

UBC School of Biomedical Engineering

SYNERGY SHOWCASE

**With keynote address by
Dr. Marissa Lithopoulos
Founder of Science, Stand-Up, & Song,
Co-Founder of Beaker Banter**

**Tuesday, August 11, 2026
SHRM B1001, 6088 University Blvd**



THE UNIVERSITY
OF BRITISH COLUMBIA
Edwin S.H. Leong
Centre for Healthy Aging
Faculty of Medicine



Dajavad Mowafaghian
CENTRE FOR BRAIN HEALTH



Centre for Aging
CARE ANYWHERE



genome science + technology
GRADUATE PROGRAM



About the School of Biomedical Engineering Synergy Program

The School of Biomedical Engineering (SBME) Synergy Undergraduate Summer Research Program is a fantastic opportunity for students to gain paid hands-on research experience in one of UBC's world-class biomedical engineering labs; partners include researchers from the Genome Science and Technology Graduate Program (GSAT), the Dajavad Mowafaghian Centre for Brain Health (DMCBH), Care Anywhere Program part of the Centre for Aging SMART, ICORD, the Edwin S. H. Leong Centre for Healthy Aging, and of course, SBME.

During the program from May to August, students worked on a defined research project with a UBC supervisor, participated in professional development programming, and networked at student socials. The Synergy Showcase is an opportunity for students to present the research they have been working on during the summer at our end-of-program event.

For more information about the Synergy program, visit our website:

<https://bme.ubc.ca/education/undergraduate-program-entry/professional-development-engagement/sbme-synergy/>

research@sbme.ubc.ca



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Agenda

Registration & Coffee: 8:30am - 9am

Keynote address: 9am - 9:30am

Trainee talks: 9:30am - 11am

Poster session: 11am - 12pm

Keynote address 9am - 9:30am

DR. MARISSA LITHOPOULOS

Founder of Science, Stand-Up, & Song
Co-Founder of Beaker Banter Post-doctoral
Fellow, University of British Columbia



Pathways to Accessibility in Science

Accessible information is critical for the progression of science, yet it remains widely undervalued.

In this keynote address, we will delve into 3 core concepts for improving accessibility in science. We will discuss creative strategies and tools that we can all use to build trust, mobilize knowledge, and foster connection. Dr. Lithopoulos will share key insights from her career in the stem cell field, in which she has led local and national science outreach initiatives for over a decade. She will also draw upon frameworks from music and comedy, to showcase how we can make science approachable, inviting, and engaging for diverse audiences. Science saves lives, but only if we can communicate it.

Dr. Marissa Lithopoulos is a scientist, musician, and comedian. She currently holds a Postdoctoral Fellowship at the University of British Columbia. Her research focuses on harnessing the potential of stem cells to treat conditions affecting the developing brain. She also provides policy interest holders with accessible information on cutting-edge biotechnologies. Dr. Lithopoulos hosts a live event called, "Science, Stand-Up, & Song" and a podcast called, "[Beaker Banter](#)". Her original science-themed music has over 25,000 listeners from across the world. Dr. Lithopoulos is the recipient of a Canadian Institutes of Health Research Postdoctoral Fellowship, a Canadian Association for Neuroscience Brain Star Award, and a Michael Smith Laboratories Pathway to Independence Award. In grade 8, Dr. Lithopoulos was voted most likely to become a millionaire. This has not yet come to fruition, but she considers it an accolade nonetheless. To connect, visit drmarissalithopoulos.com.

Trainee talks 9:30am - 11am

ABHINAV MENON

Supervised by Dr. Carolina Tropini



Keywords:
Bacteriophage
Population-dynamics
Coevolution

Persistence vs. Potency: How Directed Evolution Methods Shape Phage-Bacteria Dynamics in *E. coli*

Bacteriophages (phages) are viruses that target host bacteria and possess exciting therapeutic potential to combat antibiotic-resistant bacteria; however, there exist challenges regarding the rapid emergence of phage resistance. Since an ideal therapeutic phage would possess counter resistance mechanisms while maintaining a high level of infectivity, we are interested in directed phage evolution as a method to "train" phages. In this study, we used T4 phages evolved with two distinct methods over 30 days: either co-evolved with their host *Escherichia coli*, or evolved against a non-evolving (ancestral) host. In the first case, we found co-evolution affected counter-resistance, while in the second, independent evolution against the ancestral host affected infectivity. We aimed to identify how the two directed evolution methods affected bacterial suppression and the emergence of phage resistance in gut conditions. Hence *E. coli* cultures were placed in varying media conditions, inoculated with "trained" phages, and passaged for 7 days. Phage and bacteria concentrations were determined using plaque and colony forming assays. Our results indicated that the evolution method impacts the type of phage-bacteria population dynamics observed. Specifically, more infective independently evolved phages briefly reduced bacterial concentrations but were more likely to face extinction. Conversely, coevolved phages were more likely to persist and lead to cyclical population dynamics. Cross-lineage resistance assays showed that phage infectivity varies between bacterial lineages. These assays suggest that phage infectivity is variable over time and may continue to change with their host. We also intend to use time-shift assays to further investigate the coevolutionary dynamics present, to further determine the extent and impact of phage training on bacterial populations.



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Trainee talks 9:30am - 11am

ALBIE GONG

Supervised by Dr. Leonard Foster



Keywords:
Neuroglia
Viral infection
Immune response

Proteomic Analysis of Glucose Effects on Astrocytic Response to Human Coronavirus 229E Infection

Astrocytes are glial cells affected by hyperglycemia, contributing to altered metabolism and neuroinflammation. Under coronavirus infections, such as human coronavirus 229E, astrocytes exhibit increased reactivity and stress. Moreover, hyperglycemia exacerbates astrocyte-associated neuropathology in diabetic patients infected with coronaviruses. However, glucose impacts on glucometabolic and inflammatory proteomic responses during human coronavirus 229E infection remain unclear. Since astrocytes exhibit sex differences such as dimorphic regulation of glucose uptake via glucose transporter 2, we aim to examine glucometabolic and inflammatory protein changes in male and female astrocytes infected with human coronavirus 229E under normal and high glucose conditions. We hypothesize that both glucose and sex would significantly influence astrocytes' proteomic responses to infection. Primary human astrocytes from three male and three female donors were cultured under normal (5.5 mM) or high (25 mM) glucose and infected with human coronavirus 229E, alongside uninfected controls. Samples were processed for liquid chromatography-mass spectrometry, and outputs were processed in data-independent acquisition-neural network. Data analysis was conducted in R. Differential expression and Gene Ontology analyses revealed that female astrocytes demonstrated greater glucometabolic pathway upregulation such as oxidative phosphorylation under uninfected and high glucose conditions. Males showed increased extracellular matrix organization processes and reduced response to endoplasmic reticulum stress. Viral infection under high glucose conditions led to a greater increase in glucose-mediated protein expression in females compared to males.

CINDY ZHANG

Supervised by Dr. Mark Cembrowski



Keywords:
Transcriptomics
Hippocampus
Computation

Single-Cell Spatial Transcriptomic Profiling of Inhibitory Interneurons within the Mouse Subiculum

Inhibitory interneurons play a critical role in regulating neural excitability and oscillatory dynamics across the brain. While interneurons are traditionally thought to follow a stereotyped, mosaic-like arrangement across cortex, the spatial organization of inhibitory networks within the hippocampus, particularly the subiculum, remains underexplored. Preliminary data suggest that the subiculum may deviate from this canonical organization, exhibiting diverse gene-expression profiles that occupy distinct spatial subdomains. This project investigates whether interneuron subtypes in the mouse subiculum exhibit spatially structured gene-expression patterns that correlate with functional subdomains. Utilizing high-resolution single-cell spatial transcriptomic data from the Allen Brain Atlas (MERFISH), we employ computational clustering, dimensionality reduction, and spatial statistical modeling within the R environment to construct a high-resolution spatial atlas of subicular inhibitory populations. By integrating these transcriptionally defined subtypes with known anatomical landmarks using high-performance computing, this work aims to map the precise microarchitecture of subicular inhibition. Uncovering this localized spatial patterning is crucial for understanding how inhibitory networks shape hippocampal output and will provide essential baseline insights into circuit dysregulation underlying neurological disorders such as epilepsy, schizophrenia, and Alzheimer's disease.



Trainee talks 9:30am - 11am

HETA PATEL

Supervised by Dr. Shernaz Bamji



Keywords:
Synaptic plasticity
Protein lipidation
Functional genomics

From Pathways to Patients: Functionalizing Previously Unrecognized Isoforms and Patient Variants of zDHHHC8

Many neurodevelopmental disorders share a common feature—an imbalance in excitatory and inhibitory signaling. One gene linked to these neurodevelopmental disorders is zDHHHC8, a palmitoyl acyltransferase highly expressed in the cortex. We found zDHHHC8 exists as two previously unrecognized isoforms distinctly enriched in either inhibitory or excitatory neurons. Additionally, our clinical collaborators identified ZDHHHC8 variants in five patients with autism and other neurodevelopmental comorbidities, suggesting that disruption of isoform regulation contributes to disease pathogenesis.

Our overall objective is to determine the role of the two ZDHHHC8 isoforms in the brain and to functionalize patient derived variants.

We used a knockout-rescue approach in primary neurons to study how the loss of zDHHHC8 in excitatory or inhibitory cells impacts dendritic outgrowth, and whether either isoform rescues these defects. Similarly, to assess the functional impact of patient-derived variants, we rescued zDHHHC8-knockout neurons with either wild-type human ZDHHHC8 or the patient variants.

Our findings show that genetic ablation of zDHHHC8 reduces dendritic length in excitatory neurons, but not inhibitory neurons. Importantly, this defect was rescued by zDHHHC8-Iso2 but not zDHHHC8-Iso1, demonstrating unique isoform functions. Proximity-based protein labeling revealed that zDHHHC8-Iso1 preferentially interacts with 38 distinct proteins compared to 227 proteins with zDHHHC8-Iso2. Applying this rescue framework to patient derived variants pinpointed which specific mutations significantly disrupted dendrite outgrowth, as well as ZDHHHC8 localization and stability.

These findings functionalize patient variants and uncover two previously unrecognized zDHHHC8 splice isoforms with distinct cell-type functions, highlighting how isoform-specific dysregulation triggers neuronal circuit dysfunction in neurological disease.

KRISTA TANNANT

Supervised by Dr. Kota Mizumoto



Keywords:
Neurodevelopment
Molecular biology
Genetics

Genome engineering to investigate isoform-specific functions of SAD-1 kinase in synapse organization

SAD-1 (Synapses of Amphids Defective-1) is a highly conserved serine/threonine kinase that plays essential roles in nervous system development, including neuronal polarization and presynaptic organization. In *Caenorhabditis elegans*, alternative splicing of sad-1 exon 15 generates two structurally and functionally distinct isoforms, SAD-1L and SAD-1S, which are analogous to the mammalian Sad-A and Sad-B kinases. Despite the established importance of SAD-1 in neuronal development, the specific roles of these isoforms in synapse organization remain poorly understood.

This project investigates the isoform-specific functions of SAD-1 in regulating synaptic domain organization in *C. elegans*. We used CRISPR/Cas9 genome editing to generate mutant *C. elegans* strains expressing only the SAD-1L or SAD-1S isoform and examined synapse number and position along the DA9 motor neuron, which is known to express both SAD-1L and SAD-1S. We also introduced the T202E constitutively active mutation in wild-type, SAD-1S, and SAD-1L mutants. In the sad-1 null mutants, we observed that DA9 synapses are more spread along the axon compared to wild-type animals. In mutants expressing either SAD-1S or SAD-1L, we did not observe significant defects in synapse arrangements. Interestingly, in mutants only expressing constitutively active SAD-1L(T202E) or SAD-1S(T202E), we observed sad-1 null mutant-like synapse arrangement defects, while SAD-1(T202E) mutant animals expressing both isoforms did not exhibit such defects.

This result suggests that expression of one constitutively active isoform disrupts normal synapse arrangement. Ongoing analyses aim to further define the relationship between SAD-1 isoforms in synapse arrangement.



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Trainee talks 9:30am - 11am

LAUREN KEILTY

Supervised by Dr. Stefanie Blain-Moraes



Keywords:
Interpersonal connection
Wearable sensors
Assistive technology

Individualistic Models of Autonomic Nervous System Responses for Salient Moment Detection in Individuals with Advanced Dementia

Caregivers of individuals living with non-normalized communication, like individuals with advanced dementia, often rely on second-person perspectives to assess the emotional state and depth of engagement of those they care for in interactions of day-to-day life. Autonomic nervous system responses (ANS) such as electrodermal activity, heart rate, and peripheral skin temperature have been established to meaningfully covary with emotional responses. These responses are highly individualistic in the strength of the responses seen and the signals in which the responses are most prominent. This project assesses the quality of individualistic models of ANS responses for detecting these salient moments in individuals with advanced dementia.

Physiological and video interaction data was collected from four groups consisting of a dancer, a musician, and an individual with advanced dementia as they participated in an interactive therapy practice over 8 distinct sessions. The videos were analyzed for moments of disengagement and engagement based on criteria that included eye contact, vocal sound changes, and body movements.

For a preliminary group, physiological windows were extracted from these moments and found to have significant differences in the amplitude of the maximum EDR peak and the maximum derivative of heart rate between the engaged and disengaged classes. A linear regression model was trained, validated, and tested to give 66% accuracy, 73% precision and 76% recall in predicting engaged and disengaged moments. Continued analysis will include adjustments to the features and window sizes to better capture the full physiological responses and individualistic analysis of the data from other three groups.

MELODY WANG

Supervised by Dr. Sofia Graham/
Dr. Govind Kaigala



Keywords:
Tissue models
Organ-on-chip
High-throughput

A Plug-In Probe for Perfusable, High-Throughput Tissue Culture in Standard Well Plates

Organ-on-chip (OoC) systems promise physiologically relevant in vitro models, yet a persistent gap exists as they are powerful but low-throughput, non-standardized, demanding expert operation, and often lack the ability to capture the dynamic nature of cellular environments due to static operation.

We present the Well Probe, an open-space microfluidic device that converts conventional, unmodified multi-well plates into perfusable culture platforms without custom labware or bulky peripherals. This brings the benefits of microfluidics into routine laboratory workflows and enable the generation and maintenance of various microphysiological tissue models. The probe inserts into a standard well and, using a central injection channel paired with a surrounding aspiration ring, establishes hydrodynamically confined, recirculating flow directly over the culture surface. Because of the open-space nature, cell-laden hydrogels can be loaded by simple pipetting and retrieved intact for spatially resolved downstream analysis. Fluorescence and confocal z-stack imaging with tracer dyes and microparticles confirmed a stable, approximately radial flow profile reaching the well bottom, as well as verified surface-level shear contact.

Ongoing work addresses long-term operation stability, tapered geometries for more uniform shear, and a fluidic circuit board enabling parallelized, equal-resistance perfusion across many wells. We are also validating the biological relevance of the imposed flow using HUVECs seeded on the well surface to confirm that the probe delivers physiologically meaningful surface shear.

The Well Probe offers a simple, scalable route to bring controlled microscale perfusion to routine cultureware, lowering the barrier to physiologically relevant, high-throughput tissue models and drug screens.



Trainee talks 9:30am - 11am

MONICA MIHAILESCU

Supervised by Dr. Mahsa Khalili



Keywords:
Remote Health Monitoring
Wearables
Biosignal Processing

Photoplethysmography Signal Quality Assessment for Heart Rate Estimation: An Application-Specific Approach

Photoplethysmography (PPG) is a non-invasive optical sensing technique widely used in wearable devices and clinical monitors for cardiovascular monitoring, including heart rate estimation. While PPG enables continuous physiological monitoring, its susceptibility to noise due to motion artifact, poor sensor-to-skin contact, and temperature can degrade signal quality. To address this challenge, signal quality assessment (SQA) algorithms are commonly used to identify and remove low-quality PPG segments before analysis. However, these algorithms may be overly conservative, excluding segments that remain sufficiently reliable for accurate heart rate estimation.

This study investigates whether PPG segments labelled as lower quality by a previously established method remain suitable for heart rate estimation when compared with high-quality electrocardiogram (ECG) recordings. Using the MIMIC-III-Ext dataset, a publicly available database containing synchronized PPG and ECG segments from 6,189 intensive care unit (ICU) patients, high-quality ECG segments are selected as the reference for corresponding high- and lower-quality PPG segments. Heart rate is estimated from both signals using time- and frequency-domain approaches, with ECG-derived estimates used as the ground truth for evaluating PPG accuracy.

We hypothesize that a subset of PPG segments flagged as lower quality by the existing approach will produce accurate heart rate estimates, suggesting that this algorithm may be conservative for heart rate monitoring applications. Additionally, based on the findings of a previous study from our group, we anticipate that frequency-domain estimation methods will demonstrate greater heart rate accuracy than traditional time-domain approaches.

These findings will inform application-specific SQA methods in datasets where ECG ground truth is unavailable and provide insight into the relationship between PPG signal quality and heart rate estimation performance.

SAIGE MANN

Supervised by Dr. Christopher Moraes



Keywords:
Neonatal health
Global health
Diagnostic devices

Thromboelastograms on a Paper Microfluidic Platform for Neonatal Sepsis Diagnosis

In lower-middle-income countries, neonatal sepsis is a major cause of mortality and morbidity. Clinical signs of neonatal sepsis (respiratory distress, temperature instability, etc.) are variable and can often look indistinguishable from other conditions. A thromboelastogram (TEG) is a clinical assay that measures the viscoelastic properties of whole blood and shows promise in identifying sepsis through coagulation changes. Unfortunately, TEG has high costs, making this testing method inaccessible in resource-limited settings. This research explores the possibility of using a paper-based microfluidic platform containing a hydrogel microparticle. These microparticles will have photothermal properties, causing them to expand and contract in response to a laser and allowing them to act as actuators that measure the viscoelastic properties of the blood. Increased clot stiffness will lead to reduced microparticle expansion, enabling the quantification of the clot through fluorescent imaging. We present the fabrication of the microparticles using n-isopropylacrylamide, acrylamide, and gold nanorods as well as the development of the microfluidic platform using laminated filter paper.



Trainee talks 9:30am - 11am

ZUBINA ZAFAR

Supervised by Dr. John (Kip) Kramer



Keywords:

Locomotor networks
Supraspinal reorganization
Therapeutic targets.

Assessing Morphological Changes in Volume of the Lateral Hypothalamus for Recovery After Spinal Cord Injury

Recovery following spinal cord injury (SCI) depends not only on changes within spinal circuitry, but also on reorganization in supraspinal regions that contribute to locomotion and functional recovery. The lateral hypothalamus (LHA) has emerged as an important region in walking recovery, with hypothalamic deep brain stimulation demonstrating improved locomotor function following SCI (Cho et al., 2024). However, the role of LHA structural and volumetric remodeling following SCI remains an emerging area of research. We hypothesize that individuals with chronic SCI will demonstrate altered LHA volumetric morphology, reflecting supraspinal adaptation following injury. High-resolution T1-weighted MRI scans from individuals with chronic SCI and neurologically intact controls were analyzed. The LHA was segmented using the human hypothalamic atlas developed by Neudorfer et al and implemented within DSI Studio. Participant-specific LHA volumes were extracted following atlas-based segmentation and quality control. Group differences in LHA volume between SCI and control participants were assessed while adjusting for age, sex, and intracranial volume, while additional analyses within the SCI cohort examined associations between LHA volume and clinical characteristics, including neurological level of injury, ASIA grade, and time since injury. Diffusion MRI data from a subset of participants were processed using Q-space diffeomorphic reconstruction (QSDR) to investigate longitudinal changes in LHA microstructural measures, including fractional anisotropy (FA) and mean diffusivity (MD). This work provides insight into supraspinal adaptations following SCI by identifying structural changes within a locomotor-relevant brain region. Understanding these changes may reveal potential biomarkers of recovery and inform future rehabilitation and neuromodulation strategies.



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POSTER LIST

11am - 12pm

Poster Session 11am - 12pm

1



ABHINAV MENON

Supervised by Dr. Carolina Tropini

Persistence vs. Potency: How Directed Evolution Methods Shape Phage-Bacteria Dynamics in E. coli

Bacteriophages (phages) are viruses that target host bacteria and possess exciting therapeutic potential to combat antibiotic-resistant bacteria; however, there exist challenges regarding the rapid emergence of phage resistance. Since an ideal therapeutic phage would possess counter resistance mechanisms while maintaining a high level of infectivity, we are interested in directed phage evolution as a method to “train” phages. In this study, we used T4 phages evolved with two distinct methods over 30 days: either co-evolved with their host *Escherichia coli*, or evolved against a non-evolving (ancestral) host. In the first case, we found co-evolution affected counter-resistance, while in the second, independent evolution against the ancestral host affected infectivity. We aimed to identify how the two directed evolution methods affected bacterial suppression and the emergence of phage resistance in gut conditions. Hence *E. coli* cultures were placed in varying media conditions, inoculated with “trained” phages, and passaged for 7 days. Phage and bacteria concentrations were determined using plaque and colony forming assays. Our results indicated that the evolution method impacts the type of phage-bacteria population dynamics observed. Specifically, more infective independently evolved phages briefly reduced bacterial concentrations but were more likely to face extinction. Conversely, coevolved phages were more likely to persist and lead to cyclical population dynamics. Cross-lineage resistance assays showed that phage infectivity varies between bacterial lineages. These assays suggest that phage infectivity is variable over time and may continue to change with their host. We also intend to use time-shift assays to further investigate the coevolutionary dynamics present, to further determine the extent and impact of phage training on bacterial populations.

Keywords: Bacteriophage, Population-dynamics, Coevolution

2



ALBIE GONG

Supervised by Dr. Leonard Foster

Proteomic Analysis of Glucose Effects on Astrocytic Response to Human Coronavirus 229E Infection

Astrocytes are glial cells affected by hyperglycemia, contributing to altered metabolism and neuroinflammation. Under coronavirus infections, such as human coronavirus 229E, astrocytes exhibit increased reactivity and stress. Moreover, hyperglycemia exacerbates astrocyte-associated neuropathology in diabetic patients infected with coronaviruses. However, glucose impacts on glucometabolic and inflammatory proteomic responses during human coronavirus 229E infection remain unclear. Since astrocytes exhibit sex differences such as dimorphic regulation of glucose uptake via glucose transporter 2, we aim to examine glucometabolic and inflammatory protein changes in male and female astrocytes infected with human coronavirus 229E under normal and high glucose conditions. We hypothesize that both glucose and sex would significantly influence astrocytes' proteomic responses to infection. Primary human astrocytes from three male and three female donors were cultured under normal (5.5 mM) or high (25 mM) glucose and infected with human coronavirus 229E, alongside uninfected controls. Samples were processed for liquid chromatography-mass spectrometry, and outputs were processed in data-independent acquisition-neural network. Data analysis was conducted in R. Differential expression and Gene Ontology analyses revealed that female astrocytes demonstrated greater glucometabolic pathway upregulation such as oxidative phosphorylation under uninfected and high glucose conditions. Males showed increased extracellular matrix organization processes and reduced response to endoplasmic reticulum stress. Viral infection under high glucose conditions led to a greater increase in glucose-mediated protein expression in females compared to males.

Keywords: Neuroglia, Viral infection, Immune response



Poster Session 11am - 12pm

3



ANDERS SCHWARZ

Supervised by Dr. Jane Hill

Toward a paper-based test for rapid discrimination of bacterial causative agents of UTI

Urinary tract infections (UTIs) are among the most common bacterial infections worldwide, yet diagnosis forces a tradeoff: the paper dipstick test returns results in minutes but cannot identify the causative organism, while urine culture identifies it but requires at least 48 hours. This project develops a paper-based colorimetric test for indole, a metabolite produced by tryptophanase-expressing bacteria such as *Escherichia coli*, the predominant uropathogen, as a step toward organism discrimination on a dipstick. Using the Ehrlich reagents DMACA and Kovac's reagent, indole was detected on cellulose paper down to $\sim 5 \mu\text{M}$, and paper exposed to live *E. coli* developed colour while sterile controls stayed blank, confirming detection of biologically produced indole. Beyond this proof of concept, the work identifies the central barrier to translation. Free indole, the mechanistically specific marker, is roughly five orders of magnitude less abundant in urine than conjugates such as indoxyl sulfate, and because reported assay selectivity is measured at equal concentration, no reaction described to date is genuinely selective for free indole in urine. Establishing the uropathogenic indole concentration, validating selectivity in a urine matrix, and demonstrating a selective reaction are the key next steps toward a dipstick capable of bacterial discrimination.

Keywords: Point-of-care diagnostics, Microbial metabolite sensing, Paper-based biosensor

4



ARIA RAYMAAKERS

Supervised by Dr. Calvin Kuo

A Multi-IMU Method to Characterise Head-Trunk Motion for Mogul Skiing

Mogul skiing exposes athletes to repeated impacts that may challenge head stabilisation, affecting both injury risk and performance. Inertial measurement units (IMUs) can measure head and body motion in real-world environments, but comparing multiple sensors introduces challenges related to sensor synchronisation and alignment. Therefore, this project develops a processing method for head- and trunk-mounted IMUs, with the future goal of quantifying head stabilisation during mogul skiing.

Each IMU has an independent internal clock, which can introduce timing offsets and drift, while differences in placement orientation can distribute the same movement across different axes. Before synchronisation, corresponding head and trunk peaks were approximately one second apart, potentially misrepresenting the timing and magnitude of their relationship. This method reduced the estimated residual offset to less than one millisecond, then spatially aligned the signals before comparison.

During preliminary testing, IMUs placed on the forehead and sternum recorded acceleration and angular velocity during lateral jumps and repeated two-foot vertical jumps. Following temporal and spatial alignment, wavelet analysis was used to characterise how the head-trunk relationship changed over time and across frequencies.

Preliminary findings suggest that attenuation of head motion relative to trunk motion may occur at frequencies of approximately 5–12 Hz rather than uniformly across the movement spectrum. Identifying frequencies associated with greater relative head motion could inform training strategies that improve stabilisation and support performance and injury prevention. This method provides a foundation for future on-snow investigations and the interpretation of motion relationships measured using multiple wearable sensors.

Keywords: Sports biomechanics, Multi-sensor processing, Signal alignment



Poster Session 11am - 12pm

5



CALLA STANLEY

Supervised by Dr. Megan Levings

Evaluating the Impact of mRNA Nucleoside Modification on a Tolerogenic Lipid Nanoparticle Therapeutic for Type 1 Diabetes

Type 1 diabetes (T1D) is an autoimmune disease characterized by the destruction of insulin-producing pancreatic β cells, resulting in persistent dysregulation of blood glucose. Although insulin therapy effectively manages glycemia, it does not address the underlying autoimmune response, highlighting the need for disease-modifying therapies. Antigen-specific immune tolerance is a promising therapeutic approach that aims to selectively suppress disease-driving immune responses while preserving broader immune function. Previously, we developed a tolerizing mRNA-lipid nanoparticle therapeutic (tolLNP) to induce antigen-specific immune tolerance in T1D which demonstrated prevention and reversal diabetes in the non-obese diabetic (NOD) mouse model.

Modified nucleosides are widely used in mRNA therapeutics to reduce innate immune sensing and enable effective mRNA expression. However, different nucleoside modifications can produce distinct biological effects, making the selection of an appropriate modification particularly important for applications intended to promote immune tolerance. This study compares tolLNP formulations incorporating N1-methylpseudouridine (m¹Ψ) or 5-methoxyuridine (5moU) modified mRNA to determine whether nucleoside modification influences protection against autoimmune diabetes.

Mice were randomized to receive tolLNP formulations or buffer control during the prediabetic stage of disease and blood glucose concentrations monitored longitudinally to assess diabetes development, with animals followed until confirmed diabetes or study endpoint at 30 weeks of age. Treatment efficacy will be evaluated by comparing diabetes incidence and time to disease onset across treatment groups. These studies will determine the impact of mRNA nucleoside modification on the protective efficacy of tolLNPs for further development.

Keywords: Lipid nanoparticles (LNPs), Immunotherapy, Preclinical model

6



CINDY ZHANG

Supervised by Dr. Mark Cembrowski

Single-Cell Spatial Transcriptomic Profiling of Inhibitory Interneurons within the Mouse Subiculum

Inhibitory interneurons play a critical role in regulating neural excitability and oscillatory dynamics across the brain. While interneurons are traditionally thought to follow a stereotyped, mosaic-like arrangement across cortex, the spatial organization of inhibitory networks within the hippocampus, particularly the subiculum, remains underexplored. Preliminary data suggest that the subiculum may deviate from this canonical organization, exhibiting diverse gene-expression profiles that occupy distinct spatial subdomains. This project investigates whether interneuron subtypes in the mouse subiculum exhibit spatially structured gene-expression patterns that correlate with functional subdomains. Utilizing high-resolution single-cell spatial transcriptomic data from the Allen Brain Atlas (MERFISH), we employ computational clustering, dimensionality reduction, and spatial statistical modeling within the R environment to construct a high-resolution spatial atlas of subicular inhibitory populations. By integrating these transcriptionally defined subtypes with known anatomical landmarks using high-performance computing, this work aims to map the precise microarchitecture of subicular inhibition. Uncovering this localized spatial patterning is crucial for understanding how inhibitory networks shape hippocampal output and will provide essential baseline insights into circuit dysregulation underlying neurological disorders such as epilepsy, schizophrenia, and Alzheimer's disease.

Keywords: Transcriptomics, Hippocampus, Computation



Poster Session 11am - 12pm

7



DANYAAL ABBAS

Supervised by Dr. Rob Rohling

Nanoscale Janitors: Mopping up Dielectric Soakage in polyCMUTs

Polymer-based capacitive micromachined ultrasound transducers (polyCMUTs) offer a novel pathway toward conformal, low-cost wearable ultrasound patches. However, long-term operation can introduce signal instability due to dielectric soakage. Under the sustained high-intensity electric fields required for transducer operation, charge carriers can migrate and become trapped within the polymer dielectric layer. This charging phenomenon can cause a drift in the operating voltage and degrade acoustic sensitivity, complicating continuous ambulatory monitoring. Overcoming this bottleneck is key to transitioning wearable ultrasound technology into a reliable, 24/7 diagnostic tool.

This ongoing investigation explores the development of various microfabrication and material modifications of the transducer's insulating layer to mitigate dielectric soakage. We examine adjustments to standard photopatternable epoxy formulations alongside the integration of nanocomposite additives to influence charge behavior and mobility at the dielectric interface. Preliminary characterization indicates that these modified photopolymer formulations maintain the necessary patternability, structural homogeneity, and spin-coating characteristics required for standard polyCMUT fabrication workflows, as well as high electrical resistivity down to the micro-scale.

Work is ongoing to integrate these patterned layers into test structures to evaluate changes to dielectric soakage and charge dissipation under operational bias. Further electrical characterization and its implications for long-term device stability will be presented at the symposium, showcasing a seamless integration of the modified workflow into existing CMUT fabrication pipelines.

Keywords: Ultrasound, MEMs, Biosensors

8



ETHAN YIP

Supervised by Dr. Kelly McNagny

ILC2s enhance respiratory mucosal RNA-LNP vaccination

RNA-LNP vaccinations delivered parenterally are able to generate systemic antigen-specific IgG antibodies and memory T cells; yet they lack the ability to generate robust mucosal immunity, which is mediated by antigen-specific IgA antibodies and lymphocytes. Currently, RNA-LNP mucosal vaccination platforms that target production of IgA and tissue-resident T and B cells lack mechanistically targeted adjuvants that selectively activate innate immune cells capable of initiating the adaptive immune response. IL-33 is an alarmin that evokes the immune system when mucosal surfaces are breached. In respiratory mucosal surfaces, IL-33 can bind to IL-33R on type 2 innate lymphoid cells (ILC2s) and activate them. We hypothesize that these activated ILC2s will ultimately license the adaptive immune response, positioning IL-33 as an ideal adjuvant in mucosal vaccinations. In this study, we co-administer IL-33 with mucosal RNA-LNP vaccination in mice via intranasal administration and show that it can both activate lung ILC2s and enhance the building of antigen-specific immune memory in the lungs. We also co-administer IL-33 with mCherry-LNP vaccination to illustrate IL-33's ability to promote the uptake of the RNA-LNP vaccine into the antigen-presenting cells and their migration into the draining lymph node. We then knock out IL-33R from ILC2s and show that deleting the receptor abrogates the adjuvant effect. Altogether, these findings establish IL-33 as a potent targeted adjuvant and ILC2s as a key biological target for promoting adaptive immunity in mucosal surfaces, offering a promising strategy for the design of next-generation vaccines against respiratory pathogens.

Keywords: Innate immune memory, Tissue-resident lymphocytes, Respiratory pathogen



Poster Session 11am - 12pm



EVAN WONG

Supervised by Dr. Bin Zhao

A Super-DNA Fluorescent Probe for Monitoring pH in Lipid Nanoparticles along the Endocytic Pathway

Lipid nanoparticles (LNPs) are leading delivery vehicles for RNA therapeutics. However, inefficient endosomal escape remains a critical bottleneck for RNA delivery, with only 1–5% of LNP-encapsulated RNA reaching the cytoplasm. While endosomal acidification influences this process, the pH microenvironment experienced by the mRNA within distinct LNP formulations along the endocytic pathway remains poorly understood. The project aims to construct and characterize a pH-sensitive fluorescent DNA probe for dynamic monitoring of the local pH experienced by mRNA cargo in ionizable LNPs along the endocytic pathway in cells. A branched, self-assembled super-DNA (spDNA) probe with enhanced sensitivity was prepared and conjugated to firefly luciferase (FLuc) or enhanced green fluorescent protein (EGFP) mRNA via a bridge DNA (BDNA) linker. The spDNA-BDNA-mRNA was encapsulated in three structurally distinct LNP formulations, including benchmark (Onpattro), phase-separated (blebbed), and long-circulating LNPs. The resulting LNPs were characterized by dynamic light scattering, cholesterol assays, and cryo-electron microscopy for particle size, lipid content, and morphology. We demonstrated that the spDNA probe conjugated to mRNA retains pH-responsiveness across all formulations under buffered conditions by fluorescence measurements and in cells by confocal fluorescence microscopy. Furthermore, lysosomal colocalization studies confirmed an increased association of spDNA with the lysosomal compartment, consistent with endolysosomal pathway progression. These findings demonstrate the capabilities of the designed spDNA probe for monitoring the internal pH of the ionizable LNPs along the endocytic pathway, providing a foundation for correlating endosomal pH with RNA escape kinetics and delivery efficiency.

Keywords: Lipid nanoparticle (LNP), DNA biosensor, Endosomal escape



HALEY DHALIWAL

Supervised by Dr. Negar Harandi

A Two-Level Reflective Tool to Support Students in Connecting Skills Across the Biomedical Engineering Curriculum

Engineering students are expected to clearly articulate the knowledge and skills they develop throughout their undergraduate education, particularly when applying for co-op positions and preparing for their future careers. This can be challenging in biomedical engineering, as competencies are developed across an interdisciplinary curriculum. To address this challenge, we have developed a reflective tool to help students in this discipline identify, reflect on, and communicate the skills they've gained throughout their degree. This tool was developed through reviewing existing reflective frameworks, and consultation with engineering instructors and students, who provided feedback on the hands-on skills included in the tool and its implementation within the curriculum. It provides a simple template that can be integrated into existing laboratory and design courses with minimal changes to course structure. Students are guided to reflect on the skills they developed through course activities and consider how these skills relate to engineering practice. Initial feedback suggests that the tool is practical, easy to use, and has the potential to improve students' awareness of their learned skills. It also supports accreditation efforts by providing self-reported evidence of students' mastery of the graduate attributes throughout the curriculum. Future work will involve implementing the tool in biomedical laboratory and design courses and evaluating its impact on students' ability to recognize and articulate their skills when seeking co-op positions and careers.

Keywords: Engineering education, Self-reflection, Skill identification



Poster Session 11am - 12pm

11



HANNA KHAN

Supervised by Dr. Peter Zandstra

Inferring Off-Target Inter-Cellular Dynamics in T-cell Differentiation from Hematopoietic Stem and Progenitor Cells

Engineering T-cells from hematopoietic stem and progenitor cells (HSPCs) is a promising strategy for developing cellular therapeutics. In-vitro differentiation platforms offer a cost-effective, efficient way to produce T-cells. However, byproduct differentiated cell lineages, such as Natural Killer (NK), myeloid, or innate lymphoid cells, emerge and compete with developing T-cells. These off-target cell types have been shown to be cytotoxic and inflammatory, limiting T-cell yield, although their mechanisms remain unclear. Current modelling approaches map experimental inputs to outputs statistically but do not capture such cellular interactions. We hypothesize that direct cell-mediated killing and cytokine-driven suppression of differentiation inhibit T-cell population dynamics. Our project uses computational approaches to investigate competitive inter-cellular interactions in T-cell differentiation, aiming to optimize their production. We developed a series of three-species mechanistic ODE models, using rate constants and population dynamics theory, to test these hypothesized mechanisms among T-cells, HSPCs, and NK cells, including NK-mediated killing, secreted-factor inhibition, and a combination of both. For simplicity, we focus on NK cells, whose population predominantly expressed Granzyme A, granulysin, perforin, and TGFB-1 cytotoxic genes in CITE-seq data. Our models reproduced observed flow cytometry trends of decreasing immature Double Positive T-cell counts with increasing HSPC seeding density. These results provide insight into the fundamental mechanisms driving lineage competition, informing strategies for scaling up viable T-cell production. In the future, we will use physics-informed machine learning architectures, such as Neural ODEs, to generate equations fitting observed data by extracting key parameters from design-of-experiments studies, flow cytometry, and single-cell RNA sequencing data.

Keywords: T-cell differentiation, Lineage competition, Mathematical/Computational modelling

12



HETA PATEL

Supervised by Dr. Shernaz Bamji

From Pathways to Patients: Functionalizing Previously Unrecognized Isoforms and Patient Variants of zDHHC8

Many neurodevelopmental disorders share a common feature—an imbalance in excitatory and inhibitory signaling. One gene linked to these neurodevelopmental disorders is zDHHC8, a palmitoyl acyltransferase highly expressed in the cortex. We found zDHHC8 exists as two previously unrecognized isoforms distinctly enriched in either inhibitory or excitatory neurons. Additionally, our clinical collaborators identified ZDHHC8 variants in five patients with autism and other neurodevelopmental comorbidities, suggesting that disruption of isoform regulation contributes to disease pathogenesis.

Our overall objective is to determine the role of the two ZDHHC8 isoforms in the brain and to functionalize patient derived variants.

We used a knockout-rescue approach in primary neurons to study how the loss of zDHHC8 in excitatory or inhibitory cells impacts dendritic outgrowth, and whether either isoform rescues these defects. Similarly, to assess the functional impact of patient-derived variants, we rescued zDHHC8-knockout neurons with either wild-type human ZDHHC8 or the patient variants.

Our findings show that genetic ablation of zDHHC8 reduces dendritic length in excitatory neurons, but not inhibitory neurons. Importantly, this defect was rescued by zDHHC8-Iso2 but not zDHHC8-Iso1, demonstrating unique isoform functions. Proximity-based protein labeling revealed that zDHHC8-Iso1 preferentially interacts with 38 distinct proteins compared to 227 proteins with zDHHC8-Iso2. Applying this rescue framework to patient derived variants pinpointed which specific mutations significantly disrupted dendrite outgrowth, as well as ZDHHC8 localization and stability.

These findings functionalize patient variants and uncover two previously unrecognized zDHHC8 splice isoforms with distinct cell-type functions, highlighting how isoform-specific dysregulation triggers neuronal circuit dysfunction in neurological disease.

Keywords: Synaptic plasticity, Protein lipidation, Functional genomics



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Poster Session 11am - 12pm

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KELLY DIAO

Supervised by Dr. Fabio Rossi

ROR α Activation Improves Repair and Reduces Fibrosis Following Cardiac Injury

Fibroblast activation is crucial for tissue repair after injury. However, prolonged fibroblast activation can cause excessive scar formation (fibrosis), which impairs cardiac function after heart injury (myocardial infarction). Unlike the laboratory mouse (Mus), the spiny mouse (Acomys) exhibits reduced progressive scarring. Preliminary data shows that the Acomys activates the transcription factor protein ROR α which may control fibroblast behaviour as it regulates the transition of activated fibroblast back to resting state. To investigate the role of ROR α , ROR α was inhibited in Acomys to see the effect when losing the transcription factor activity, and ROR α was activated in Mus, after myocardial infarction and induced high blood pressure. Cardiac function was assessed using echocardiography by measuring ejection fraction and fractional shortening. The Acomys and Mus hearts were stained for histology and immunofluorescence to evaluate fibrosis and myofibroblast abundance. Quantitative image analysis was performed to assess fibrosis area and myofibroblast density. Findings suggest that ROR α modulation influences cardiac remodeling after injury. Activation of ROR α in Mus appears to improve functional recovery and reduce fibroblast activation, while inhibition of ROR α in Acomys impairs its regenerative response. These findings identify ROR α as a promising regulator of fibroblast fate and its therapeutic potential for limiting fibrosis while promoting effective cardiac repair. These findings may help guide treatments for heart disease and other fibrotic conditions, by targeting pathways that promote healing and limit tissue damage.

Keywords: Tissue remodeling, Regenerative biology, Stromal biology

14



KRISTA TANNANT

Supervised by Dr. Kota Mizumoto

Genome engineering to investigate isoform-specific functions of SAD-1 kinase in synapse organization

SAD-1 (Synapses of Amphids Defective-1) is a highly conserved serine/threonine kinase that plays essential roles in nervous system development, including neuronal polarization and presynaptic organization. In *Caenorhabditis elegans*, alternative splicing of sad-1 exon 15 generates two structurally and functionally distinct isoforms, SAD-1L and SAD-1S, which are analogous to the mammalian Sad-A and Sad-B kinases. Despite the established importance of SAD-1 in neuronal development, the specific roles of these isoforms in synapse organization remain poorly understood.

This project investigates the isoform-specific functions of SAD-1 in regulating synaptic domain organization in *C. elegans*. We used CRISPR/Cas9 genome editing to generate mutant *C. elegans* strains expressing only the SAD-1L or SAD-1S isoform and examined synapse number and position along the DA9 motor neuron, which is known to express both SAD-1L and SAD-1S. We also introduced the T202E constitutively active mutation in wild-type, SAD-1S, and SAD-1L mutants. In the sad-1 null mutants, we observed that DA9 synapses are more spread along the axon compared to wild-type animals. In mutants expressing either SAD-1S or SAD-1L, we did not observe significant defects in synapse arrangements. Interestingly, in mutants only expressing constitutively active SAD-1L(T202E) or SAD-1S(T202E), we observed sad-1 null mutant-like synapse arrangement defects, while SAD-1(T202E) mutant animals expressing both isoforms did not exhibit such defects.

This result suggests that expression of one constitutively active isoform disrupts normal synapse arrangement. Ongoing analyses aim to further define the relationship between SAD-1 isoforms in synapse arrangement.

Keywords: Neurodevelopment, Molecular biology, Genetics



Poster Session 11am - 12pm

15



LAUREN KEILTY

Supervised by Dr. Stefanie Blain-Moraes

Individualistic Models of Autonomic Nervous System Responses for Salient Moment Detection in Individuals with Advanced Dementia

Caregivers of individuals living with non-normalized communication, like individuals with advanced dementia, often rely on second-person perspectives to assess the emotional state and depth of engagement of those they care for in interactions of day-to-day life. Autonomic nervous system responses (ANS) such as electrodermal activity, heart rate, and peripheral skin temperature have been established to meaningfully covary with emotional responses. These responses are highly individualistic in the strength of the responses seen and the signals in which the responses are most prominent. This project assesses the quality of individualistic models of ANS responses for detecting these salient moments in individuals with advanced dementia.

Physiological and video interaction data was collected from four groups consisting of a dancer, a musician, and an individual with advanced dementia as they participated in an interactive therapy practice over 8 distinct sessions. The videos were analyzed for moments of disengagement and engagement based on criteria that included eye contact, vocal sound changes, and body movements.

For a preliminary group, physiological windows were extracted from these moments and found to have significant differences in the amplitude of the maximum EDR peak and the maximum derivative of heart rate between the engaged and disengaged classes. A linear regression model was trained, validated, and tested to give 66% accuracy, 73% precision and 76% recall in predicting engaged and disengaged moments. Continued analysis will include adjustments to the features and window sizes to better capture the full physiological responses and individualistic analysis of the data from other three groups.

Keywords: Interpersonal connection, Wearable sensors, Assistive technology

16



MELODY WANG

Supervised by Drs. Sofia Graham and Govind Kaigala

A Plug-In Probe for Perfusable, High-Throughput Tissue Culture in Standard Well Plates

Organ-on-chip (OoC) systems promise physiologically relevant in vitro models, yet a persistent gap exists as they are powerful but low-throughput, non-standardized, demanding expert operation, and often lack the ability to capture the dynamic nature of cellular environments due to static operation.

We present the Well Probe, an open-space microfluidic device that converts conventional, unmodified multi-well plates into perfusable culture platforms without custom labware or bulky peripherals. This brings the benefits of microfluidics into routine laboratory workflows and enable the generation and maintenance of various microphysiological tissue models. The probe inserts into a standard well and, using a central injection channel paired with a surrounding aspiration ring, establishes hydrodynamically confined, recirculating flow directly over the culture surface. Because of the open-space nature, cell-laden hydrogels can be loaded by simple pipetting and retrieved intact for spatially resolved downstream analysis. Fluorescence and confocal z-stack imaging with tracer dyes and microparticles confirmed a stable, approximately radial flow profile reaching the well bottom, as well as verified surface-level shear contact.

Ongoing work addresses long-term operation stability, tapered geometries for more uniform shear, and a fluidic circuit board enabling parallelized, equal-resistance perfusion across many wells. We are also validating the biological relevance of the imposed flow using HUVECs seeded on the well surface to confirm that the probe delivers physiologically meaningful surface shear.

The Well Probe offers a simple, scalable route to bring controlled microscale perfusion to routine cultureware, lowering the barrier to physiologically relevant, high-throughput tissue models and drug screens.

Keywords: Tissue models, Organ-on-chip, High-throughput



Poster Session 11am - 12pm

17



MONICA MIHAILESCU

Supervised by Dr. Mahsa Khalili

Photoplethysmography Signal Quality Assessment for Heart Rate Estimation: An Application-Specific Approach

Photoplethysmography (PPG) is a non-invasive optical sensing technique widely used in wearable devices and clinical monitors for cardiovascular monitoring, including heart rate estimation. While PPG enables continuous physiological monitoring, its susceptibility to noise due to motion artifact, poor sensor-to-skin contact, and temperature can degrade signal quality. To address this challenge, signal quality assessment (SQA) algorithms are commonly used to identify and remove low-quality PPG segments before analysis. However, these algorithms may be overly conservative, excluding segments that remain sufficiently reliable for accurate heart rate estimation.

This study investigates whether PPG segments labelled as lower quality by a previously established method remain suitable for heart rate estimation when compared with high-quality electrocardiogram (ECG) recordings. Using the MIMIC-III-Ext dataset, a publicly available database containing synchronized PPG and ECG segments from 6,189 intensive care unit (ICU) patients, high-quality ECG segments are selected as the reference for corresponding high- and lower-quality PPG segments. Heart rate is estimated from both signals using time- and frequency-domain approaches, with ECG-derived estimates used as the ground truth for evaluating PPG accuracy.

We hypothesize that a subset of PPG segments flagged as lower quality by the existing approach will produce accurate heart rate estimates, suggesting that this algorithm may be conservative for heart rate monitoring applications. Additionally, based on the findings of a previous study from our group, we anticipate that frequency-domain estimation methods will demonstrate greater heart rate accuracy than traditional time-domain approaches.

These findings will inform application-specific SQA methods in datasets where ECG ground truth is unavailable and provide insight into the relationship between PPG signal quality and heart rate estimation performance.

Keywords: Remote health monitoring, Wearables, Biosignal processing



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MUHAMMAD AL MUHTADIN

Supervised by Dr. Lillian Hung

The Pepper Robot Demonstrates Potential for Person-Centered Dementia Care Despite Software Limitations

Person-centered care (PCC) is a gold standard for dementia care, tailoring to individual history, preferences, and needs. In order to assist with PCC, we have previously developed the Whatmatters app that provides nurses with patient's preferences in the form of images, videos, and audio. Despite its effectiveness, it still relies on healthcare providers to actively engage with it. This opens the opportunities to explore the use of a humanoid social robot known as Pepper to reduce the burden of healthcare providers in delivering PCC. We explored Pepper's capabilities and limitations, with the goal of being able to install the Whatmatters app and allow interactivity. We then performed an intervention with a patient and conducted gamified staff training for the app to then reiterate our development on Pepper based on our findings. Pepper was found to have a significant software limitation running on an outdated Android 5.1 and NAOqi 2.5 making it unfeasible to install the Whatmatters app. We improvised by installing a stripped-down mock application. Pepper's built in interactivity was limited to pre-programmed greetings and short questions for basic conversations, along with installable animations including dances and simple gestures. These simple interactivity received positive reactions from patients and staff during intervention and staff training. We reiterated by connecting to an AI model for enhanced interactivity, but were unable to test due to the project's ethical scope. While Pepper shows promising results, a more modern robot with better software and extensibility should be explored to overcome Pepper's current limitation.

Keywords: Artificial intelligence, Gamification, SoftBank robotics

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MUTSUMI ITO

Supervised by Dr. Nozomu Yachie

TEVp-inducible lentiviral particle assembly and production system

Lentivirus is a widely used platform for stable gene delivery in cell engineering and cancer immunotherapy, in part due to engineered safety features that minimize the formation of replication-competent virus. In such applications, the ability to control the timing and location of viral particle assembly is valuable. However, existing inducible systems, including transcription-based Tetracycline-inducible systems, are often limited by background leakage, slow induction kinetics, and limited spatial control.

To address these limitations, we utilize the RELEASE (Retained Endoplasmic Cleavable Secretion) system to regulate viral production. In this system, viral structural and envelope proteins are retained within the ER through an ER retention signal. Upon TEVp-mediated cleavage of the retention signal, the proteins escape the ER and assemble into viral particles. We have demonstrated the compatibility of this RELEASE system with viral production with the envelope protein VSVG and are currently evaluating its compatibility with Gag and Pol.

Overall, we present a TEVp-triggered system for controlling lentiviral particle production, in which ER retention coupled to proteolytic cleavage enables conditional assembly of functional viral particles.

Keywords: Viral vector engineering, Post-translational regulation, Protein trafficking

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NICOLA SMITH

Supervised by Drs. Ajinkya Ghagre and Peter Zandstra

Spatial Visualization of Notch Signalling During T Cell Differentiation

Natural shrinking of the thymus (thymic involution) severely impairs naive T cell production with age, weakening adaptive immunity and resilience against infection and cancer. To restore T cell output, synthetic hydrogels mimicking the thymic microenvironment can differentiate hematopoietic stem cells into progenitor T (Pro-T) cells. This process relies on activation of the mechanosensitive Notch pathway via ligand-receptor interactions between adjacent cells and the hydrogel environment. However, how 3D spatial constraints, cell colony architecture, and hydrogel mechanics collectively govern Notch activation is poorly understood. This project aims to spatially map Notch signalling in 3D hydrogels by staining and quantifying downstream Notch targets across varied hydrogel conditions with the goal of better understanding how matrix mechanics and spatial organization regulate Pro-T cell yield.

Keywords: Immunology, Biomaterials, Cell niches



Poster Session 11am - 12pm

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NINA GLIOSCA

Supervised by Dr. Jenna Uspreh

Where are the Women in STEM? Bridging the Gap Between STEM Interest and Education

Women, girls, and gender-expansive (e.g., trans or non-binary) people, particularly from low socio-economic status (SES) backgrounds, face chronic underrepresentation in Canada's STEM education fields and occupations. Hundreds of Canadian STEM outreach programs aim to reach these populations, yet long-term data shows that girls' interest in science and engineering has little correlation with their persistence in STEM education. The long-term impacts of these outreach programs on the STEM identity and persistence of girls and gender-expansive youth (G+GEY) from different SES backgrounds remain unclear. It is predicted that there will be higher rates of positive STEM identity and persistence among G+GEY of higher SES, especially those whose parents work in STEM fields. This study uses a mixed-methods approach, combining surveys and interviews over an eighteen-month period, with G+GEY attending youth STEM outreach programs across Canada as the population of interest. Participants entering grades 9 and 11 will complete four surveys: one before camp, one immediately after, one at twelve months, and one at eighteen months. Parents will also complete a survey to understand how their access to and exposure to STEM may influence their child's STEM identity and trajectory. Surveys draw on sociological frameworks measuring STEM interest, science and engineering identity, science capital, and sense of belonging in STEM environments. Interviews will explore facilitators and barriers that parents and youth perceive to pursuing STEM or accessing outreach resources. Findings will identify key timepoints and forms of intervention to support lower-SES G+GEY in their pursuit of science and engineering, benefiting outreach programs, funding bodies, and parents.

Keywords: Equity and inclusion, Social identity theory, Longitudinal study design

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RAISA ALLARAKHIA

Supervised by Drs. Jordan Hamden and Annie Ciernia

Impaired microglial transcriptional & morphological activation and downstream A β phagocytosis & plaque compaction in a humanized mouse model of comorbid inflammatory bowel & Alzheimer's disease

Inflammatory bowel disease (IBD) is a chronic inflammatory condition of the gastrointestinal tract which alters microbiome composition and gut-brain signalling metabolite production. IBD patients experience earlier onset of proteinopathies, such as Alzheimer's Disease (AD), in which misfolded proteins aggregate into neurotoxic, immune-resistant structures. Interestingly, both IBD & AD patients are deficient in colon bacteria that convert dietary fiber into short-chain fatty acids (SCFAs).

SCFAs cross the blood-brain barrier and inhibit histone deacetylases; in microglia, CNS-resident immune cells, SCFAs upregulate TREM2 receptors. In AD, a neuronal membrane protein is cleaved into extracellular amyloid- β (A β) peptides, which polymerize into protofibrils, fold into fibrils, and aggregate into plaques with an inert fibril core & neurotoxic protofibril halo. Microglia detect A β plaques via TREM2 and undergo morphological transformation to reduce plaque protofibril-to-fibril ratio. Hypertrophic microglia branches compact plaque cores to reduce protofibril affinity; amoeboid microglia intralysosomally aggregate protofibrils into fibrils.

We hypothesize that IBD depletes SCFA-producing bacteria—reducing gut-derived brain SCFAs, downregulating microglial TREM2, shifting plaques to neurotoxic forms, and accelerating neurodegeneration in AD patients. To create a mouse model of comorbid IBD & AD, 5xFAD (transgenic A β pathology model) mice were colonized with fecal microbiota from a human IBD patient or healthy control and serum SCFA reduction was confirmed in IBD mice.

In 2 month brains, immunofluorescence, widefield & confocal microscopy, and 2D ImageJ & 3D Imaris analysis were used to characterize plaque core density, plaque protofibril-to-fibril ratio, plaque-associated neuritic dystrophy, coverage & polarization by plaque-associated microglia, and morphology of plaque-associated/proximal/distal microglia. IBD mice have globally elevated plaque burden & reduced neuron density, and elevated plaque size & diffuseness correlating with altered microglia plaque interaction at cortex, hippocampus, & thalamus.

Keywords: Gut-brain axis, Neurodegeneration, Immunology



Poster Session 11am - 12pm

23



REID CHASE

Supervised by Dr. Peter Zandstra

Gene regulatory network modelling predicts human CD4 versus CD8 T cell lineage specification

Engineered T cell therapies have emerged as transformative treatments for haematological malignancies. The production of T cells from pluripotent stem cells (PSCs) is a more scalable and accessible alternative to using patient-derived T cells. Importantly, commitment to CD4 versus CD8 T cell lineages can be controlled by tuning the strength and duration of different signalling pathways. However, the gene regulatory networks driving single-positive (SP) lineage specification and selection have yet to be fully elucidated. In particular, it remains unclear how Notch signalling fits into larger regulatory circuits, and how it interacts with T cell receptor (TCR) signalling to specify CD4 versus CD8 T cell fates. In this study, we develop a mechanistic Hill-based model of double-positive to SP lineage commitment in human induced PSC-derived T cells. We compare mechanistic and statistical models to evaluate whether a biologically informed design improves predictive performance. Using the model, we delineate the lineage biases conferred by Notch- and TCR-stimulating conditions, and we optimise these signalling inputs to produce desired fate outcomes. Next, we will extend our model to capture cell survival decisions during selection, allowing optimisations to maximise both lineage specification and T cell yields. This work establishes a predictive framework for understanding the regulatory interactions driving T cell survival and fate decisions during SP induction, enabling more precise control of T cell differentiation for cell therapies.

Keywords: T cell differentiation, Gene regulatory networks, Mechanistic modelling

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ROBBEN LIU

Supervised by Dr. Nika Shakiba

Expansion and Controlled Settlement of hPSC Aggregates in a Microfluidic System for Differentiation and Downstream Analysis

Human pluripotent stem cells (hPSCs) have an unlimited capacity to self-renew and differentiate into any cell type of the body, serving as a powerful source for regenerative medicine. The in vivo counterparts of both naïve and primed hPSCs (corresponding to cells at the pre- and post-implantation stages of human embryos, respectively) exist as aggregates and are exposed to fluid flow during development. Although bioreactors are currently used to expand hPSC aggregates, they lack the adaptability to control individual aggregates for downstream applications. In this project, we aim to develop an integrated system to expand hPSC aggregates under controlled flow conditions while allowing precise control of their settlement for differentiation and the formation of organ-like models. To establish a flow-circulating system with scalability potential, we combined a microfluidic pump with medium reservoirs. Additionally, we incorporated a microfluidic chip to regulate the settlement of individual aggregates into small buckets. In preliminary results, we maintained continuous growth of hPSC aggregates under a flow rate ranging from 0.1 to 1.4 mL/min, with average sizes comparable to those generated by conventional bioreactors. We also achieved precise control over aggregate settlement within the chip's small buckets. In our future work, we will assess the quality of our hPSC aggregates by comparing their transcriptomic profiles with those cultured in a conventional bioreactor and evaluate their functionality through differentiation assays. Overall, this project represents significant advancements in the hPSC bioprocessing (for both primed and naïve cells), offering a controlled technology for downstream applications.

Keywords: Microfluidics, Stem cells, Organoid



Poster Session 11am - 12pm

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SAIGE MANN

Supervised by Dr. Christopher Moraes

Thromboelastograms on a Paper Microfluidic Platform for Neonatal Sepsis Diagnosis

In lower-middle-income countries, neonatal sepsis is a major cause of mortality and morbidity. Clinical signs of neonatal sepsis (respiratory distress, temperature instability, etc.) are variable and can often look indistinguishable from other conditions. A thromboelastogram (TEG) is a clinical assay that measures the viscoelastic properties of whole blood and shows promise in identifying sepsis through coagulation changes. Unfortunately, TEG has high costs, making this testing method inaccessible in resource-limited settings. This research explores the possibility of using a paper-based microfluidic platform containing a hydrogel microparticle. These microparticles will have photothermal properties, causing them to expand and contract in response to a laser and allowing them to act as actuators that measure the viscoelastic properties of the blood. Increased clot stiffness will lead to reduced microparticle expansion, enabling the quantification of the clot through fluorescent imaging. We present the fabrication of the microparticles using n-isopropylacrylamide, acrylamide, and gold nanorods as well as the development of the microfluidic platform using laminated filter paper.

Keywords: Neonatal health, Global health, Diagnostic devices

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SHAHZAD SHAMS

Supervised by Dr. John Madden

Feeling Through a Prosthetic Hand: A Bypass-Limb Platform Integrating Soft E-Skin Sensing with Wearable Haptic Feedback

Upper-limb amputation results in the loss of motor and sensory function of the hand. Myoelectric prostheses, prostheses controlled by electrical signals from the muscles of the residual limb, can restore movement but provide little sense of touch, forcing users to rely on constant visual attention and mental effort during grasping. Although non-invasive sensory feedback has been studied for decades, few systems reach daily use, in part because sensing, control, and feedback components are rarely integrated into a single wearable platform. Our lab has developed soft capacitive electronic skin (e-skin) sensors that measure grip force and shear (sliding) direction, motivating a platform that connects these sensors to a prosthetic hand and a wearable feedback interface. We therefore developed a "bypass limb": a robotic prosthetic hand worn alongside the intact arm of a user without limb difference, allowing prosthesis technologies to be tested without requiring participants with amputation. The 3D-printed hand carries e-skin sensors read by a microcontroller that wirelessly transmits three-axis contact data to a wearable haptic interface: a rack-and-pinion plunger presses into the upper arm at nine levels to convey grip force, while four vibration motors encode shear direction along two axes at three intensities. The user opens and closes the hand using muscle signals measured at the forearm, completing a closed sensorimotor loop. We are now developing pick-and-place testing to gauge how well the haptic feedback helps users regulate grip force, supporting future studies on how artificial touch can reduce cognitive burden and improve grasp control for prosthesis users.

Keywords: Prosthetics, Haptic feedback, Wearables



Poster Session 11am - 12pm

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SOPHIA DUMONT

Supervised by Dr. Alex Burden

Upgrading CHIMERA with a Teensy 4.1 for Improved Timing Precision

Mild traumatic brain injury (mTBI) is one of the most common types of brain injury however, the long term impacts and mechanisms are not fully understood. The Closed-Head Impact Model of Engineered Rotational Acceleration is a device that was designed to be able to deliver controlled and repeatable impacts to animal models (specifically mouse, rat and ferret) to allow researchers to study injury biomechanics and the neurological outcomes. The existing CHIMERA uses an Arduino Uno microcontroller whose timing precision limits the accuracy and consistency of the studies done with it. This project's objective was to replace the Arduino Uno with a Teensy 4.1 which would provide a greater processing speed and timing resolution. This required modifying the existing code to be compatible with the new microcontroller, adapting the hardware connections, troubleshooting the connection between sensors and the controller and finally validating the performance of the new controller. Throughout the project several challenges were identified, such as differences in the use of interrupts between the two controllers leading to repeated photogate triggering. Such issues were resolved through troubleshooting and revising the device's original literature. The final validations concluded that the Teensy 4.1 had been successfully integrated into the CHIMERA system and the accuracy of velocity readings had been improved. Enhancing the precision and reliability of CHIMERA strengthens the quality and reproducibility of biomechanical data in mTBI research.

Keywords: mTBI, Embedded systems, Data acquisition

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SOPHIE PERRY

Supervised by Dr. Govind Kaigala

Microfluidic-Assisted Localized Drug Delivery for Analysis of Spatial Response Heterogeneity in Cancer Cell Migration

Tumour heterogeneity is a key characteristic of cancer, presenting a challenge for developing effective cancer therapeutics. Heterogeneity is a leading contributor to drug resistance by exerting selective pressure, thereby promoting the growth of resistant cells. Notably, leader cells, which drive cancer cell migration, are shown to exhibit therapeutic resistance due to their stem-like characteristics and ability to alter their phenotypes. Deconvolving such resistance mechanisms requires methods that can allow for specific treatment of cell sub-populations and their spatial phenotyping, however current approaches are limited. Here we build on a previously established technology named the microfluidic probe (MFP), which enables the localization of reagents on a surface at the microscale. We develop a workflow to analyze spatial therapeutic responses of migrating and non-migrating cells through MFP-assisted collection of cellular material, followed by qPCR and mRNA sequencing. We also design and optimize a new MFP device that allows for highly localized drug treatment. Such spatially restricted treatment can help to separate direct and indirect responses, providing insight into the involvement of paracrine feedback and potential spread of compensatory mechanisms among neighboring cells. This local treatment MFP will be used together with time-lapse imaging and velocimetry analysis to reveal insights into migration and recovery dynamics. By combining both approaches, we can evaluate spatial cellular phenotypic changes in response to drugs, as well as molecular gene expression patterns. Overall, this work presents a promising tool to strengthen our understanding of collective cancer cell migration and the role of heterogeneity in cancer resistance mechanisms.

Keywords: Spatiotemporal analysis, Microfluidics, Differential cellular response



Poster Session 11am - 12pm

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ZUBINA ZAFAR

Supervised by Dr. John (Kip) Kramer

Assessing Morphological Changes in Volume of the Lateral Hypothalamus for Recovery After Spinal Cord Injury

Recovery following spinal cord injury (SCI) depends not only on changes within spinal circuitry, but also on reorganization in supraspinal regions that contribute to locomotion and functional recovery. The lateral hypothalamus (LHA) has emerged as an important region in walking recovery, with hypothalamic deep brain stimulation demonstrating improved locomotor function following SCI (Cho et al., 2024). However, the role of LHA structural and volumetric remodeling following SCI remains an emerging area of research. We hypothesize that individuals with chronic SCI will demonstrate altered LHA volumetric morphology, reflecting supraspinal adaptation following injury. High-resolution T1-weighted MRI scans from individuals with chronic SCI and neurologically intact controls were analyzed. The LHA was segmented using the human hypothalamic atlas developed by Neudorfer et al and implemented within DSI Studio. Participant-specific LHA volumes were extracted following atlas-based segmentation and quality control. Group differences in LHA volume between SCI and control participants were assessed while adjusting for age, sex, and intracranial volume, while additional analyses within the SCI cohort examined associations between LHA volume and clinical characteristics, including neurological level of injury, ASIA grade, and time since injury. Diffusion MRI data from a subset of participants were processed using Q-space diffeomorphic reconstruction (QSDR) to investigate longitudinal changes in LHA microstructural measures, including fractional anisotropy (FA) and mean diffusivity (MD). This work provides insight into supraspinal adaptations following SCI by identifying structural changes within a locomotor-relevant brain region. Understanding these changes may reveal potential biomarkers of recovery and inform future rehabilitation and neuromodulation strategies.

Keywords: Locomotor networks, Supraspinal reorganization, Therapeutic targets

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ARTHUR ELLIS

Supervised by Dr. Dena Shahriari

Experimental and Computational Optimization of an Implantable Device for Neurogenic Bladder Management

An underactive bladder occurs when a person cannot sense bladder fullness and/or is unable to empty the bladder effectively, often due to spinal cord injury or other neurological disorders. As a result, many patients rely on long-term catheterization, which can lead to infections, tissue damage, and reduced quality of life. This project aims to develop a soft implantable device for neurogenic bladder management as an alternative to catheterization. The device integrates two key components. The first is a shape memory alloy-based actuator embedded within an elastomer that contracts the bladder to assist urination. The second is a flexible strain sensor that monitors bladder filling by measuring bladder wall stretching. To better understand the interaction between the device and the bladder, simplified computational models will be developed in COMSOL Multiphysics. Hyperelastic (Neo-Hookean) and linear elastic material models will be used to represent the mechanical properties of the bladder and device. Anatomical and physical constraints will be incorporated through appropriate boundary conditions, while applied variables will be defined using physiological and physical relationships. The models will evaluate strain distributions, sensor stability and signal reliability, and actuator-induced bladder contraction. In parallel, device prototypes will be fabricated and experimentally evaluated. Ex vivo testing will characterize the relationship between applied voltage and actuator contraction, while in vivo testing will assess the strain sensor's ability to monitor bladder filling and evaluate the animal's recovery following implantation. Together, these computational and experimental studies will guide the optimization of the implant for future neurogenic bladder applications.

Keywords: Soft embedded electronics, Actuators, Sensors



Poster Session 11am - 12pm

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SANIDH SHAH

Supervised by Dr. Joerg Gsponer

Modelling the Structural Effects of Mutagenesis on Ribosomal Skipping in 2A Peptides

Eukaryotic translation typically produces one polypeptide per mRNA, but 2A peptides are a notable exception, triggering ribosomal skipping—termed StopGo—to yield two products from a single reading frame. These nascent oligopeptides demonstrate autonomous and co-translational processing within the peptidyl transferase centre (PTC) in eukaryotic ribosomes, inhibiting their own downstream peptide bond formation as they are being synthesised. Prior mutagenesis studies of the F2A and P2A variants within this 2A family have mapped StopGo activity to specific mutations, and a cryo-EM structure of F2A shows how it engages the PTC during ribosomal skipping. P2A, however, despite comparable activity data, lacks any solved ribosome-bound structure, and upstream motifs are non-interchangeable across 2A family members. The structural basis of most StopGo-modulating mutations remains undefined, and it is unclear how individual mutations reshape 2A peptide conformation to alter skipping efficiency. We build on this data, showing that AlphaFold3 can predict 2A peptide conformations by modelling a reduced ribosomal subset across a mutagenesis panel, where cryo-EM cannot resolve individual mutant conformations at scale. This approach better discerns the various positions taken by mutated 2A peptides and extends structural inference to P2A. In doing so, we establish a generalisable computational framework for probing the 2A mechanism in the absence of variant-specific structural data. This work has implications for the rational design of high-efficiency 2A linkers in multicistronic expression systems, protein-based biotechnology, and gene therapy vectors.

Keywords: AlphaFold3, Homology modelling, Structural biology



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Synergy Showcase - Poster List

Poster #	Presenter	Poster Title
1	Abhinav Menon	Persistence vs. Potency: How Directed Evolution Methods Shape Phage-Bacteria Dynamics in <i>E. coli</i>
2	Albie Gong	Proteomic Analysis of Glucose Effects on Astrocytic Response to Human Coronavirus 229E Infection
3	Anders Schwarz	Toward a paper-based test for rapid discrimination of bacterial causative agents of UTI
4	Aria Raymaakers	A Multi-IMU Method to Characterise Head-Trunk Motion for Mogul Skiing
5	Calla Stanley	Evaluating the Impact of mRNA Nucleoside Modification on a Tolerogenic Lipid Nanoparticle Therapeutic for Type 1 Diabetes
6	Cindy Zhang	Single-Cell Spatial Transcriptomic Profiling of Inhibitory Interneurons within the Mouse Subiculum
7	Danyaal Abbas	Nanoscale Janitors: Mopping up Dielectric Soakage in polyCMUTs
8	Ethan Yip	ILC2s enhance respiratory mucosal RNA-LNP vaccination
9	Evan Wong	A Super-DNA Fluorescent Probe for Monitoring pH in Lipid Nanoparticles along the Endocytic Pathway
10	Haley Dhaliwal	A Two-Level Reflective Tool to Support Students in Connecting Skills Across the Biomedical Engineering Curriculum
11	Hanna Khan	Inferring Off-Target Inter-Cellular Dynamics in T-cell Differentiation from Hematopoietic Stem and Progenitor Cells
12	Heta Patel	From Pathways to Patients: Functionalizing Previously Unrecognized Isoforms and Patient Variants of zDHHc8
13	Kelly Diao	ROR α Activation Improves Repair and Reduces Fibrosis Following Cardiac Injury
14	Krista Tannant	Genome engineering to investigate isoform-specific functions of SAD-1 kinase in synapse organization
15	Lauren Keilty	Individualistic Models of Autonomic Nervous System Responses for Salient Moment Detection in Individuals with Advanced Dementia
16	Melody Wang	A Plug-In Probe for Perfusable, High-Throughput Tissue Culture in Standard Well Plates

Poster #	Presenter	Poster Title
17	Monica Mihailescu	Photoplethysmography Signal Quality Assessment for Heart Rate Estimation: An Application-Specific Approach
18	Muhammad AlMuhtadin	The Pepper Robot Demonstrates Potential for Person-Centered Dementia Care Despite Software Limitations
19	Mutsumi Ito	TEVp-inducible lentiviral particle assembly and production system
20	Nicola Smith	Spatial Visualization of Notch Signalling During T Cell Differentiation
21	Nina Gliosca	Where are the Women in STEM? Bridging the Gap Between STEM Interest and Education
22	Raisa Allarakhia	Impaired microglial transcriptional & morphological activation and downstream A β phagocytosis & plaque compaction in a humanized mouse model of comorbid inflammatory bowel & Alzheimer's disease
23	Reid Chase	Gene regulatory network modelling predicts human CD4 versus CD8 T cell lineage specification
24	Robben Liu	Expansion and Controlled Settlement of hPSC Aggregates in a Microfluidic System for Differentiation and Downstream Analysis
25	Saige Mann	Thromboelastograms on a Paper Microfluidic Platform for Neonatal Sepsis Diagnosis
26	Shahzad Shams	Feeling Through a Prosthetic Hand: A Bypass-Limb Platform Integrating Soft E-Skin Sensing with Wearable Haptic Feedback
27	Sophia Dumont	Upgrading CHIMERA with a Teensy 4.1 for Improved Timing Precision
28	Sophie Perry	Microfluidic-Assisted Localized Drug Delivery for Analysis of Spatial Response Heterogeneity in Cancer Cell Migration
29	Zubina Zafar	Assessing Morphological Changes in Volume of the Lateral Hypothalamus for Recovery After Spinal Cord Injury
30	Arthur Ellis	Experimental and Computational Optimization of an Implantable Device for Neurogenic Bladder Management
31	Sanidh Shah	Modelling the Structural Effects of Mutagenesis on Ribosomal Skipping in 2A Peptides