^6A in RNA. Following this optimization, chemical labelling tools will be tasked with transcriptome-wide single-nucleotide resolution sequencing and quantification of m^6A, and a computational workflow will be developed.

ALYSSA DUHON

BIOMEDICAL SCIENCES

PROJECT

A new low-cost dynamic light scattering device and method towards virus pathogen characterizations

SUPERVISOR

Ozzy Mermut
William Petro

Dynamic light scattering (DLS) is a noninvasive photonic technique for examination of nano- to micron- sized particles in liquid suspensions. Current state-of the-art DLS systems are large and expensive, rendering them inaccessible for routine analysis. My research focuses on advancing the development of a DLS method for the detection of pathogens based on a new low-cost detection architecture and nanoparticle assay. Although other methods have been used to study viruses, DLS is an effective characterization technique because of its specificity, speed, and nanometer sensitivity to particle size and shape. Our DLS configuration will aim to measure the size distribution of gold-functionalized virus nanoparticles by capturing the intensity fluctuations of scattered light at different angles. In my project, I have been conducting a literature survey on nanoparticle assays for DLS measurement of viral particles. These will feed as design inputs for our DLS prototype under development. Our approach uses optical fibers, a low-cost laser, software-based autocorrelation, and a new rapid photon counting silicon photomultiplier detector. The small footprint, and low-cost design features will enable wide accessibility of DLS equipment for use in undergraduate labs, and clinician offices for educational use, biomedical testing, as well as virus characterization.

JACQUELINE DUHON

BIOMEDICAL SCIENCES

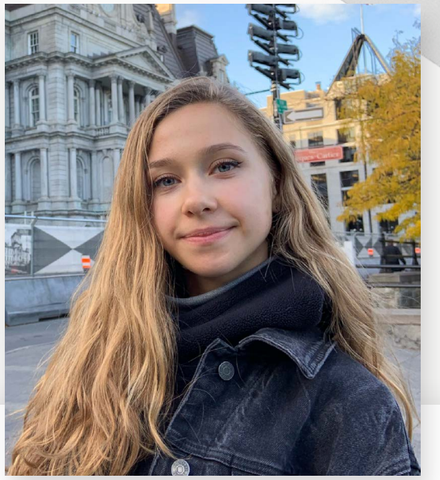
PROJECT

The association between public health interventions; demographic, social, and climatic factors, and COVID-19 growth across countries: a correlational study

SUPERVISOR

Jude Kong

My research focuses on using control measures implemented by governments around the world, as well as demographic, social, and climatic factors to explain, by correlations, the COVID-19 peak value and time across countries.
While some countries are still seeing a steady daily increase in the number of new cases, containment strategies in other countries have managed to slow the transmission of COVID-19. As the spread of the virus is contained, policy makers around the world are preparing for future waves by determining the efficacy of each measure that was put in place by different governments. Using the knowledge of R coding as well as data analysis and manipulation that I have acquired during the summer, I am utilizing statistical methods to determine the association that COVID-19 growth has with public health interventions; and demographic, social, and climatic factors. My findings will be used to inform the non-pharmaceutical interventions strategies that should be put in place during future outbreaks.



ALICE FOURS

BIOCHEMISTRY

PROJECT

Structural and functional analysis of F-plasmid protein complex

SUPERVISOR

Gerald Audette

I have been working alongside Gerald Audette towards the structural and functional analysis of F-plasmid proteins TraW and TrbC. These proteins are involved in bacterial conjugation and are found in T4SS of gram-negative bacteria. Bacterial conjugation is the contact dependant mechanism by which genetic material is transferred from a donor bacterial cell to a recipient bacterial cell using a pilus that brings cells closer together. TraW and Trb C interact to form a complex called R27 which is required in pilus assembly.

We are using several techniques in the lab to determine the structure of the protein complex. Once the protein complex is purified, using ThermoFluor assay we measure the temperature at which protein dentures to find the optimal buffer for protein stability. Using size-exclusion chromatography combined with multi-angle light scattering, we will be able to find the size of the protein complex. Using small-angle x-ray scattering we will be able to find the overall shape of the protein complex. Finally, using nuclear magnetic resonance will provide us with a more detailed protein structure, greater insight into protein dynamics and how mobile DNA elements like virulence factors and genes for antibiotic resistance are transferred between bacteria.

MICHAEL KROL

BIOLOGY

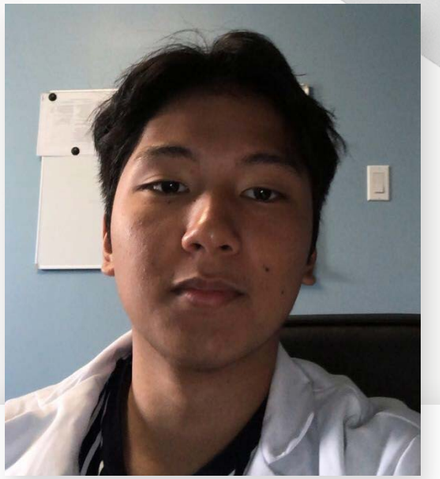
PROJECT

Structural and functional analysis of insulin resistance biomarkers

SUPERVISOR

Gary Sweeney

Michael worked on the of discovery of various biomarkers of insulin resistance specifically, adiponectin. Insulin resistance is one of the underlining factors in the development of prediabetes and eventually type 2 diabetes. Thus, early detection of insulin resistance using biomarkers is critical for disease prevention and pharmacotherapy. We studied adiponectin, an adipokine responsible for glucose regulation and fatty acid metabolism, in greater detail. In human studies, higher levels of adiponectin have been associated with reduced risk of cardiovascular complications and type 2 diabetes based on studies on healthy patients. However, the opposite was observed in patients with pre-existing conditions. As a result, correctly interpreting adiponectin with other biomarkers will allow for earlier diagnoses of some metabolic diseases and allow for the understanding of changes in biological pathways. Moreover, he analyzed flow cytometer data on various biological problems using the FlowJo software.



JARRED LAGANAS

BIOMEDICAL SCIENCE

PROJECT

Small RNA sequence annotation in the *Tetrahymena thermophila* genome

SUPERVISOR

Ronald E. Pearlman

Tetrahymena thermophila, is a ciliate protozoan, a useful model organism in studies of important conserved biological pathways. This organism employs asexual, vegetative cell division and sexual reorganization in a process called conjugation and has led scientific advances including the Nobel Prize winning discoveries of telomeres and catalytic RNAs. *T. thermophila*'s diploid germline micronucleus and its somatic macronucleus containing 45 copies of 275 chromosomes are fully sequenced and data are available in genomic and proteomic databases.

The sequences of transfer RNAs, small nuclear RNAs involved in the processing of pre-mRNA into mature mRNA by processing introns, and other small RNAs are not annotated in the present iterations of the available genome databases. The focus of Jarred's work is to find tRNA, small nuclear RNA and other small RNA sequences identified in the literature and to use bioinformatics to locate and annotate the chromosome location of these small RNA sequences. Using bioinformatics and the very recent 2020 update of the *T. thermophila* genome sequence we are able to annotate small RNA sequences more precisely and the new information will be valuable for the scientific community studying *T. thermophila* and its use as an important model organism for studies in the life sciences.

RACHEL LYSENKO

PSYCHOLOGY

PROJECT

Analysis of the structural and functional similarities between the TrhG and TraG proteins for the type IV secretion system

SUPERVISOR

Gerald Audette

Currently, my research concerns trying to confirm similarities in structural organization between the TrhG protein from the F-like plasmid R27 and the TraG protein from the F plasmid, the sequences of which were taken from the organisms *Salmonella enterica subsp. Typhi* and *Escherichia coli K-12* respectively. With this goal in mind, I have been performing modeling and sequence comparisons, bioinformatics work, concerning these two proteins. Despite the two proteins having low sequence homology, I have been contributing in the effort to observe the solubility of the periplasmic C-terminal region of TraG*, and subsequently TrhG*, to see if a flexible linker region exists between the N- and C-terminal domain of these proteins, as is predicted in the analysis of TraG*. I am currently in the process of constructing primers and further constructs so that the Audette Lab can perform in vitro experiments to confirm the found bioinformatic predictions in silico. The results of this research may allow for new analogies or distinctions to be made between the F and R27 T4SS. This information aids in knowing what parts of the T4SS may be useful for targeting in the creation of various drugs against conjugative pili, which allow for the transfer of DNA between bacteria.

DYLAN MARTINEZ

BIOMEDICAL SCIENCE

PROJECT

Generating CRISPR/CAS9 constructs and nanoparticles for bioengineering cannabis

SUPERVISOR

Nikola Kovinich

Malaria is a deadly disease that poses global health problems. As a result various antimalarial drugs are currently being developed, however disease control is impeded by the multidrug resistant strains of the malaria parasite Plasmodium falciparum . To combat this parasite, artemisinin was found to be highly effective against it. Although total synthesis is difficult and expensive, semi-synthesis of it as well as any derivative from microbially sourced artemisinic acid is a more cost-effective and reliable source of artemisinin. Throughout the summer Dr. Kovinich and I have been working on a project that involves using CRISPR/CAS9 technology to bioengineer a purple kush strain of cannabis. Specifically, are goals are to use CRISPR/CAS9 to knockout the THCAS gene to prevent THC biosynthesis and replace them with genes that would allow artemisinic acid biosynthesis through sequential transformation. If we are successful in this project it would be a great help to people in need of malaria treatment because although pharmaceutical research is going into engineering artemisinic-acid producing yeast, cannabis that produces artemisinic-acid is a far cheaper and more available alternative.

DANIEL PATOLSKY

BIOCHEMISTRY

PROJECT

Investigating the role of H3 phosphorylation in transcriptional regulation of immediate early genes

SUPERVISOR

Peter Cheung

Histone phosphorylation plays a major role in a diverse range of nuclear processes, including transcriptional regulation, chromosome condensation, and DNA damage repair. The N-terminal tail of histone H3 contains two serine residues, S10 and S28. Phosphorylation of H3S10 and H3S28 is mediated by upstream kinases of the ERK and p38 signaling cascades, in response to mitogens and other stress related factors. Subsequently, phosphorylated H3S10 and H3S28 temporarily activate immediate early genes by making the DNA template more accessible to transcription factors and creating binding platforms for the recruitment of additional regulatory proteins. Numerous studies have shown that H3 phosphorylation forms crosstalks with other histone modifications that contribute to its role in immediate early gene expression.

Daniel has been carefully analyzing and compiling significant discoveries from a vast collection of different research papers involving H3 phosphorylation. He is currently writing a detailed up-to-date literature review on the biological processes behind H3 phosphorylation and their roles in orchestrating essential cellular events. Daniel's focus is to uncover connections between the histone modifications and regulatory proteins associated with phosphorylation of H3 specifically at S10 and S28, in order to create a collective understanding of the mechanisms that regulate immediate early gene activation.

ALEEZA QAYYUM

BIOMEDICAL SCIENCE

PROJECT

Bioinformatic analysis of nuclear protein import in *Tetrahymena thermophila*

SUPERVISOR

Ronald E. Pearlman

The Pearlman Lab uses the eukaryotic ciliate protozoan Tetrahymena thermophila as a model organism to address fundamental biological questions with practical applications. Research with T. thermophila has led to many notable scientific contributions, including the role of small RNAs and the connection of nuclear histone acetylation to the activation of transcription, and catalytic RNAs which is Nobel Prize recognized.

Aleeza's work focuses on repurposing FDA approved drugs to possibly aid in the treatment of COVID-19. Due to inaccessibility to wet labs, Aleeza is using bioinformatic approaches with the fully sequenced Tetrahymena thermophila genome, alongside extensive genomic and proteomic databases to work virtually. In eukaryotic organisms, nuclear protein import is performed by importin carrier proteins. A well characterized mechanism of nuclear import involves the importin alpha and beta 1 heterodimer, which controls what enters the nucleus, including viruses. FDA approved drug ivermectin has been shown to inhibit the replication of viruses through the importin alpha and beta 1 heterodimer. Through bioinformatic analysis of nuclear import pathways in T. thermophila, Aleeza hopes to address mechanistic questions about importin involvement in nuclear transport to possibly shed light on ivermectin and its potential role in inhibiting the replication of the COVID-19 virus SARS-CoV-2.

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