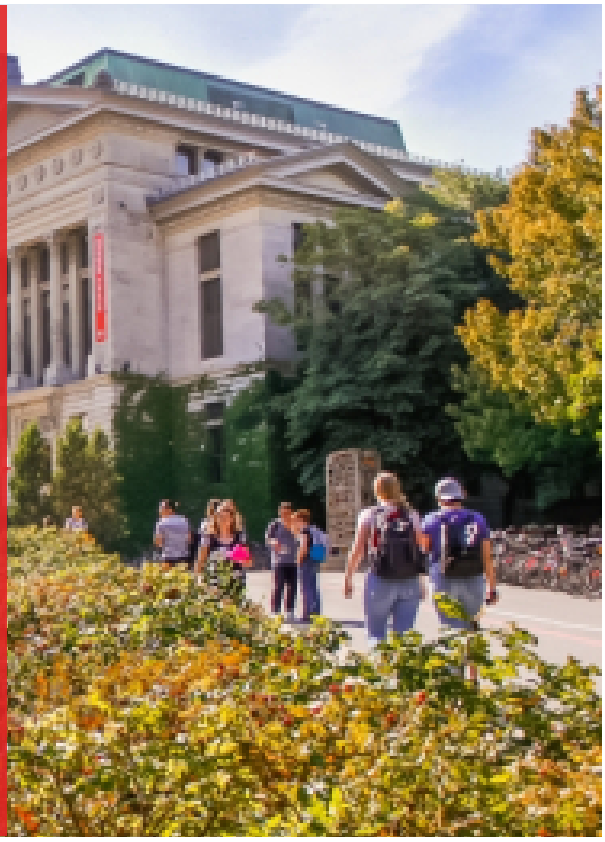
BBMESS
Biological and Biomedical Engineering Student Society

McGill

# BBME Symposium

## May 5-6, 2025
## 8:30 am - 6:15 pm
## SSMU Ballroom



## Keynote Speakers:

**The Hon. Dr. Marc Garneau**
Formerly Canadian Space Agency and Government of Canada

**Prof. Emily Porter**
McGill University, Assistant Professor

**Prof. Louis Collins**
McGill University, James McGill Professor

**Prof. Samir Mitragotri**
Harvard University, Hiller Professor and Hansjorg Wyss Professor

Contact: bbmess.pgss@mail.mcgill.ca

Links for program and voting: linktr.ee/bbmess

THE 8TH

# BIOLOGICAL AND BIOMEDICAL ENGINEERING SYMPOSIUM

**MAY 5-6, 2025**

SSMU Ballroom

3480 Rue McTavish

**BBMESS**

**Biological and Biomedical Engineering Student Society**

MCGILL SUSTAINABLE EVENT

SILVER

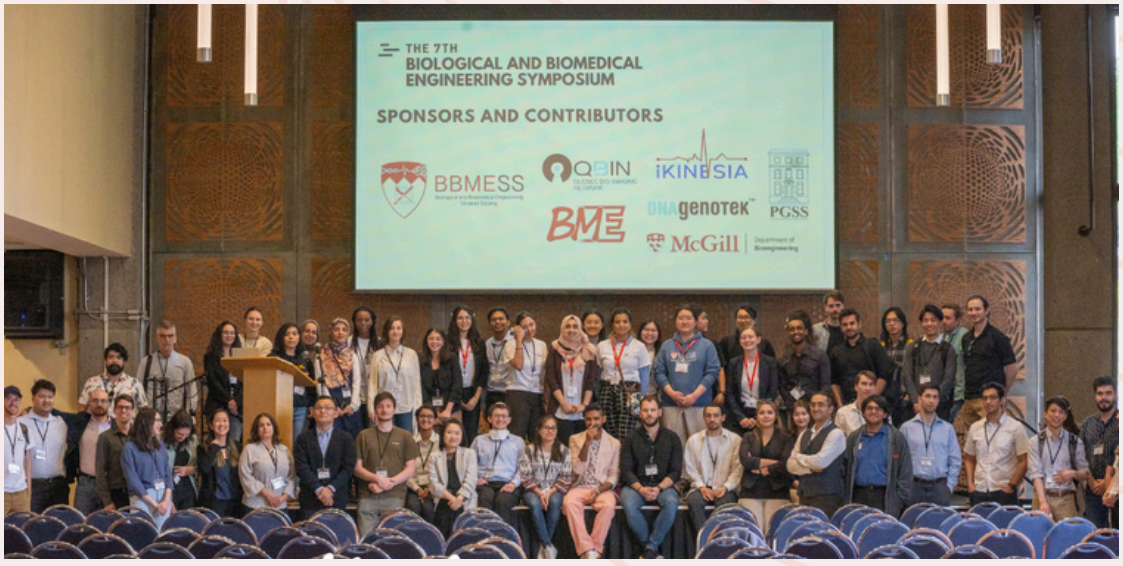
# TABLE OF CONTENTS

# WHO ARE WE?

The Biological and Biomedical Engineering Student Society (BBMESS) is a volunteer-based student run society that represents the graduate students of the Biological and Biomedical Engineering (BBME) program at McGill University.

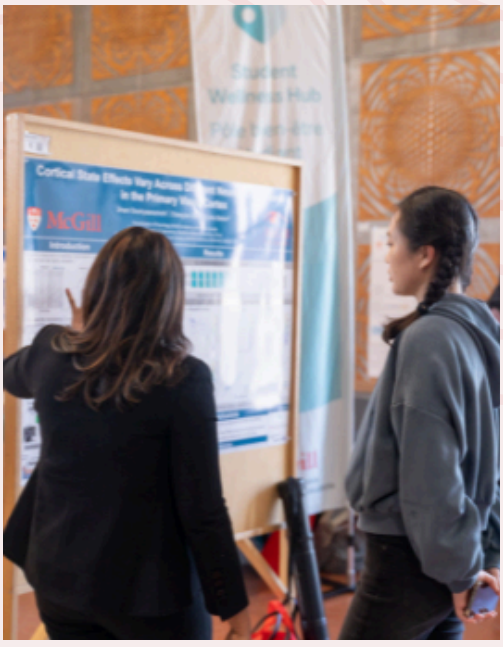
Our main goals are to:

- Foster a sense of community through social events
- Provide soft-skills development and networking opportunities through academic events
- Advocate for the BBME student body



# WHAT IS THE BBME SYMPOSIUM?

The Biological and Biomedical Engineering (BBME) Symposium is a biennial event hosted by the BBME student council. Its main goal is to provide students an opportunity to showcase their work and network with peers, faculty, and invited guests. In addition, it is an opportunity for students to learn about the different research fields under the biological and biomedical engineering umbrella.



# SCHEDULE - DAY 1
# Monday, May 5, 2025

| | | |
|---|---|---|
| 8:30 AM - 4:30 PM | **Registration**<br>*Ballroom, Room 301* | |
| 8:30 AM - 9:15 AM | **Breakfast**<br>*Ballroom, Room 301* | |
| 9:15 AM - 9:30 AM | **Welcome and Opening Remarks**<br>Jason Zhu, BBMESS President and Prof. David Juncker, Chair of Biomedical Engineering<br>*Ballroom, Room 301* | |
| 9:30 AM - 10:30 AM | **Believe in the importance of what you are doing**<br>Opening keynote by The Hon. Dr. Marc Garneau, Formerly Canadian Space Agency and Government of Canada<br>*Ballroom, Room 301* | |
| 10:30 AM - 11:00 AM | **Break**<br>*Ballroom, Room 301* | |
| 11:00 AM - 12:30 PM | **Thematic sessions** | |
| | **Biosensors, Diagnostics, and Therapeutics**<br>Chaired by Prof. Dan Nicolau<br>*Ballroom, Room 301* | **Microscopy, Imaging, and Neuroimaging**<br>Chaired by Prof. Georgios Mitsis<br>*Lev Bukhman Room, Room 203* |

# SCHEDULE - DAY 1
# Monday, May 5, 2025

**continued**

| | |
|---|---|
| 12:30 PM - 1:30 PM | **Lunch**<br>*Ballroom, Room 301* |
| 1:30 PM - 2:30 PM | **Commercializing University Intellectual Property: the McGill Perspective**<br>Dr. Mark Weber, Director, Innovation and Partnerships, McGill University<br>*Ballroom, Room 301* |
| 2:30 PM - 3:30 PM | **Poster Session**<br>*Ballroom, Room 301* |
| 3:30 PM - 4:30 PM | **Startup Law 101 Workshop**<br>Compass Startup Legal Clinic<br>*Ballroom, Room 301* |
| 4:30 PM - 5:00 PM | **Break**<br>*Ballroom, Room 301* |
| 5:00 PM - 6:00 PM | **Microwave medical technologies: advances and clinical challenges**<br>Faculty keynote by Prof. Emily Porter<br>*Ballroom, Room 301* |

# SCHEDULE - DAY 2
# Tuesday, May 6, 2025

| | | |
|---|---|---|
| 8:30 AM - 4:30 PM | **Registration**<br>*Ballroom, Room 301* | |
| 8:30 AM - 9:15 AM | **Breakfast**<br>*Ballroom, Room 301* | |
| 9:15 AM - 9:30 AM | **Welcome and Day 2 Opening Remarks**<br>Prof. Adam Hendricks, Chair of Bioengineering<br>*Ballroom, Room 301* | |
| 9:30 AM - 10:30 AM | **Modelling and computational methods for the analysis of Alzheimer's disease**<br>Faculty keynote by Professor Louis Collins, James McGill Professor<br>*Ballroom, Room 301* | |
| 10:30 AM - 11:00 AM | **Break**<br>*Ballroom, Room 301* | |
| 11:00 AM - 12:30 PM | **Thematic sessions** | |
| | **Bioinformatics, Modelling, and Computational Biology**<br>Chaired by Prof. Louis Collins<br>*Ballroom, Room 301* | **Biomaterials, Tissue Engineering, and Regenerative Medicine**<br>Chaired by Prof. Allen Ehrlicher<br>*Lev Bukhman Room, Room 203* |

# SCHEDULE - DAY 2
# Tuesday, May 6, 2025
**continued**

| | |
|---|---|
| 12:30 PM - 1:30 PM | **Lunch**<br>*Ballroom, Room 301* |
| 1:30 PM - 2:30 PM | **Government-Oriented Careers Panel**<br>**National Research Council of Canada**<br>Prof. Lidija Malic, Dr. Felix Lussier, Dillon Da Fonte, Mojra Janta-Polczynski<br>*Ballroom, Room 301* |
| 2:30 PM - 3:30 PM | **Poster Session**<br>*Ballroom, Room 301* |
| 3:30 PM - 4:30 PM | **Intellectual Property Workshop**<br>Legal Information Clinic at McGill<br>*Ballroom, Room 301* |
| 4:30 PM - 5:00 PM | **Break**<br>*Ballroom, Room 301* |
| 5:00 PM - 6:00 PM | **A Hitchhiker and Backpacker's Guide to Drug Delivery**<br>Closing keynote by Prof. Samir Mitragotri, Harvard University<br>*Ballroom, Room 301* |
| 6:00 PM - 6:15 PM | **Awards Ceremony and Closing Remarks**<br>Prof. Maryam Tabrizian, BBME Graduate Program Director<br>*Ballroom, Room 301* |

# COMMUNITY GUIDELINES

BBMESS is dedicated to providing inclusive and harassment-free events and we will not tolerate any offensive behaviour. Please keep these guidelines in mind for the duration of the symposium:

**Be kind, open-minded and respectful:** participate in the events with the mindset that everyone deserves to be present at the symposium. Whether through an oral or poster presentation, or as an attendee, everyone is welcome and respected at our conference.

**Update your LinkedIn:** connect with our speakers using your professional social media profiles, so update your LinkedIn to make those connections!

**Trash disposal**: to ensure that our event remains sustainable, follow the waste disposal guidelines available on-site for recycling, garbage, plastic, and compost.

**Be present in the sessions:** remember that you are here to both learn and teach. This is an opportunity for you to engage with peers and grow your network, so we ask that you attend all the events and participate in the sessions by asking questions and engaging in discussion with the invited speakers to show your interest and desire to learn

# ACCESSING THE VENUE

## Address

University Centre (3480 rue McTavish),
SSMU Ballroom (Room 301, 3rd Floor),
Montreal, QC, H3A0E7 Canada


## Directions

Take Sherbrooke Street until McTavish Street. The University Centre (3480 McTavish Street) and the Brown Building (3600 McTavish Street) are situated on the left side of the street, just before the road bends to the right at the foot of the staircase leading to Dr. Penfield Street. Please note McTavish street is pedestrian only.

## Accessible Public Transportation Options

**Bus:** The STM bus routes 144 and 24 stop close to the building.

**Metro:** The nearest metro is Peel Station on the Green Line, within a 5-minute walk.

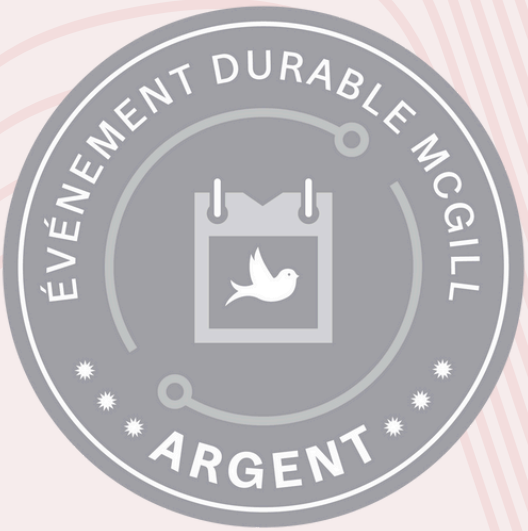
**Train:** If you're coming from outside of Montreal, you can take a train to the Montreal Central Station and transfer to the metro or bus to reach University Centre.

**Bike:** Campus bike racks are available near the entrance. You can also rent a Bixi bike from one of the many stations around the city and on campus.

# SUSTAINABLE EVENTS CERTIFICATION

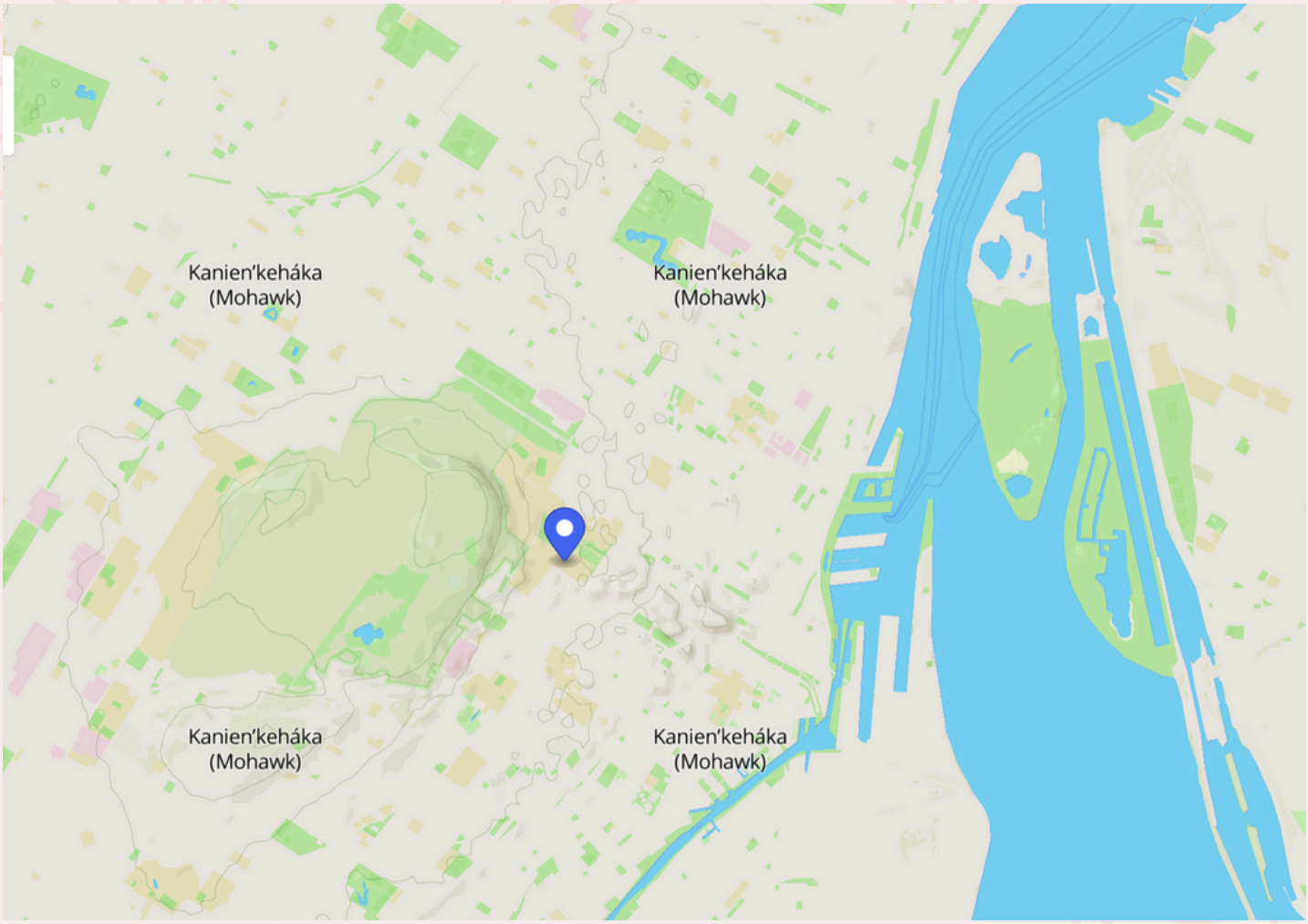
We are proud to announce that our event has been awarded Silver Sustainable Event certification by the McGill Sustainable Events program run by the McGill Office of Sustainability.

Nous sommes fiers d'annoncer que notre événement a été certifié comme événement D'Argent par le programme Événements durables McGill du Bureau du développement durable de l'Université McGill.

# LAND ACKNOWLEDGEMENT

McGill University is on land which has long served as a site of meeting and exchange amongst Indigenous peoples, including the Haudenosaunee and Anishinabeg nations. We acknowledge and thank the diverse Indigenous peoples whose presence marks this territory on which peoples of the world now gather.



# BBMESS COUNCIL 2024-2025

**Jason Zhu**
President

**Breona Martin**
Chair

**Lina El Kesti**
VP Communications

**Hannah Bernstein**
VP Social Media

**Danielle Schutt**
VP Finance

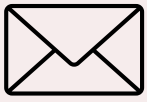
**John Nguyen**
VP Academics

**Ojasvini Ahluwalia**
VP Academics

**Karim Saadé**
VP Social Events

**Jackson McCormack**
VP Social Events

# CONTACT US



bbmess.pgss@mail.mcgill.ca

https://bbmess.wixsite.com/bbmess

Biological and Biomedical Engineering Student Society of McGill University

@bbmess_mcgill

https://linktr.ee/bbmess

# THANK YOU TO OUR SPONSORS AND CONTRIBUTORS!

McGill | Faculty of Medicine and Health Sciences | Faculté de médecine et des sciences de la santé

BIOMEDICAL ENGINEERING

BIOENGINEERING

MDPI

bioengineering

LabGiant

# KEYNOTE SPEAKERS

# OPENING KEYNOTE SPEAKER

# THE HON. DR. MARC GARNEAU

## BELIEVE IN THE IMPORTANCE OF WHAT YOU ARE DOING

**MAY 5**
**9:30 AM - 10:30 AM**

Born 23 February 1949 in Quebec City, Canada. Received a Bachelor of Science degree in Engineering Physics from the Royal Military College of Kingston in 1970, and a Doctorate in Electrical Engineering from the Imperial College of Science and Technology, London, England, in 1973.

**Naval career:**

Marc Garneau served as a Combat Systems Engineer in the Royal Canadian Navy from 1973 until 1984.

**Astronaut career:**

He was one of six Canadians selected for astronaut training in December 1983. He became the first Canadian to fly in Space on Shuttle Mission STS 41-G in October 1984.

He flew on two more missions: STS-77 in 1996 and STS-97 in 2000, logging over 677 hours in space.

In November 2001, he was appointed President of the Canadian Space Agency (CSA), a post he held until December 2005.

**Political career:**

Marc Garneau was elected as a Liberal Member of Parliament in October 2008. He became minister of Transport in November 2015, a post he held for 5 years until January 2021 when he was named Foreign Affairs minister, a post he occupied until October 2021. He retired from politics in March 2023.

He is a Companion of the Order of Canada (2003). He served as Chancellor of Carleton University from 2003 to 2008. He is a Recipient of the NASA Exceptional Service Medal (1997), three NASA Space Flight Medals (1984, 1996, 2000), and eleven Honorary Doctorates.

On 8 October 2024, his autobiography, *"A Most Extraordinary Ride: Space, Politics and the Pursuit on a Canadian Dream"* was published by McClelland & Stewart.

# FACULTY KEYNOTE SPEAKER

# PROF. EMILY PORTER

## MICROWAVE MEDICAL TECHNOLOGIES: ADVANCES AND CLINICAL CHALLENGES

**MAY 5**
**5:00 PM - 6:00 PM**

Dr. Porter is an Assistant Professor in the Department of Biomedical Engineering at McGill University, and a Scientist in the Cancer Research Program at the Research Institute of the McGill University Health Centre.

She was an Assistant Professor with the Department of Electrical and Computer Engineering at The University of Texas (UT) at Austin, from 2015-2019, where she initiated the Electromagnetic Technologies (EMT) Lab. Prior to UT Austin, she was an NSERC Postdoctoral Fellow and then an EU Marie-Curie Research Fellow with the Translational Medical Device Laboratory at National University of Ireland Galway, from 2015-2019. Dr. Porter was granted her Ph.D. (Electrical Engineering) in 2015 from McGill University, Montreal, Canada. Her Ph.D. work was in the area of Computational and Applied Electromagnetics, and focused on microwave breast health monitoring. She also has an M.Eng. and a B.Eng. in Electrical and Computer Engineering, completed in 2008 and 2010, respectively.

In the Electromagnetic Medical Technologies (EMT) Lab, they are interested in electromagnetic (EM)-based solutions with applications in diagnostic, therapeutic, supportive or assistive medical technologies. Primarily based in the radio-frequency and microwave frequency ranges, these EM-based technologies are promising due to their low-cost, minimally invasive nature, ability to provide highly frequent scan data, and the potential for combined diagnosis and treatment (i.e., theranostics), or combined monitoring and proactive intervention or correction. Their research approach incorporates innovation in engineering with knowledge from multiple fields in order to deliver results that are timely, and of interest to both the medical and engineering communities. They strive to keep research driven by concrete needs, with a clinically-informed and commercially-validated approach to medical technologies. Working in this area can be very rewarding, as any contributions they make can hopefully directly help both patients and the general public, and improve their health and quality of life.

# FACULTY KEYNOTE SPEAKER

# PROF. LOUIS COLLINS

## MODELLING AND COMPUTATIONAL METHODS FOR THE ANALYSIS OF ALZHEIMER'S DISEASE

**MAY 6**
**9:30 AM - 10:30 AM**

Dr. Collins is a full professor in the departments of Neurology & Neurosurgery and Biomedical Engineering, associate member of the Center for Intelligent Machines at McGill, and associate member of the McGill Centre for Studies in Aging. He teaches BDME650, the Advanced Medical Imaging course in the Department of Biomedical Engineering. He heads the NeuroImaging and Surgical Technologies (NIST) laboratory in the Brain Imaging Centre at the Montreal Neurological Institute of McGill University.

In the NIST lab, their research involves automated anatomical segmentation and atlasing in a neurological and neurosurgical context. Computerized image processing techniques, such as non-linear image registration and model-based segmentation, are used to automatically identify structures within the human brain. These techniques are applied to a large database of magnetic resonance (MR) data from normal subjects to quantify anatomical variability and to compare the brains of people with a neurological disease to the brains of healthy controls. In image guided neurosurgery (IGNS), similar techniques provide the surgeon with computerized tools to assist in interpreting anatomical, functional and vascular image data to effectively plan and carry out minimally-invasive neurosurgical procedures. He was previously the Graduate Program Director in Biomedical Engineering (2013-2017) and Graduate Program Director in Biological and Biomedical Engineering (2015-2017).

Dr. Collins has a B.Sc. in Computer Science from Concordia University (1987), a Master's in Electrical Engineering from McGill University (1990) and a Ph.D. in Biomedical Engineering from McGill University (1994). He has been a Professor at McGill University since 1999, and a James McGill Professor since 2019.

# CLOSING KEYNOTE SPEAKER

# PROF. SAMIR MITRAGOTRI

## A HITCHHIKER AND BACKPACKER'S GUIDE TO DRUG DELIVERY

**MAY 6**
**5:00 PM - 6:00 PM**

Professor Mitragotri's research is focused on drug delivery. His research has advanced fundamental understanding of biological barriers and has led to the development of new materials as well as technologies for the treatment of various ailments including diabetes, cancer, skin diseases, multiple sclerosis, and infections, among others. Many of his inventions have advanced to clinical technologies. His research has led to a number of start-up companies. At the same time, the fundamental knowledge developed through his research has advanced the understanding of the biology of barriers in the human body. Prof. Mitragotri has pioneered novel technologies using ultrasound and ionic liquids to enable transdermal delivery of proteins, peptides, and siRNA. He has also developed novel technologies including ionic liquids for oral delivery of proteins such as insulin and other peptides. Prof. Mitragotri has invented systems that make use of synthetic carriers hitchhiking on natural cells such as red blood cells, macrophages, neutrophils, T cells, and NK cells for targeted delivery of drugs and cells.

Professor Mitragotri is the Hiller Professor of Bioengineering and Hansjörg Wyss Professor of Biologically Inspired Engineering at Harvard University. He has authored over 400 publications, is an inventor on over 225 issued/pending patents, and he has given over 500 invited lectures. He is an elected member of the National Academy of Engineering, National Academy of Medicine and National Academy of Inventors. He is also an elected fellow of AAAS, CRS, BMES, AIMBE, and AA PS. He received BS in Chemical Engineering from the Institute of Chemical Technology, India and PhD in Chemical Engineering from the Massachusetts Institute of Technology.

# THEMATIC SESSIONS

## THEMATIC SESSION #1

# BIOSENSORS, DIAGNOSTICS, AND THERAPEUTICS

## PROF. DAN NICOLAU

PROFESSOR, MARIKA ZELENKA ROY CHAIR IN BIOENGINEERING
DEPARTMENT OF BIOENGINEERING

**MAY 5**
**11:00 AM - 11:30 AM**

Dan V. Nicolau is the founding Chair of McGill University's Department of Bioengineering at the Faculty of Engineering. He has degrees in Chemical Engineering (PhD., MEng) and in Statistics, Cybernetics & Information Technology (M.Sc.). His research has covered polymer chemistry and physico-chemistry, surface science and engineering, micro- and nanofabrication for semiconductor and biomedical devices, process modeling and control, molecular modeling, protein adsorption, and biomimetics.

ORAL PRESENTATION

MAY 5, 11:30 AM

# 3D PRINTED MICROFLUIDIC CHANNEL IMPACTOR FOR EXHALED BIOAEROSOL CAPTURE

**Yonatan Morocz**[1], Justin De Vries[1], Xavier Lefebvre[2], Etienne Robert[2], David Juncker[1]

1 McGill University, Biomedical Engineering
2 Polytechnique Montreal

Aerosols provide real-time insights into respiratory health and pathogen transmission yet remain an underutilized sample source compared to nasopharyngeal swabs or blood tests. Airborne pathogens such as SARS-CoV-2, influenza, tuberculosis, measles, and respiratory syncytial virus are carried in fine particles ranging from 100 nm to 100 µm, and while conventional diagnostics quantify viral load from established sampling sites, only aerosol measurements reflect a patient's true infectivity. Recent developments in aerosol capture devices have shown promise for early detection, but their reliance on complex peripherals and expensive, bulky analytical methods hinders widespread clinical adoption, particularly given the inherently low abundance of aerosolized biomolecules. To overcome these limitations, we propose a Microfluidic Channel Impactor (MCI), a self-contained device that integrates an impaction substrate directly within a microfluidic channel. As aerosol-laden air accelerates through a precisely engineered network of slits, particles are directed by inertial forces onto a capture surface, achieving capture rates above 85% for particles larger than 1 µm while operating under physiological expiratory pressures (6–9 kPa) and accommodating flow rates up to 50 L/min. By embedding the impaction substrate directly into the microfluidic channel, our design drastically cuts down on sample dilution, allowing us to extract and resolubilize analytes in as little as 2 µL of solution—a reduction that can be 10–10,000 times lower than that of current methods. The device is manufactured using high-resolution digital light processing 3D printing with custom PEGDA-based photopolymers, enabling the fabrication of complex embedded and open channels. The channel system prevents leakage and minimizes the dilution volume. Rigorous testing with phase Doppler anemometry and confocal microscopy has verified both the capture efficiency and the on-target capture rate. Overall, this fresh approach to aerosol sampling could pave the way for rapid, non-invasive, point-of-care respiratory pathogen diagnostics, thereby lowering transmission risks and enhancing patient outcomes.

ORAL PRESENTATION

MAY 5, 11:45 AM

# ROLE OF SOLUBLE SPHINGOMYELIN PHOSPHODIESTERASE ACID-LIKE 3B IN THE PATHOPHYSIOLOGY OF ME/CFS

**Bita Rostami-Afshari,**[1,2,3,4] Wesam Elremaly,[1,3,4] Anita Franco,[1,3,4] Mohamed Elbakry,[1,3,4,5] Marie-Yvonne Akoume,[1,3,4,6] Ines Boufaied,[7] Atefeh Moezzi,[1,2,3,4] Corinne Leveau,[1,2,3,4] Pierre Rompré,[8] Christian Godbout,[9] Olav Mella,[10] Øystein Fluge,[10] and Alain Moreau[1,2,3,4,11,*]

1 Viscogliosi Laboratory in Molecular Genetics of Musculoskeletal Diseases, Azrieli Research Center, CHU Sainte-Justine, Montreal, QC, Canada;
2 Department of Biochemistry and Molecular Medicine, Faculty of Medicine, Université de Montréal, Montreal, QC, Canada;
3 Open Medicine Foundation ME/CFS Collaborative Center at CHU Sainte-Justine/Université de Montréal, Montreal, QC, Canada;
4 ICanCME Research Network, Azrieli Research Center, CHU Sainte-Justine, Montreal, QC, Canada;
5 Department of Chemistry, Biochemistry Section, Faculty of Science, Tanta University, Tanta, Gharbia Governorate, Egypt
6 Department of Cellular, Molecular Biology and Genetics, Université des Sciences de la Santé de Libreville (USS), Libraville, Gabon;
7 Flow Cytometry Platform, Azrieli Research Center, CHU Sainte-Justine, Montreal, QC, Canada;
8 Faculty of Dentistry, Université de Montréal, Montreal, QC, Canada;
9 Patient-partner, ICanCME Research Network, Azrieli Research Center, CHU Sainte-Justine, Montreal, QC, Canada;
10 Department of Oncology and Medical Physics at the University of Bergen, Haukeland University Hospital, Bergen, Norway;
11 Department of Stomatology, Faculty of Dentistry, Université de Montréal, Montreal, QC, Canada;

**Background.** Myalgic encephalomyelitis (ME) is a debilitating multisystemic disease affecting ~0.2% of Canadians, primarily women. Diagnosis remains challenging due to the lack of specific biomarkers. ME is associated with immune and metabolic dysfunctions, often triggered by viral infections. Key immune abnormalities include T and B cell imbalances, impaired NK cell function, and elevated pro-inflammatory cytokines (IL-6, TNF-α). SMPDL3B, a regulator of immune signaling, suppresses TLR4 activation in macrophages and dendritic cells. Its absence leads to excessive TLR4 signaling and cytokine production, potentially exacerbating ME-related inflammation.

**Rationale.** Our prior studies identified differential methylation of SMPDL3B in discordant ME twin pairs, suggesting its role in disease pathophysiology. SMPDL3B regulates sphingomyelin metabolism, and metabolomic studies reveal reduced ceramides in ME patients. Preliminary data suggest PI-PLC cleaves membrane-bound SMPDL3B, increasing its soluble form. Given sphingolipids' role in immune regulation, SMPDL3B dysregulation may contribute to ME's immune dysfunction.

**Hypothesis & Objectives.** We hypothesize that loss of membrane-bound SMPDL3B, coupled with increased soluble SMPDL3B, contributes to ME pathophysiology by altering immune responses and lipid metabolism. Our objectives are to: characterize soluble vs. membrane-bound SMPDL3B in ME, assess soluble SMPDL3B's impact on immune activation, and explore PI-PLC/SMPDL3B-targeting therapies.

**Methods.** This study includes a cross-sectional analysis of 326 ME patients and 63 matched controls from a prospective cohort initiated in 2015. Soluble SMPDL3B levels are measured by ELISA, while membrane-bound SMPDL3B is quantified by flow cytometry. We hypothesize that the reduction of membrane-bound SMPDL3B leads to sphingomyelin accumulation and increased pro-inflammatory cytokines, such as IL-6, via TLR4 signaling.

**Results.** Elevated soluble SMPDL3B correlates with ME severity, while ME PBMCs exhibit reduced membrane-bound SMPDL3B, likely due to enhanced PI-PLC activity. Vildagliptin, a PI-PLC inhibitor, reduces soluble SMPDL3B and restores its membrane form.

**Conclusion.** SMPDL3B dysregulation disrupts immune and lipid homeostasis in ME. Targeting PI-PLC may provide a novel therapeutic strategy.

ORAL PRESENTATION

MAY 5, 12:00 PM

# IMPACT OF CLIMATIC FACTORS ON THE SURVIVAL OF RESPIRATORY VIRUSES IN MUCOSALIVARY PARTICLES

**Marc Amin**[1], Élise Caron[2], Audray Fortin[2], Florent Rossi[3], Nathalie Turgeon[3], Nathalie Grandvaux[2], Caroline Duchaine[3], Caroline E. Wagner[1]

1 Department of Bioengineering, McGill University

2 Department of biochemistry and molecular medicine, Université de Montréal

3 Department of Biochemistry, Microbiology and Bioinformatics, Université Laval

Airborne transmission of respiratory viral infections is mainly driven by virus-containing particles originating from the respiratory fluids of infected hosts. The viability of viruses in these suspended particles depends on environmental conditions, which influence virus survival both directly and by modulating droplet evaporation rates, which affects particle suspension time and the physicochemical particle environment. Previous experimental studies have found temperature and relative humidity (RH) to have an important impact on viral survival: higher temperatures accelerate evaporation and virus inactivation, while higher RH slows evaporation, but has an overall non-linear effect on virus viability. Particle composition, notably the presence of mucosal proteins like mucin, also affects evaporation and virus survival, potentially by forming a protective layer at the interface that reduces rates of water loss. This project aims to functionally quantify how the survival of respiratory syncytial virus (RSV), a leading cause of lower respiratory tract infections in infants, depends on temperature and RH in a physiologically relevant fluid system for respiratory fluids. Using a climate-controlled enclosure, mucosalivary solutions containing mucin or saliva are dispensed and imaged using a high-speed camera to characterize evaporation profiles over time under various climate conditions. Additionally, using a climate-controlled particle suspension drum, the survival time of RSV in nebulized mucosalivary solutions is evaluated by collecting air samples and assessing survival using plaque assays and qPCR. The findings will provide insights into the biophysical process of virus survival and transmission in particles with physiologically relevant composition. This research will advance predictive models for seasonal virus transmission patterns, which may inform public health interventions by improving projections for how climate change could reshape respiratory virus transmission dynamics.

ORAL PRESENTATION

MAY 5, 12:15 PM

# LABEL-FREE SIZING AND MULTIPLEXED PROTEIN DETECTION ON SINGLE EXTRACELLULAR VESICLES

**Andreas Wallucks**[1], Philippe DeCorwin-Martin[1], Molly Shen[1], Lucile Alexandre[1], Hugues Martin[1], Andy Ng[1], David Juncker[1]

1 McGill University

Just as single-cell RNA sequencing has revolutionized studying cellular diversity, high multiplex single EV proteomics will be transformative our understanding of EV heterogeneity by identifying distinct subpopulations and accurately mapping shifts in the EV proteome under various cellular states or applied stimuli. Current single EV proteomic technologies, such as flow cytometry, fall short of establishing single EV proteomic atlases due to high detection thresholds, limited protein multiplexing, or both. Here we introduce EV-ID, a platform with a detection limit around 35 nm, capable of detecting dozens of proteins simultaneously in tens of thousands of single EVs from a 10 µL sample with fully automated, scalable data acquisition.

EV-ID employs in-house functionalized glass substrates forming both universal EV capture surfaces, and affinity surfaces for the enrichment of specific subpopulations. EVs are counted and sized using previously introduced EV size photometry (SP), enabled by label-free interferometric scattering microscopy (iSCAT) on a widefield epifluorescence microscope. EV protein expression is mapped via DNA exchange imaging, employing cyclic immunofluorescence imaging on DNA-barcoded antibodies. Oligo labelling and erasure are performed fully automated in under 5 minutes each for multiple samples in parallel.

Detection efficiencies of membrane and intraluminal EV proteins were optimized and validated on EVs from GFP reporter cell lines, and the absence of steric hindrance in single- vs. multiplex detection was confirmed. Surface chemistries were optimized for capture of EVs from purified samples, as well as from raw cell supernatant to eliminate purification biases. EV-ID was employed measuring an initial panel of 20 proteins on tens of thousands of EVs from HUVEC, HEK293T, HT29, and MDA-MB-231 cells, revealing cell-specific and conserved co-expression patterns.

EV-ID enables high-throughput, ultrasensitive, multiplexed profiling of single EVs from minimal samples, generating protein distribution atlases with the potential to transform EV biology and diagnostics.

## THEMATIC SESSION #2

# MICROSCOPY, IMAGING, AND NEUROIMAGING

## PROF. GEORGIOS MITSIS

ASSOCIATE PROFESSOR, WILLIAM DAWSON SCHOLAR
DEPARTMENT OF BIOENGINEERING

**MAY 5**
**11:00 AM - 11:30 AM**

Georgios Mitsis is an Associate Professor and William Dawson Scholar in the Department of Bioengineering. He has a Ph.D., M.S. (EE), and M.S. (BME) from the University of Southern California in Los Angeles, and a Diploma from the National Technical University of Athens in Athens, Greece.

His lab is interested in the application of signals and systems theory to the life sciences. In this context, they are conducting research related both to algorithm development with a focus on nonlinear and time-varying systems modeling, and their applications to biological/physiological signals and systems, with a focus on cerebral hemodynamics and autoregulation. Specifically, they are conducting research in the following areas: Modeling of nonlinear and time-varying dynamic systems, cerebral hemodynamics and autoregulation, time-varying functional brain connectivity, and computational oncology and optimal therapy design for cancer treatment.

ORAL PRESENTATION

MAY 5, 11:30 AM

# PERIVENTRICULAR GRADIENTS IN AXONAL AND MYELIN MICROSTRUCTURE ARE PRESENT EARLY IN MULTIPLE SCLEROSIS AND PERSIST DURING PROGRESSION

**Hannah R. Bernstein**[1,2,3], Vladimir Grouza[1,2], Joseph S. Gati[4], Sarah A. Morrow[4,5], Ravi S. Menon[4], Sridar Narayanan[1,2], Douglas L. Arnold[1,2], David A. Rudko[1,2,3]

1 McConnell Brain Imaging Centre, The Neuro. Montreal Neurological Institute-Hospital, Montréal, Canada
2 McGill University, Department of Neurology and Neurosurgery, Montréal, Canada
3 McGill University, Department of Biomedical Engineering, Montréal, Canada
4 Western University, Robarts Research Institute, Centre for Functional and Metabolic Mapping, London, Canada
5 Hotchkiss Brain Institute, Clinical Neurosciences, Calgary, Canada

**Background:** MS imaging studies have demonstrated an ependymal 'surface-in' distribution of white matter damage. However, the origin of this effect and how it impacts myelinated axons in people with MS (PwMS) is poorly understood.

**Objectives:** To investigate (i) whether there is clear evidence of tract-wise, periventricular damage, based on fractional anisotropy, mean diffusivity, axonal water fraction (AWF) and myelin volume fraction (MVF), in PwMS, (ii) if such tissue damage is associated with T1-'black-hole' (T1-BH) and/or non-BH lesions and (iii) if periventricular quantitative MRI abnormalities are correlated with lateral ventricle (LV) and choroid plexus (CP) enlargement.

**Methods:** We applied structural, MT-weighted, and multi-shell diffusion MRI in healthy controls and PwMS to quantify periventricular gradient damage to axons and myelin. We also evaluated the correlation between such gradient damage and both non-BH and T1-BH lesion loads. Finally, we measured associations between gradient damage and local brain enlargement.

**Results:** Clear periventricular gradients exist in both AWF and MVF measures in the Association and Projection Tracts. They are strongly correlated with T1-BH lesion load, and with LV and CP enlargement in PwMS having higher disability.

**Conclusions:** The present work demonstrates clear evidence of tract-specific, periventricular, band-wise damage in both AWF and MVF of PwMS

ORAL PRESENTATION

MAY 5, 11:45 AM

# IMPROVED MRI-BASED ESTIMATION OF CEREBRAL WHITE MATTER TRACT G-RATIO ALTERATIONS IN INDIVIDUALS WITH AN INCREASED GENETIC RISK FOR AUTISM

**Wen Da Lu**[1,2], Mark Nelson[2,3], Charles Olivier[4], Khadije Jizi[4], Sebastien Jacquemont[4,5], Christine Tardif[1,2,3]

1 Department of Biomedical Engineering, McGill University, Montreal, Canada
2 McConnell Brain Imaging Centre, Montreal Neurological Institute and Hospital, Montreal, Canada
3 Department of Neurology and Neurosurgery, McGill University, Montreal, Canada
4 Sainte Justine Hospital Research Center, Montreal, Canada
5 Department of Pediatrics, University of Montréal, Montreal, Canada

The g-ratio, defined as the ratio between the inner to outer diameter of the myelin sheath around an axon, is a fundamental characteristic of cerebral white matter microstructure. The g-ratio modulates the balance between transmission efficient and metabolic cost. The g-ratio can be mapped non-invasively in vivo using magnetic resonance imaging (MRI) by combining quantitatives maps of myelin and axonal volume fraction. This provides an estimate of the aggregate g-ratio at the voxel level, which are subsequently averaged across the voxels belonging to a white matter tract. But most voxels contain multiple tracts, each with a distinct g-ratio. This partial voluming effect can obscure biologically meaningful differences between tracts and introduce biases, particularly in regions with complex white matter architecture.

To overcome these limitations, we introduce a tract-specific approach where the g-ratio is computed at the level of individual white matter tracts. Instead of averaging voxel-wise estimates, this method directly aggregates myelin and axonal volumes along streamlines reconstructed from diffusion MRI, providing a more anatomically precise estimate of white matter g-ratio. In a typical brain, this tract-specific approach reveals distinct spatial trends compared to voxel-based estimates, suggesting that important tract-level differences may be hidden by conventional methods.

This novel approach is of particular interest for studying neurodevelopmental disorders (NDDs), such as autism, where specific white matter tracts or networks may be altered. In individuals with copy number variants at the 16p11.2 locus, a well-established genetic risk factor for autism, our novel tract-specific method reveals the effects of 16p11.2 gene dosage on g-ratio. Specifically, 16p11.2 deletions are associated with higher g-ratio values (i.e. thinner myelin sheaths), while duplications correspond to lower g-ratio values.

ORAL PRESENTATION

MAY 5, 12:00 PM

# INFLUENCE OF ARTERIAL BLOOD PRESSURE ON BOLD-FMRI DURING REST AND AUTONOMIC TASKS: INTRODUCING THE ARTERIAL RESPONSE FUNCTION.

**Rémi Dagenais**[1], Georgios D. Mitsis[1]

1 Bioengineering, McGill

The respiratory and cardiac response functions are widely used in fMRI analysis to account for the systemic physiological component of the BOLD signal. However, and despite its relevance, the contribution of arterial blood pressure has been ignored in the past due to the experimental challenges related to collecting this signal in the MRI environment. With recent progress in terms of arterial blood pressure (ABP) estimation in the MRI environment using the photoplethysmography (PPG) signal, it is now possible to study the contribution of this systemic physiological contribution on the BOLD signal. We hypothesize that including the ABP fluctuations along with the respiratory and cardiac responses can account for significant variance otherwise not taken into consideration. In this context, we propose a novel physiological response function – the arterial response function – to account for the ABP contribution to the systemic component of the BOLD signal and assess its relative significance with respect to the well-established respiratory response and cardiac response functions. The arterial response function may provide valuable insights into denoising BOLD-fMRI and studying intrinsic regulatory mechanisms of the cerebrovascular system such as autoregulation.

Overall, the ARFs presented a faster dynamic than the CRF and RRF for all conditions in the 14 subjects tested. It also explained an additional 2.6, 3.4, and 2.9% of variance from the BOLD signal that was not accounted for by the CRF and RRF during rest, controlled-breathing, and cold pressor challenge respectively. The extra variance accounted for was localized similarly to the cardiac and respiratory responses around highly vascularized regions of the brain.

These results suggest that ABP should be collected in fMRI experiments to reduce physiological noise but also offers the potential to study the origin of the systemic physiological components of the BOLD signal such as cerebral autoregulation with improved spatial resolution.

ORAL PRESENTATION

MAY 5, 12:15 PM

# CRANIOFACIAL CONE BEAM CT: ADDRESSING "VOLUME-VS-RESOLUTION DILEMMA" USING GENERATIVE AI

**Seyedmahdi Hosseinitabatabaei**[1], Andrew Nelson[2], Nicolas Piche[3], Didem Dagdeviren[4], Natalie Reznikov[1,2,4,5]

1 Department of Bioengineering, McGill University, Montreal, Canada
2 Department of Anthropology, University of Western Ontario, London, Canada
3 Comet Technologies Canada Inc. Montreal, Canada
4 Faculty of Dental Medicine and Oral Health Sciences, McGill University, Montreal, Canada
5 Department of Anatomy and Cell Biology, McGill University, Montreal, Canada

In imaging, reconciling a wide field-of-view with resolution is a dilemma, despite both being critical for diagnostic imaging. In craniofacial radiology, cone-beam computed tomography (CBCT) is a method of 3D imaging producing either a large field-of-view with coarse-resolution or vice-versa. When the field-of-view is large, fine features like root canals become diffuse, as sharp "edges" soften. Super-resolution is a digital technique for recovery of sharp edges, but risks generating artificial features or distorting existing features. This project aims to achieve super-resolution of CBCT scans using Generative-Adversarial-Networks (GANs) for accurate recovery of fine features.

CBCT scans of 4 cadaveric human heads and 6 sheep heads were acquired at 270µm and 135µm voxel size, and a GAN was designed to recover fine image details in low-resolution images. The low- and high-resolution pairs were registered and used for GAN training and testing. The loss-function included terms for pixel, edge, and perceptual accuracy. The performance of the GAN was benchmarked against bicubic interpolation using peak-signal-to-noise ratio (PSNR) and learned-perceptual-image-patch-similarity (LPIPS).

The GAN outperformed bicubic interpolation, achieving higher PSNR (+2.03 for seen, +2.44 for unseen-set) and lower LPIPS (-0.07 for seen, -0.07 for unseen), indicating improved recovery of image details. GAN's similar performance on seen and unseen test sets indicates its generalization, effectively learning, "recognizing" and interpolating the sharp features from diffuse or fuzzy features.

This is the first CBCT super-resolution study to use real low-resolution 3D-images of anatomical objects, instead of artificially downgraded images or phantoms. This project will allow us to simultaneously achieve large volume and high-resolution in clinical CBCT, hence improving diagnostic accuracy.

We thank the donors of McGill University Body Donation Program and the division of Human Anatomy.

## THEMATIC SESSION #3

# BIOINFORMATICS, MODELLING, AND COMPUTATIONAL BIOLOGY

## PROF. LOUIS COLLINS

### JAMES MCGILL PROFESSOR, PROFESSOR IN NEUROLOGY AND NEUROSURGERY AND BIOMEDICAL ENGINEERING

Dr. Collins is a full professor in the departments of Neurology & Neurosurgery and Biomedical Engineering, associate member of the Center for Intelligent Machines at McGill, and associate member of the McGill Centre for Studies in Aging. He teaches BDME650, the Advanced Medical Imaging course in the Department of Biomedical Engineering. He heads the NeuroImaging and Surgical Technologies (NIST) laboratory in the Brain Imaging Centre at the Montreal Neurological Institute of McGill University.

In the NIST lab, their research involves automated anatomical segmentation and atlasing in a neurological and neurosurgical context. Computerized image processing techniques, such as non-linear image registration and model-based segmentation, are used to automatically identify structures within the human brain. These techniques are applied to a large database of magnetic resonance (MR) data from normal subjects to quantify anatomical variability and to compare the brains of people with a neurological disease to the brains of healthy controls. In image guided neurosurgery (IGNS), similar techniques provide the surgeon with computerized tools to assist in interpreting anatomical, functional and vascular image data to effectively plan and carry out minimally-invasive neurosurgical procedures. He was previously the Graduate Program Director in Biomedical Engineering (2013-2017) and Graduate Program Director in Biological and Biomedical Engineering (2015-2017).

Dr. Collins has a B.Sc. in Computer Science from Concordia University (1987), a Master's in Electrical Engineering from McGill University (1990) and a Ph.D. in Biomedical Engineering from McGill University (1994). He has been a Professor at McGill University since 1999, and a James McGill Professor since 2019.

ORAL PRESENTATION

MAY 6, 11:00 AM

# HEART RATE ANALYSIS TO IDENTIFY AT-RISK FETUSES FOR HYPOXIC-ISCHEMIC ENCEPHALOPATHY DURING FEVER

**Ethan Grooby**[1], Aditi Lahiri[2], Yvonne W. Wu[3], Lawrence Gerstley[2], Michael Kuzniewicz[2], Marie-Coralie Cornet[3], John Parker[4], Philip Warrick[1,4], Robert Kearney[1]

1 McGill University, Montreal, Canada
2 Kaiser Permanente Northern California, Oakland, USA
3 University of California, San Francisco, USA
4 PeriGen Inc., North Carolina, USA

**Introduction:** During labour, severe, prolonged, or frequent fetal hypoxia can lead to hypoxic-ischemic encephalopathy (HIE), potentially causing permanent brain injury or fetal death.

**Objective:** To investigate how maternal fever affects fetal and maternal heart rates (MHR and FHR) during labour and whether this modifies the association with HIE.

**Methods:** We analysed maternal temperature, MHR, FHR, and uterine con-traction data from a retrospective cohort of singleton infants (≥35 weeks) delivered at 16 Northern California Kaiser Permanente hospitals (2011–2019). PeriGen Patterns was used to obtain FHR patterns (decelerations, baseline, accelerations). Outcomes were classified into three groups based on umbilical cord or early infant blood gas results, neurological exams, and clinical interventions: (1) HIE, (2) Acidosis without HIE, and (3) Healthy. Data were stratified by presence of intrapartum fever (≥38°C). To examine the maternal and fetal response to fever, data was analysed two hours following fe-ver onset. In the no-fever group, hourly records were obtained. Active phase of the first stage of labour was examined in both the fever and no-fever groups. As features are time-varying, they were corrected by binning labour hour and subtracting the median feature value.

**Results:** In the fever group, all outcome classes showed statistically significant increases in FHR baseline, fetal deceleration time, and MHR, along with decreased fetal acceleration time, compared to the no-fever group. Differences in these features between the HIE and Healthy outcome classes were larger in the presence of fever.

**Conclusion:** Maternal fever during labour is a known risk factor for HIE. The observed changes in MHR and FHR patterns suggest increased physiological stress, supporting this association. Moreover, the distinction between HIE and Healthy outcomes becomes more pronounced with fever. These findings highlight the need to consider fever status when defining clinical guide-line thresholds or developing machine learning models based on FHR data.

ORAL PRESENTATION

MAY 6, 11:15 AM

# EVOLVING DIVERSE GENE NETWORKS

**Qichen Huang**[1], Nacer Eddine Boukacem[1], Philippe Martin[1], Paul François[1]
1 University of Montreal, Mila Quebec AI Institute

Gene regulatory networks (GRNs) underlie key developmental processes, yet the landscape of diverse network architectures capable of achieving the same function remains largely unexplored. We propose a novel approach using a Generative Flow Network (GFlowNet) to efficiently explore and evolve GRNs that fulfill specific developmental tasks. We designed the GFlowNet to perform both global search and local refinements in the space of network configurations. Initially applied to classical genetic oscillators, GFlowNet efficiently navigates the state space, where each state represents a directed network with edges corresponding to gene regulation. Our approach reveals that, for a given target function multiple distinct topological motifs can achieve the desired behavior. Moreover, even within a fixed network topology, diverse interaction strengths (weights) can yield similar developmental patterns, underscoring the inherent flexibility of GRNs. Furthermore, we extend our analysis to more complex functions in developmental patterning of somitogenesis, we uncover common core modular motifs that emerge during network evolution, and find diverse design principles and evolutionary trajectories from simple oscillator network to segmentation network. Dimensionality reduction techniques further help us visualize these evolutionary pathways, aligning our findings with the core and periphery hypothesis of network evolution. Additionally, our exploration into larger networks indicates that increased node counts contribute to enhanced robustness and diversity, as more weight configurations within a given topology can produce similar target patterns. Overall, our results demonstrate that the generative model (GFlowNet) efficiently explores GRN configurations to identify both conserved and diverse motifs, offering new insights into the evolutionary plasticity of genetic networks and paving the way for the rational design of synthetic networks with improved performance and robustness.

ORAL PRESENTATION

MAY 6, 11:30 AM

# CHILDREN WITH MALFORMED INNER EARS REQUIRE PERSONALIZED COCHLEAR IMPLANT PROGRAMMING

**Carina Sabourin**[1], Dr Steve Lomber[1], Jaina Negandhi[2], Dr Sharon Cushing[2], Dr Blake Papsin[2], Dr Karen Gordon[2]

1 Department of Biological and Biomedical Engineering, McGill University, Montreal, Canada
2 Department of Otolaryngology-Head and Neck Surgery, The Hospital for Sick Children, Toronto, Canada

**Purpose:** Cochlear implants (CIs) deliver current to the auditory nerve to provide children with hearing loss access to sound. This study evaluated the impact of inner ear malformations on CI function. CI electrodes target sites along the auditory nerve to convey sound cues, but malformations may hinder stimulation and distort auditory cues. Many children with abnormal cochleae receive CIs, however programming can be clinically challenging and outcomes are variable. This study tested whether children with abnormal inner ears show: 1) wider CI current spread, 2) reduced neural responsivity, 3) higher electrical stimulation parameters, and 4) poorer behavioral outcomes than peers with typical inner ears.

**Methods:** CI stimulation parameters, electrophysiological recordings, transimpedance measurements, and available audiometric/speech perception data were analyzed in children with bilateral CIs (n = 184 typically developed and n = 27 malformed inner ears). Mixed effects modeling was conducted. Child-specific voltage spread models were optimized to reproduce clinical measurements.

**Results:** Wider current spread was observed in children with malformed inner ears than the typically developed group (mean(SE) = 1.43(0.43), $p < 0.05$). Moreover, in the malformed group, higher auditory nerve electrophysiological thresholds and lower amplitude growth function slopes occurred for electrodes with wider current spread (mean(SE) = 0.83(0.59), $p < 0.05$ for thresholds; mean(SE) -0.76(0.39), $p < 0.05$ for slopes), but not the typically developed group ($p = 0.21$ for thresholds; $p = 0.42$ for slopes). Higher CI electrical stimulation levels were required for electrodes with wider current spread in both groups. Behavioral outcomes were more variable in the malformed group, especially for those with extreme current spread. Child-specific models of intracochlear current spread reveal individual differences.

**Conclusion:** Abnormal current spread occurs in children with inner ear malformations. Personalized models could help optimize CI programming to enhance auditory nerve stimulation and best support hearing development in each child.

ORAL PRESENTATION

MAY 6, 11:45 AM

# AUTOMATED CELL SURVIVAL COLONY COUNTING FOR CLONOGENIC ASSAYS

**Wanrong Mona Wang**[1], Joanna Li[2,3], Laya Rafiee Sevyeri[2,3], Shirin A. Enger[2,3]

1 Department of Bioengineering, Faculty of Engineering, McGill University, Montréal, Québec, Canada

2 Medical Physics Unit, Gerald Bronfman Department of Oncology, McGill University, Montréal, Québec, Canada

3 Lady Davis Research Institute for Medical Research, Jewish General Hospital, Montréal, Québec, Canada

The radiosensitivity of cancer cells varies significantly between cancer types and individual patients. Assessing the radiosensitivity of a given cancer cell type is crucial for understanding the effectiveness of radiotherapy. The clonogenic assay is a cell biology technique that quantifies viable cell colonies, defined as clusters containing 50 or more cells, after administering radiation dose. It is considered the gold standard for measuring radiosensitivity. However, the technique is currently performed manually, which is time-consuming and prone to interobserver variability. Computer vision methods can help automate the cell counting process. In this study, we collected 787 samples from HCT116 human cancer cell lines and developed a computer vision-based pipeline to automate colony counting. Our pipeline addressed several challenges that we faced: (i) the lack of annotated data due to the laborious nature of manually labelling colonies; (ii) variability in data collection, which leads to differences in images that require preprocessing; (iii) the unavailability of microscopic-resolution images, which necessitates the use of morphological features for accurate counting. The Python OpenCV library performed morphological alterations on the images and created masks to filter unwanted background objects. Furthermore, we augmented the existing marker-based watershed segmentation algorithm to separate bordering colonies in the assay images. To evaluate the segmentation module, we calculated average accuracy on all the 787 samples, referring to the difference between the number of the colonies counted by the openCV moments to the number of colonies in the ground truth. The model achieved an accuracy of 78.53%. For future work, we will continue to work on improving the pipeline to be robust to differences in collected images, and test the pipeline on different cell lines.

ORAL PRESENTATION

MAY 6, 12:00 PM

# AUTOMATING LINEAR MOTIF PREDICTIONS TO MAP HUMAN SIGNALING NETWORKS

**Eric Sun**[1], Yu (Brandon) Xia[1], Jasmin Coulombe-Huntington[1]

1Department of Bioengineering, McGill University, Montréal, QC, Canada

Short linear motifs (SLiMs) are critical mediators of protein-protein interactions, yet only a small fraction (0.2% of the estimated total) have been experimentally characterized. Unlike well-conserved, long, and structured protein domains, SLiMs are short (3–11 residues), fast-evolving, often located in intrinsically disordered regions, and facilitate transient interactions such as cell signaling. These characteristics make SLiM discovery a challenging but essential area of research.

To address these challenges and enable de novo SLiM discovery, we present a computational framework that integrates AlphaFold (AF), protein language models (ProtT5), and Gibbs sampling to predict SLiMs at a proteome-wide scale. Our approach leverages AF-derived structural features, such as solvent accessibility surface area (SASA) and intrinsic disorder predictions, alongside ProtT5 embeddings, all of which significantly distinguish motif residues from background residues ($p < 0.01$, Fisher's exact test). Additionally, we incorporate multiple-sequence protein alignments across 100 vertebrates to capture the evolutionary dynamics of SLiMs. A key innovation is the use of hidden Markov models to identify and model motifs, accounting for insertions and deletions, a limitation of conventional motif discovery tools such as MEME.

Applying this framework, we identified a novel MAPK1 (ERK2)-mediated phosphorylation motif in RUNX1, characterized by significantly elevated feature scores relative to background residues (disorder: >1.0 SD, SASA: >1.2 SD, ProtT5 embeddings: >1.8 SD). Biochemical validation (Varshney et al., 2012) confirms RUNX1 phosphorylation at this site, providing new insights into its regulatory role in tumor progression and highlighting a potential therapeutic target. By systematically mapping SLiM-mediated interactions, our approach enables a deeper reconstruction of human cell signaling networks, shedding light on the intricate regulatory mechanisms that drive cellular communication.

ORAL PRESENTATION

MAY 6, 12:15 PM

# EXPLORING TISSUE COMPLEXITY THROUGH VR-BASED INTEGRATION OF 3D IMAGING AND SPATIAL TRANSCRIPTOMICS

**Isabel Carballo Rueda**[1], **Noelia Redondo Bort**[1], Darcy Wagner[2]

1 Faculty of Experimental Sciences. Francisco de Vitoria University. Ctra. Pozuelo-Majadahonda 1800, 28223, Pozuelo de Alarcón, Madrid, Spain.

2 Research Institute of the McGill University Health Centre. 1001 Décarie Blvd., Block E, Montreal, QC, CANADA H4A 3J1

Light Sheet Fluorescence Microscopy (LSFM) and optical clearing techniques have revolutionized the ability to acquire high-resolution 3D images of large and intact, fixed tissues and organs up to the size of whole mice. However, integrating 3D LSFM datasets with complementary molecular analysis, such as traditional histology or immunofluorescence, remains a challenge due to differences in resolution and acquisition modalities, tissue deformation during histological processing, and limitations of traditional flat, 2D screens.

Co-registration of these multimodal datasets is crucial for enhancing tissue analysis and gaining deeper insights into tissue morphology, especially in clinical contexts. In this study, we explore the use of Virtual Reality (VR) to improve the alignment and visualization of 2D histological slices and 3D LSFM datasets, enhancing co-registration accuracy and spatial perception.

The broader goal is to innovate in omic sciences, such as spatial transcriptomics, by combining VR-based 3D visualizations with high dimensionality molecular data, enabling more effective mapping of gene expression and cellular phenotypes in tissue samples.

Spatial transcriptomics has emerged as a key tool in molecular biology, enabling not only the identification of gene expression patterns but also their precise spatial localization within tissues. Among the most advanced technologies in this area, MERFISH (Multiplexed Error-Robust Fluorescence In Situ Hybridization) is notable for its capacity to achieve subcellular resolution through a robust barcoding system. This makes MERFISH particularly effective for single-cell RNA analysis while preserving spatial information.

This project focuses on analyzing spatial transcriptomics data from lung tissue, aiming to identify distinct cell types and characterize spatial gene expression in disease. To support this, we are developing a Python-based interactive platform for data visualization and interpretation, enabling researchers—regardless of coding expertise—to explore and generate biologically meaningful insights through intuitive tools like UMAP plots, dot plots, and heatmaps that can eventually be integrated with the 3D LSFM datasets for analysis in VR.

# THEMATIC SESSION #4
# BIOMATERIALS, TISSUE ENGINEERING, AND REGENERATIVE MEDICINE

## PROF. ALLEN EHRLICHER

ASSISTANT PROFESSOR, DEPARTMENT OF BIOENGINEERING

**MAY 6**
**11:00 AM - 11:30 AM**

Dr. Allen Ehrlicher has a Ph.D. and M.Sc. from University of Leipzig, Germany and a B.S. from University of Texas, Austin.

As Canada Research Chair in Biological Mechanics, Dr. Allen Ehrlicher is examining and exploiting the principles of biological mechanics by pursuing two interrelated themes. First, he and his research team will study the interplay between physical forces and cell biology. Second, they will engineer synthetic biology and new materials that build on the robust mechanics of biological systems. By leading to new insights into biological mechanics, Ehrlicher's research will have applications in areas like medicine and materials science.

ORAL PRESENTATION

MAY 6, 11:30 AM

# ANDROGEN RECEPTOR SIGNALING INHIBITION ENABLES BIOPHYSICAL CHANGES IN PROSTATE CANCER ASSOCIATED WITH INCREASED METASTATIC POTENTIAL

**Clayton Molter**[1], Taisei Fu[1], Ke Du[1], Dongyue Xie[1], Allen Ehrlicher[1]

1 Bio-Active Materials Laboratory, Department of Bioengineering, McGill University, Montreal, Quebec, Canada

Prostate cancer (PCa) is a common health hazard for men displaying androgen-dependent growth - mediated by Androgen Receptor (AR) signalling - at early stages, thus inspiring androgen deprivation therapy (ADT) to be the gold standard clinical treatment. However, in later stages, PCa transitions to androgen-independence with a loss of AR, accompanied by a drastic increase in invasiveness and metastasis. Critically, ADT is known to induce PCa invasiveness by promoting the epithelial-to-mesenchymal transition (EMT), which has been associated with biophysical changes. Indeed, during metastasis cells change their biophysical properties to facilitate migration through crowded microenvironments, namely in the form of reduced cell stiffness and increased contractility. Notably, metastatic PCa cells deviate from these conventional biophysical trends for reasons that are not yet understood. Given AR's essential role in PCa progression, we hypothesize AR signalling may also regulate mechanical transitions required for PCa metastasis during ADT, and may clarify PCa's unique biophysical properties.

We quantify ADT-driven biophysical changes in terms of cell motility, contractility, and nuclear stiffness. We model the progression of PCa under ADT pressure using highly metastatic, AR-negative PCa cells stably re-expressing AR. We observe that AR re-expression suppresses androgen-induced motility, whereas ADT uniquely increases motility and directional persistence in AR-positive cells, promoting an emerging amoeboid-like phenotype characterized by reduced adhesion and contractility. Furthermore, we observe that ADT promotes increased nuclear stiffness and lamin A/C expression. Increased lamin A/C – a structural scaffolding protein responsible for nuclear rigidity - and reduced adhesion have indirectly been associated with invasive PCa, and this study is the first to quantitatively characterize their associated biophysical changes as a direct result of ADT. Moreover, these findings are consistent with the PCa's unique deviation from conventional cancer biophysical trends, suggesting dysregulation of AR may be a critical determining factor in the pro-metastatic mechanical adaptations throughout PCa progression.

ORAL PRESENTATION

MAY 6, 11:45 AM

# MECHANICAL UNLOADING INDUCED CHANGES IN BLOOD FLOW AND BONE LOSS IN MURINE HINDLIMB

**Taylor deVet**[1,2], Mahmoud S Moussa[2,3], Svetlana Komarova[2,3,4], Bettina Willie[2,3]

1 BBME McGill University

2 Shriners Hospital for Children Canada

3 Dental Medicine and Oral Health Sciences, McGill University

4 Biomedical Engineering, University of Alberta

Mechanical forces acting on the skeleton are essential for bone remodeling. Removal of mechanical stimuli such as in microgravity or prolonged bed rest can result in extreme bone loss. Limb loading and mechanical unloading both affect blood pressure, but the active role the vascular network plays in bone adaptation to unloading is still unknown. We hypothesize that hindlimb paralysis will cause changes to the vasculature surrounding bone, inducing bone loss.

Twenty-six-week-old C57Bl/6J female mice were randomized to either Botox (BTX) injection or sham-injected groups. BTX was injected in the hindlimb targeting the quadriceps and calf muscles. Mice tibiae were imaged with microCT and the hindlimb and heart were assessed for blood flow using ultrasound. Following euthanasia at day 21, the animal was perfused with a contrast agent to assess changes in vascular architecture surrounding the tibia. The tibiae were imaged with synchrotron tomography to assess lacunae and vasculature within the bone.

The BTX injected group lost significant body weight and did not fully recover from paralysis. BTX-injected limbs had 16% lower cortical thickness, and 66% lower trabecular volume fraction compared to baseline. Timelapse morphometry showed bone loss was predominantly on the endocortical surfaces. Lacunar properties did not differ between groups, but significant changes were measured in vascular porosity. In-vivo ultrasound demonstrated increased velocity time integral for blood flow in femoral and popliteal arteries, but not in saphenous artery.

BTX induced bone loss in hindlimbs while also increasing flow in the femoral and popliteal arteries. Unloading decreased the amount of vasculature present in the hindlimb, proportional to the amount of limb mass that was lost. The increase in blood flow in the larger vessels may be attributed to the loss in complexity of the vascular network. This work shows for the first time that BTX induced unloading alters blood flow surrounding the bone.

ORAL PRESENTATION

MAY 6, 12:00 PM

# IN VITRO 3D MODELING OF DILATED CARDIOMYOPATHY IN A BEATING HEART-ON-A-CHIP USING PATIENT-DERIVED HUMAN INDUCED PLURIPOTENT STEM CELLS

**Ali Mousavi**[1,2,3,4], Ludovic Mouttet[4], Shihao Cui[2], Yasaman Hekmatnia[4], Mehran Mottahedi[4], Ida Derish[4], Nadia Giannetti[4], Renzo Cecere[4], Houman Savoji[1,2,3]

1 Institute of Biomedical Engineering, Department of Pharmacology and Physiology, Faculty of Medicine, Université de Montréal, Montreal, QC, Canada

2 CHU Sainte-Justine Research Center, Montreal, QC, Canada,

3 Montreal TransMedTech Institute, Montreal, QC, Canada,

4 Division of Cardiology and Cardiac Surgery, McGill University Health Centre, Montreal, QC, Canada

Dilated cardiomyopathy (DCM) is the leading cause of heart transplantation, with a 50% risk of progression to heart failure within five years of diagnosis. Traditional disease models, such as animal studies, often fail to mimic the complex physiology of the human heart. As an alternative, heart-on-a-chip platforms offer real-time monitoring of disease progression and pathological mechanisms by engineering biomimetic mini-heart tissues. Here, we developed a functional heart-on-a-chip model for personalized medicine using patient-specific human induced pluripotent stem cells (hiPSCs), reprogrammed from the patients' blood samples. The chip features two cell seeding chambers with flexible silicone pillar pairs to support tissue formation and fits into standard 12-well plates for high-throughput performance. Healthy and DCM hiPSCs were differentiated into cardiomyocytes (CMs) and purified via lactate starvation. An optimized ratio of ventricular human cardiac fibroblasts was further added to hiPSC-CMs, and the cells were encapsulated in a fibrin/Geltrex hydrogel (containing fluorescent beads) and seeded in each chamber of the device. The tissue gradually compacted and started beating spontaneously. Immunofluorescence analysis revealed structural abnormalities in DCM tissues, including reduced cell alignment and elongation. The tissue functional responses (e.g., calcium transient and beating) were investigated based on pillar deflection and bead movement after two weeks of culture, showing ventricular tachycardia in DCM tissue and highlighting the functional hallmarks of the disease. Interestingly, bulk RNA sequencing was performed on these 3D microtissues, which demonstrated the gene expression changes in the DCM group and identified the specific biomarkers associated with the disease. Finally, the platform was validated using two drug candidates (norepinephrine and lidocaine), and their expected chronotropic and inotropic effects were successfully observed in our model. Notably, norepinephrine treatment restored the normal rhythm in DCM tissue. Therefore, our platform demonstrated great potential in drug screening, disease modeling, and personalized medicine, while providing mechanistic insights into DCM.

ORAL PRESENTATION

MAY 6, 12:15 PM

# LARGE-SCALE EXPANSION OF HUMAN MESENCHYMAL STEM CELLS USING THERMORESPONSIVE MICROCARRIERS IN A STIRRED BIOREACTOR

**Saeideh Maleki**[1,2], Mouna Kammoun[1], Ali Mousavi[1,2], Arman Jafari[1,2], Naimeh Rafatian[2], Amir Seyfoori[3], Mohsen Akbari[3], Houman Savoji[1,2]

1 Institute of Biomedical Engineering, Department of Pharmacology and Physiology, Faculty of Medicine, University of Montreal, Montreal, QC, Canada.

2 Research Center, Centre Hospitalier Universitaire Sainte-Justine, Montreal, QC, Canada.

3 Laboratory for Innovations in Microengineering (LiME), Department of Mechanical Engineering, University of Victoria, Victoria, BC V8P 5C2, Canada

I**ntroduction:** Mesenchymal stem cells (MSCs) play a pivotal role in regenerative medicine due to their differentiation potential and therapeutic applications in diseases such as cardiovascular disorders, diabetes, and neurodegenerative conditions. However, the limited availability of human MSCs (hMSCs) in adult tissues necessitates efficient ex vivo expansion to generate tens of millions to billions of cells required for clinical applications. Conventional two-dimensional (2D) culture systems are inadequate for large-scale production, emphasizing the need for scalable technologies. Bioreactors integrated with microcarriers offer a controlled environment that optimizes cell growth, significantly improving cell yields and volumetric efficiency. **Objective:** This study explores the large-scale expansion of hMSCs using thermoresponsive microcarriers (MCs) in a stirred bioreactor. **Methods:** MCs were fabricated via a flow-focusing microfluidic chip, producing a uniform size distribution (100–300 µm). These smart MCs, composed of a hydrogel network of poly(N-isopropylacrylamide), poly(ethylene glycol) diacrylate, and gelatin methacryloyl, enable enzyme-free cell harvesting, enable enzyme-free cell harvesting through temperature reduction, eliminating the need for proteolytic enzymes such as trypsin, which can compromise cell viability and stemness. hMSCs were cultured in both static and dynamic bioreactor conditions, followed by thermal and trypsin-mediated harvesting. Seeded MCs were transferred to (1) a 3D static well-plate culture system and (2) a 3D dynamic bioreactor culture system. Cell viability assays and Phalloidin-DAPI immunostaining were performed during the exponential (Day 5) and plateau growth phases. Flow cytometry confirmed MSCs stemness using ISCT (International Society of Cell Therapy)-recommended markers. **Results:** Bioreactor cultures yielded significantly higher cell numbers than static cultures. Viability assays and flow cytometry (positive for CD 90, Cd75, CD105 (>95%) and negative for CD45(<2%)), demonstrated that thermally harvested MSCs maintained viability and stemness. **Conclusion:** Thermoresponsive MCs in a stirred bioreactor enhance hMSC expansion while minimizing enzymatic exposure, providing a scalable solution for large-scale cell production in regenerative medicine.

# WORKSHOPS AND PANEL

# WORKSHOP #1
# COMMERCIALIZING UNIVERSITY INTELLECTUAL PROPERTY: THE MCGILL PERSPECTIVE

## DR. MARK WEBER

DIRECTOR, INNOVATION AND PARTNERSHIPS AT MCGILL UNIVERSITY

**MAY 5**
**1:30 PM - 2:30 PM**

Dr. Mark Weber has a Ph.D., M.Eng. and B.Eng. in Chemical Engineering from McGill University. He has been working at McGill University for over 12 years, and has been the Director of Innovation and Partnerships for over 6 years. His specialties include commercialization, product development, and technical service.

This workshop will address how to overcome the entry-to-market barriers and scale in the biomedical field, as well as what more we can do to support professors and students who seek entrepreneurial opportunities.

# WORKSHOP #2
# STARTUP LAW 101

## COMPASS STARTUP LEGAL CLINIC

**MAY 5**
**3:30 PM - 4:30 PM**

Compass assists the Montreal startup community by offering free legal information to aspiring entrepreneurs.

They will walk through the fundamentals of equity and legal structures for startups, tailored to bioengineering startups. They'll break down the meaning of share capital, covering voting vs. non-voting shares, while also exploring key legal instruments like founders' and shareholders' agreements. The session will also include a focused discussion on intellectual property rights, with specific insights into how McGill's IP policies apply to student-led ventures. As well as an overall explanation of a startups life cycle.

# PANEL DISCUSSION
# GOVERNMENT-ORIENTED CAREERS

# PANEL DISCUSSION
# NATIONAL RESEARCH COUNCIL OF CANADA

**MAY 6**
**1:30 PM - 2:30 PM**

**Prof. Lidija Malic**
Team Lead, Precision Diagnostics

**Dr. Felix Lussier**
Research Associate

**Dillon Da Fonte**
Technical Officer

**Mojra Janta-Polczynski**
Technical Officer

# WORKSHOP #3
# INTELLECTUAL PROPERTY

Legal Information Clinic at McGill

**MAY 6**
**3:30 PM - 4:30 PM**

The LICM is committed to increasing access to justice for McGill and Montreal communities and to meeting the needs of students and marginalized groups because justic matters for everyone.

Join the Legal Information Clinic at McGill (LICM) in their presentation on the fundamentals of intellectual property law. They will break down the key concepts behind copyrights, trademarks, patents, and trade secrets.

# POSTER PRESENTATIONS

## MAY 5
## 2:30 PM - 3:30 PM

Biomedical sensors, diagnostics, and therapeutics

M01, M09, M11, M25, M27, M40, M44

Microscopy, imaging, and neuroimaging

M15, M17, M38

Bioinformatics, modelling, and computational biology

M19, M30, M34, M36

Tissue engineering and regenerative medicine

M06, M20, M29

Other

M08, M28

# TARGETING AUTONOMIC IMBALANCE IN MYALGIC ENCEPHALOMYELITIS: A SEARCH FOR CRITICAL MODULATORS

**Yasaman Vahdani**[1,2,3,4], Evguenia Nepotchatykh[2,3,4,5], Wesam Elremaly[2,3,4], Iurie Caraus[2,3,4], Mohamed Elbakry[2,3,4], Anita Franco[2,3,4], Moreau Alain[1,2,3,4,5,6]

1 Department of Biochemistry and Molecular Medicine, Faculty of Medicine, Université de Montréal

2 Viscogliosi Laboratory in Molecular Genetics of Musculoskeletal Diseases, Sainte-Justine University Hospital Research Center

3 Open Medicine Foundation ME/CFS Collaborative Center at CHU Sainte-Justine/Université de Montréal

4 ICanCME Research Network, Sainte-Justine University Hospital Research Center

5 Molecular Biology PhD Program, Faculty of Medicine, Université de Montréal

6 Department of Stomatology, Faculty of Dentistry, Université de Montréal

Background: Myalgic Encephalomyelitis (ME) is a complex disease that predominantly affects women, with a 3:1 female-to-male ratio. According to the Canadian Consensus Criteria, ME is characterized by persistent fatigue lasting over six months. Many ME patients show autonomic nervous system dysregulation, impacting the vascular system and leading to conditions such as Orthostatic Intolerance (OI) and Postural Orthostatic Tachycardia Syndrome (POTS). POTS, defined by a heart rate increase of over 120 bpm upon standing, affects 25-50% of ME patients, while broader OI symptoms are seen in 50-90% of cases. The causes of ME remain poorly understood, though potential triggers include viral infections, genetic and epigenetic predispositions. While POTS is clinically recognized in ME patients, its molecular underpinnings remain unclear, limiting the development of targeted treatments.

Objectives: To address these knowledge gaps by examining the epigenetic and molecular factors contributing to POTS and OI in ME patients.

Methodology: The Agilent expression array-Human miRNA 8×60k harboring 2549 human miRNAs was used to identify candidate miRNAs differentially expressed in POTS sufferers with and without ME when compared with ME patients without POTS and matched sedentary healthy controls. Only miRNAs exhibiting ± two-fold changes were considered statistically significant. By validation and replication analysis of selected miRNAs by qPCR, a panel of 9 miRNAs was identified as significant in different cohorts of study. To explore the connections between different molecules, such as miRNAs of interest, genes, diseases (POTS with/without ME), and pathways, we utilized IPA (Ingenuity Pathway Analysis) software.

Results: miR-150-5p overexpression downregulates norepinephrine transporter (NET) protein levels by targeting SLC6A2 mRNA, with elevated levels of this microRNA observed in ME patients with POTS. Additionally, two other microRNAs, miR-181a-5p and miR-5010-3p, were found to be upregulated specifically in ME patients with POTS, targeting SLC8A1 (sodium-calcium exchanger, NCX1) and DRD1 (dopamine receptor D1), respectively. Conclusion: These findings point to possible molecular mechanisms that underlie POTS in the context of ME by disrupting norepinephrine, calcium, and dopamine balance, setting the foundation for further biomarker validation and functional studies.

M06

# COLD ATMOSPHERIC PLASMA ACTIVATED HYDROGEL FOR CHRONIC WOUND HEALING

**Mo Chen**[1], Qiujie Fang[1], Bingzheng Shen[1], Zhitong Chen[2], Guojun Chen[1]

1 McGill University

2 Chinese Academy of Sciences

Chronic wounds often exhibit delayed healing due to heightened inflammation and inadequate blood vessel formation. In response to these challenges, our investigation delved into a treatment approach utilizing cold atmospheric plasma (CAP) incorporated into an injectable Pluronic hydrogel. This intervention stimulated cell migration, promoted blood vessel proliferation, and eradicated bacteria, evincing potential as a promising therapeutic avenue for addressing intricate wound healing.

M08

# ACOUSTOFLUIDIC DEVICES FOR 3D MULTICELLULAR SPHEROIDS FORMATION

**Bryan Daniel Herrera Lozada**[1], Maryam Tabrizian[1]

1 McGill University

Acoustofluidics is an emerging field that combines the use of acoustic waves for the manipulation of fluid dynamics in the micro-scale. These kinds of platforms are capable of manipulating particles in a gentle, label-free manner based on their characteristics like size, shape, density, and compressibility. All these attributes have sparked interest in using this technology specifically for cell manipulation and cell culture. In the previous work in our laboratory, we demonstrated the manipulation of cancer lines MCF-7 and MDA-MB-231 by using acoustic waves for the formation of cell spheroid structures. In this project, we are interested in developing a new type of acoustofluidic device capable of manipulating cells and forming spheroids under higher viscosity conditions. We are interested in using viscous solutions like hydrogels or bio-inks to incorporate these platforms in 3D bioprinting technologies. This perspective will make it possible to use cell spheroids as building blocks in 3D bioprinting technologies for tissue engineering applications. Cell spheroids in tissue engineering are of special interest due to the advantages compared to using single cells for bioprinting, specifically because they will allow cell-cell interactions in the model, using materials with properties like the extracellular matrix as spheroids agglutinant, and using different cell types that not present cell spheroid formation commonly. To reach this purpose, this project focuses on the use of fluid dynamics simulations to optimize the platform performance, develop a new methodology for the fabrication of platforms with the desired characteristics, and test their performance with different bio-inks and cell lines.

# A DIGITAL MICROFLUIDIC PLATFORM FOR THE PRODUCTION OF FUNCTIONAL IMMUNE CELL THERAPIES FROM PRIMARY HUMAN T-CELLS

Samuel R. Little, **Niloufar Rahbari**[1], Fatemeh Gholizadeh[2], Mehri Hajiaghayi[2], Joel Philips[1], Peter J. Darlington[3], Steve C.C. Shih[4]

1 Centre for Applied Synthetic Biology, Concordia University
2 Department of Biology, Concordia University
3 PERFORM Center Department of Health Kinesiology and Applied Physiology, Concordia University
4 Department of Electrical and Computer Engineering, Concordia University

Payload delivery into mammalian cells is crucial for developing cell therapies. Currently, most of the focus has been on creating high throughput platforms for clinical scale manufacturing where a single type of payload is rapidly inserted into as many cells as possible.1 However, little has been done on a platform for R&D-scale cell engineering, where numerous unique payloads or conditions need to be screened in parallel while limiting consumption costs. Recently, we showed a novel tri-drop liquid structure using digital microfluidics for efficient electroporation (DMF-EP) containing small numbers (< ~ 50,000) of cells.2 In this work, we present our DMF-EP platform for generating functionally engineered primary human T-cells for immunotherapeutic applications. We compare directly against two gold-standard techniques and demonstrate that our platform can achieve comparable delivery efficiencies to commercially available platforms, while having improved viability, proliferation, and functionality post-transfection, and significantly reducing the consumption of patient cells and expensive materials normally required by the cell engineering process.

M11

# ADVANCED DETECTION AND IDENTIFICATION OF CANCER BIOMARKERS THROUGH LIPOSOME DOCORATION, SURFACE-ENHANCE RAMAN SPECTROSCOPY AND ML-MODEL TRAINING

**Yueru Zhou,** Sajad Shiekh, Walter Reisner, Sara Mahshid

The advancement of biosensing platforms is essential for the enhancement of early-stage cancer diagnostics through the accurate identification of biomarkers. Here we introduce a novel methodology that synergistically combines surface-enhanced Raman spectroscopy (SERS) with engineered liposomal systems to effectively detect cancer biomarkers. In contrast to traditional approaches, we utilize liposomes and liposome that functionalized with epidermal growth factor receptor (EGFR) proteins—as versatile and biocompatible nanocarriers for SERS detection. The SERS signal amplification was acquired on an advanced single-vesicle resolution plasmonic platform with nanocavities. The platform enabled to acquire distinct SERS spectra from our homemade and further analyze with machine learning algorithm to realize biomarker detection and identification. This work demonstrates the potential of using synthetic liposomal system to build a machine learning model for sensitive and specific biomarker detection, offering a transformative strategy for advancing SERS detection for liquid biopsy applications in cancer diagnostics.

# MAGNETIC RESONANCE (MR)-GUIDED LASER INTERSTITIAL THERMAL THERAPY (MRGLITT) PLANNING TOOL IMPROVEMENT: THE EFFECT OF SEGMENTED ANATOMICAL MRI TO PREDICT MR THERMOMETRY IMAGES USING ARTIFICIAL INTELLIGENCE (AI)- BASED MODELS

S. Sadatamin[1,3,4], S. Robbins[4], **E. Donszelmann-Lund[2,3]**, Y. Hau Wallace Lee[3,5], T. Latypov[3], R. Tyc[4], G. M. Ibrahim[1,3], L. A. Kahrs[1], A. C. Waspe[1,3], J. M. Drake[1,3]

1 University of Toronto

2 McGill University 3 The Hospital for Sick Children, Toronto, ON (CA)

4 Monteris Medical, Plymouth, MN (US)

5 University of Waterloo (CA)

MR-guided laser interstitial thermal therapy is a minimally invasive brain tumor treatment involving a fixed trajectory laser probe. To minimize the amount of damage from the heat source, an AI-based model can predict MR thermometry heat propagation. This prediction can assist the surgeon choose an ideal laser location prior to treatment. One important consideration is different tissues of the brain due to their heat-sinking effects. Currently, the AI model is trained using anatomical MRI images and MR thermometry images. Integrating brain segmentation into the model has potential to improve predictions by accounting for heat absorption effects of the brain. Objective: To assess the effectiveness of brain MRI segmentation for thermometry image prediction using an AI-based planning model for MRgLITT treatment. Methods: An AI algorithm was used to predict MR thermometry images from anatomical MRI planning images. Epilepsy patients from the Monteris Medical dataset were used as target ground-truth. MRI images were segmented using N4 Bias Field Correction, Skull Stripping and the DIPY Segmentation library. Segmentation regions included white matter, gray matter, and CSF. A U-Net will be trained using cropped and centered treatment area images, along with the additional segmentation input channel. To evaluate the results, SSIM, RMSE, Max-Difference and L1 loss of the ground truth and predicted thermometry images will be used.Results: MR tthermometry prediction improved with segmentation information qualitatively and quantitatively compared to the baseline results. Segmentation of anatomical MRIs incorporated useful thermal information of the brain to help combat the challenge of heatsinks during treatment. Conclusions: Brain segmentation for three major regions was implemented using Bias Field Correction, Skull Stripping and the DIPY segmentation library. The results show improved AI-based MR thermometry prediction by incorporating thermal properties of the brain.

M17

# EXTRACELLULAR VESICLES SUBPOPULATIONS YIELD DIFFERENT DNA ENCAPSULATION EFFICIENCIES

**Oscar Boyadjian**[1,2], Stephanie Lehoux[2], Maryam Tabrizian[1,3]

1 Department of Biomedical Engineering, McGill University

2 Lady Davis Institute for Medical Research, Jewish General Hospital

3 Faculty of Dental Medicine and Oral Health Sciences, McGill University

Introduction:

Extracellular vesicles (EVs) are membrane-bound nanoparticles with high potential as gene therapy delivery systems. However, current protocols for loading exogenous nucleic acids into EVs suffer from low efficiency. To optimize this, it is critical to understand DNA-EV interactions at the single-vesicle level. dSTORM microscopy offers the resolution needed to uncover this complexity.

Methods:

Red blood cell-derived EVs were isolated from three human donors and loaded with Cy5-labeled DNA using a PEI-based method. Bulk loading was quantified with picogreen after EV lysis. EVs were captured on chips targeting GYPA+ or phosphatidylserine (PS+ via Annexin V) subpopulations. Membranes were stained with DiI, and CD9 was labeled with CF488. Imaging was performed using a dSTORM ONI Nanoimager, with analysis in CODI Alto. Statistical comparisons were made using Student's t-test.

Results:

Picogreen revealed significant DNA association with EVs ($p<0.01$), but single-vesicle imaging showed heterogeneous interactions. Most EVs were DNA-free; others showed DNA on the surface ("stick" mode) or throughout ("mixed" mode). GYPA+ EVs were more abundant than PS+ EVs ($p<0.01$), but PS+ EVs expressed CD9 twice as often ($p<0.001$) and encapsulated 2.4 times more DNA per vesicle ($p<0.01$). DNA localization did not correlate with CD9 levels or size, suggesting loading is influenced by EV surface composition rather than general properties.

Conclusion:

PS+ EVs exhibit superior DNA encapsulation efficiency compared to GYPA+ EVs. Targeting this subpopulation—present in EVs from many cell types—may improve nucleic acid loading and enhance the efficacy of EV-based gene therapies.

M19

# UPSAMPLING MRI SCANS CAN SIGNIFICANTLY INCREASE ROBUSTNESS OF NBM SEGMENTATION

**Neda Shafiee**[1], D. Louis Collins[1]

1 McConnell Brain Imaging Centre, Montreal Neurological Institute, McGill University, Montreal, QC, Canada

The nucleus basalis of Meynert (NbM) is the primary source of cholinergic projections to the cortex and is among the earliest sites affected by Alzheimer's disease (AD). Postmortem studies have shown early neurofibrillary tangle accumulation in NbM, and its degeneration may precede entorhinal and neocortical changes, making it a potential early biomarker. However, accurately delineating the NbM using MRI is challenging due to its small size, limited MR contrast, and indistinct anatomical boundaries. To address this, we tested whether increasing MRI resolution prior to deformation-based morphometry (DBM) analysis improves sensitivity to disease-related atrophy in NbM.

We analyzed MRI scans from 896 participants in the ADNI dataset, including cognitively normal amyloid-negative (CN–, n=219), cognitively normal amyloid-positive (CN+, n=117), early MCI (EMCI, n=131), late MCI (LMCI, n=242), and AD patients (n=187). All scans were upsampled to 0.5 mm isotropic resolution using Manjón et al.'s method, then nonlinearly registered to an ADNI template. Jacobian determinant maps were computed to assess local volume change within the NbM, using the atlas by Zaborszky et al. for masking. We repeated the same analysis on the original 1 mm scans for comparison.

Both resolutions detected NbM atrophy with disease progression, but the high-resolution pipeline revealed greater distinction between diagnostic groups. Specifically, Cohen's d and t-values comparing EMCI vs. LMCI were higher using the upsampled data, indicating enhanced sensitivity to subtle atrophic changes.

Our findings suggest that for small, poorly defined brain structures such as the NbM, upsampling MRI data can improve DBM-based atrophy detection. This approach may support earlier and more accurate identification of neurodegenerative changes in Alzheimer's disease.

M20

# VASCULARIZED LIVER-ON-A-CHIP FOR COLORECTAL CANCER METASTASIS MODELLING

**Qihui Zhu**[1], David Juncker[1]

1 McGill University

Colorectal cancer liver metastases (CRCLM) are the most common outcome for colorectal cancer patients which ultimately leads to fatality. Although much effort has been put into developing a disease model, most models have pros and cons. Most in-vitro models, such as patient-derived organoids, face issues with vascularization, and hypoxic core and lack tissue-tumor interactions. Various liver-on-a-chip models have been established, with different disease applications. However, CRCLM, being one of the most prominent diseases related to the liver has yet to be established. To address this, we are developing a liver-on-a-chip model that utilizes immortalized human hepatocytes (IHH) with fully self-assembled human umbilical vein endothelial cell (HUVEC) vasculatures. Currently, we address the angiogenic properties of the IMR-90 lung fibroblast cell line in the context of self-assembled HUVEC vasculatures. The immortalized IMR-90 cells showed an anti-angiogenic nature compared to the pro-angiogenic properties of those shown in the primary IMR-90 cells. We also showed self-assembled HUVEC vasculature formation in a fibrin gel co-culture system with the primary IMR-90 in a microfluidic chip. Lastly, we are also demonstrating some preliminary attempts at implementing IHH cells in such self-assembled HUVEC vasculatures where we monitored the albumin and CYP3A4 production daily.

# SPLIT-AND-POOL SYNTHESIS OF A COMBINATORIAL NANOPARTICLE-BOUND SSDNA OLIGONUCLEOTIDE LIBRARY

**John V. L. Nguyen**[1], Ahlem Meziadi[1], Lidija Malic[1,2], Christina Nassif[2], Dillon Da Fonte[2], Maryam Tabrizian[1,3]

1 Department of Biomedical Engineering, McGill University, 3775 University Street, Montreal, QC
2 Life Sciences Division, National Research Council of Canada, Boucherville, QC
3 Faculty of Dental Medicine and Oral Health Sciences, McGill University

Aptamers are short oligonucleotides with high target specificity, making them valuable tools for biosensing and diagnostics. However, the conventional SELEX method for aptamer discovery is labor-intensive and constrained by the limited theoretical diversity of commercial aptamer libraries. This limitation necessitates extensive amplification, slowing down the discovery process. A more efficient approach is needed to enhance detection capabilities while eliminating intermediate amplification steps.

We present a combinatorial aptamer library synthesis method based on split-and-pool synthesis using magnetic nanoparticles (MNPs). This approach involves conjugating an oligonucleotide primer to MNPs, followed by sequential ligation of short DNA fragments containing restriction enzyme sites. Repeated pooling and splitting generate unique sequences on individual beads, streamlining synthesis and facilitating downstream screening via microfluidic biosensors. MNPs enable efficient magnetic separation, yielding a sequence-diverse library that scales with the number of synthesis cycles and fragment combinations. Characterization through UV-Vis spectroscopy, zeta potential analysis, nanoparticle tracking analysis, fluorescence dsDNA assays, circular dichroism spectroscopy, automated electrophoresis, and massive parallel sequencing confirms successful synthesis.

Our method produces single-stranded DNA (ssDNA) that is anticipated to self-anneal into three-dimensional structures. Zeta potential measurements indicate cumulative decreases of zeta potential, while nanoparticle tracking analysis reveals gradual size growth, with both characteristics increasing with successive split-and-pool iterations. UV-Vis and circular dichroism spectroscopy show signals characteristic of DNA on nanoparticles, indicating the successful formation of DNA-nanoparticle complexes. Automated electrophoresis shows oligonucleotides of the expected size and successful integration of library products into plasmids for subsequent DNA sequencing. Bioinformatics analysis further demonstrates substantial sequence diversity, sequence length variability, and decreasing synthesis efficiency with successive cycles.

Given the limitations of SELEX, our novel library synthesis approach offers a promising alternative for generating oligonucleotide libraries which could be used to discover new aptamers for diagnostic or therapeutic applications.

M27

# HIGHLY MULTIPLEXED PROTEOMICS OF SINGLE MEDULLOBLASTOMA EXTRACELLULAR VESICLES SEPARATE VESICLES BY SUBGROUP

**Fabian Svahn**[1], Andreas Wallucks[1], Ana Castillo Orozco[2], Livia Garzia[3], Janusz Rak[4], David Juncker[1]

1 Biomedical Engineering Department, McGill University
2 Department of Human Genetics, Research Institute of the McGill University Health Centre
3 Department of Surgery, Research Institute of the McGill University Health Centre
4 Department of Pediatrics, Research Institute of the McGill University Health Centre

Medulloblastoma (MB) is a pediatric brain tumor with significant morbidity and mortality classified into molecular subgroups WNT, SHH, Group 3, and Group 4. Current diagnostics like MRI and CSF cytology are inadequate for monitoring MB progression, recurrence or profiling its molecular evolution. Extracellular vesicles (EV) play a key role in intercellular communication and cancer progression. MB-derived EVs, linked to poor prognosis, may contribute to metastasis and are accessible through liquid biopsy. Technologies capturing the complexity of MB via EVs could significantly improve MB management, by allowing for a non-invasive way to profile and monitor MB patients and detect recurrence, treatment response or molecular evolution. This benefits from single EV resolution for at least two reasons: (i) ability to detect rare EV; (ii) ability to detect distinct EV populations as a reflection of the cellular landscape of the disease. High multiplexing allows for the combination of both general cancer and/or progenitor markers with Medulloblastoma-specific markers, and the co-localization of several proteins increases specificity even for highly rare populations. The “EV-ID” platform enables highly multiplexed single EV analysis, overcoming limitations of current single EV methods by combining label-free interferometric scattering microscopy for vesicle sizing and enumeration with DNA exchange imaging for multiplexed proteomic analysis with minimal sample input. Using the EV-ID platform, preliminary 13-plex single vesicle proteomics of single EV from in vitro models of Group 3, Group 4 and SSH Medulloblastoma reveals the existence of heterogeneous vesicular subpopulations that allow for bagged decision tree classification of EV according to Medulloblastoma subgroups with AUC 0.84 for molecularly similar Group 3 and Group 4, and AUC 0.91 for comparing SHH with the others. Medulloblastoma EV-ID highlights the promise for non-invasive liquid biopsy to characterize MB via proteomic analysis of circulating extracellular vesicles.

M28

# A SELF-OSCILLATING FLUIDIC MICRO HEAT ENGINE (SOFHE) FOR ENERGY APPLICATION

**Nooshin Karami**[1,2], Etienne Leveille[2], Amrid Amnache[2], Luc G. Frechette[2]

1 McGill University

2 Universite de Sherbrooke

A self-oscillating fluidic micro heat engine (SOFHE) consists of a vapor bubble trapped by a liquid plug (acting as a piston) within a capillary tube. The vapor bubble–liquid plug system is set into oscillation through the cyclic evaporation and condensation of a thin liquid film. The mechanical power generated by these oscillations can be harnessed to perform mechanical work, such as fluid pumping (when coupled with a mechanism like a jet pump), or converted into electrical energy (when integrated with a transducer). A micro-jet pump has recently been designed, integrated, and characterized with a SOFHE, demonstrating a pumping capacity in the milliliter-per-minute range—an encouraging result for applications in microfluidic lab-on-a-chip devices or microelectronics cooling.

M29

# SUBSTRATE STIFFNESS REGULATES COLLECTIVE ELECTRO-MECHANICAL RESPONSE OF HUMAN IPSC CARDIOMYOCYTES

**Pouria Tirgar**[1,2,3], Miguel Romero Sepulveda[3], Luv Srivastava[1], Ali Amini[1,4,5], Allen Ehrlicher[1,2,4]

1 Department of Bioengineering, McGill University, Montreal, QC H3A 0C3, Canada
2 Center for Structural Biology. McGill University, Montreal, QC H3A 0C3, Canada
3 Department of Physiology, McGill University, Montreal, QC H3A 0C3, Canada
4 Department of Mechanical Engineering, McGill University, Montreal, QC H3A 0C3, Canada
5 Physical Intelligence Department, Max Planck Institute for Intelligent Systems, 70569 Stuttgart, Germany

Cardiac performance emerges from intricate coupling between electrical and mechanical activity of cardiomyocytes, a bidirectional process modulated by mechano-electric feedback (MEF). Extracellular-matrix stiffness rises sharply during development and in fibrotic disease, yet how such mechanical cues reshape MEF in human systems remains unclear. Here we quantify the collective electro-mechanical behaviour of human induced-pluripotent-stem-cell-derived cardiomyocyte (hiPSC-CM) monolayers cultured on silicone substrates spanning healthy and pathological Young's moduli (2, 12, and 32 kPa). Using fluorescent calcium imaging and traction-force microscopy, we show that, unlike murine cells, increasing substrate stiffness accelerates calcium kinetics (faster rise time, shorter calcium duration), elevates transient amplitude, and boosts contractile work under both spontaneous beating and paced conditions (0.5–2 Hz). On the stiffest matrix (E=32 kPa), calcium rise was ~40 % faster, and contractile work almost tripled relative to the softest substrate (E=2 kPa). Pharmacological uncoupling of actin-myosin interaction with the myosin-ATPase inhibitor Mavacamten selectively blunted these stiffness-dependent gains, reducing calcium amplitude and prolonging transients in proportion to baseline force generation. This indicates that active contractility is a critical mediator that converts external mechanical cues into electrophysiological output.

M30

# CO-REGISTRATION OF 3D DATASETS WITH COMPLIMENTARY 2D IMAGES USING VIRTUAL REALITY AND ARTIFICIAL INTELLIGENCE

**Noelia Redondo Bort**[1,2], Leonor Simoes[1], Darcy Wagner[1]
1 McGill University
2 Universidad Francisco de Vitoria

Light Sheet Fluorescence Microscopy (LSFM) and optical clearing have revolutionized the ability to acquire high-resolution 3D images of large and intact, fixed tissues and organs up to the size of whole mice. While fluorescent labeling of specific structures in 3D is possible, multiplexing approaches in whole organs remain costly.

Co-registering LSFM datasets with complimentary molecular analysis, such as thin histological sections, can significantly enhance tissue analysis. However, this process presents significant challenges due to differences in resolution and acquisition modalities, tissue deformation during histological processing, and limitations of traditional flat, 2D screens.

In this work, we propose a novel approach for 2D-3D co-registration using Virtual Reality (VR) to overcome these challenges. This methodology improves spatial perception through immersive interaction, enabling more accurate manual alignment and a better understanding of morphological relationships.

Our methodology consists of two key steps: first, manual registration in a VR environment using a conventional workstation with 32Gb RAM GPUs to manually manipulate and align the histological slices with the 3D model to learn how this task can be performed. We will then use this knowledge to automate this process with computer vision and/or machine learning. We first performed manual co-registration with syGlass software and a VR headset (Meta Quest 3) to estimate the approximate region where the slice might be located. Once it was identified, we systematically explored different planes within this area, utilizing Python to extract individual planes from the 3D volume with different orientations. We then used the Oriented FAST and Rotated BRIEF (ORB) algorithm to find the best match between the 3D volume extracted slices and the original 2D slice. Ongoing work is to iterate this process until a nearly identical match can be found.

This study demonstrates VR's potential in biomedical imaging by integrating immersive interaction and spatial perception with automated techniques, offering an innovative solution to multimodal imaging data.

M34

# DEVELOPING ARTIFICIAL VISION THROUGH V4-TARGETED CORTICAL PROSTHESES

**Younes Valibeigi**[1], Christopher Pack[2]
1 Integrated Program in Neuroscience, McGill University, Quebec, Canada
2 Montreal Neurological Institute, McGill University, Quebec, Canada

The development of visual cortical prosthetics has traditionally focused on stimulating the primary visual cortex (V1), where each electrode elicits a simple phosphene—a circular flash of light—requiring hundreds or thousands of electrodes to approximate image perception pixel by pixel. However, this pixel-based approach faces several challenges: phosphenes often have indistinct shapes, risk tissue damage or seizures, and suffer from neural adaptation.

In contrast, we propose a novel prosthetic strategy targeting area V4, a mid-level visual area where neurons encode semi-complex features such as curvature and textures. Unlike V1, stimulating V4 enables the evocation of percepts that more closely resemble meaningful components of natural scenes, requiring fewer electrodes. Furthermore, unlike the inferotemporal cortex (IT), where receptive fields are large and diffuse, neurons in V4 have spatially localized receptive fields. This makes V4 uniquely suited to generate visual percepts at specific locations in the visual field—a key requirement for spatially accurate artificial vision.

To maximize the effectiveness and specificity of stimulation, we developed a new procedure involving simultaneous stimulation of two sites with opposite polarities. This approach focuses current flow within a restricted cortical region, enhancing local circuit engagement while minimizing spread, with the goal of producing clearer and more stable visual percepts.

To test this approach, we trained non-human primates to perform a delayed match-to-sample task involving circular and radial gratings. These stimuli were selected based on prior findings in our lab demonstrating that they evoke distinct patterns of neural activity in V4.

Our data suggest that microstimulating clusters of feature-selective neurons in V4 significantly biases the monkeys' perceptual decisions toward the corresponding patterns. These results highlight the potential of V4-targeted prosthetics to manipulate visual experience with high spatial and feature specificity, laying the groundwork for more naturalistic and efficient artificial vision systems.

M36

# AUTOMATING LINEAR MOTIF PREDICTIONS TO MAP HUMAN SIGNALING NETWORKS

**Eric Sun**[1], Yu (Brandon) Xia[1], Jasmin Coulombe-Huntington[1]

1 Department of Bioengineering, McGill University, Montréal, QC, Canada

Short linear motifs (SLiMs) are critical mediators of protein-protein interactions, yet only a small fraction (0.2% of the estimated total) have been experimentally characterized. Unlike well-conserved, long, and structured protein domains, SLiMs are short (3–11 residues), fast-evolving, often located in intrinsically disordered regions, and facilitate transient interactions such as cell signaling. These characteristics make SLiM discovery a challenging but essential area of research.

To address these challenges and enable de novo SLiM discovery, we present a computational framework that integrates AlphaFold (AF), protein language models (ProtT5), and Gibbs sampling to predict SLiMs at a proteome-wide scale. Our approach leverages AF-derived structural features, such as solvent accessibility surface area (SASA) and intrinsic disorder predictions, alongside ProtT5 embeddings, all of which significantly distinguish motif residues from background residues ($p < 0.01$, Fisher's exact test). Additionally, we incorporate multiple-sequence protein alignments across 100 vertebrates to capture the evolutionary dynamics of SLiMs. A key innovation is the use of hidden Markov models to identify and model motifs, accounting for insertions and deletions, a limitation of conventional motif discovery tools such as MEME.

Applying this framework, we identified a novel MAPK1 (ERK2)-mediated phosphorylation motif in RUNX1, characterized by significantly elevated feature scores relative to background residues (disorder: >1.0 SD, SASA: >1.2 SD, ProtT5 embeddings: >1.8 SD). Biochemical validation (Varshney et al., 2012) confirms RUNX1 phosphorylation at this site, providing new insights into its regulatory role in tumor progression and highlighting a potential therapeutic target. By systematically mapping SLiM-mediated interactions, our approach enables a deeper reconstruction of human cell signaling networks, shedding light on the intricate regulatory mechanisms that drive cellular communication.

# BRAINS IN ORDER: LEARNING TO RANK FOR BETTER BRAIN AGE PREDICTION

**Reza Rajabli**[1], D. Louis Collins[1]

1 McConnell Brain Imaging Centre, Montreal Neurological Institute, McGill University, Montreal, Canada

Background:

Deep learning models trained on healthy T1-weighted brain MRIs can predict an individual's age, with the difference between predicted and actual age—known as the brain age gap—serving as a potential biomarker for neurodegeneration or brain maintenance. However, the relatively limited availability of brain imaging data, compared to datasets in other deep learning domains, hinders model generalizability and reduces the reliability of this biomarker. We have previously shown that a robust preprocessing pipeline, extensive data augmentation, and effective model regularization are critical for training generalizable brain age estimators. Still, existing models often fail to extrapolate beyond the training age range and tend to regress toward the mean, introducing bias. This issue is particularly problematic when applying models to older adults, who are frequently the focus in studies of neurodegenerative disease.

Methods:

To address these limitations, we developed a rank-based regression model that learns to assign scores for ranking brain images by age, rather than directly predicting chronological age. This ranking approach mitigates bias toward the mean by implicitly modeling the trajectory of brain aging. Additionally, training on image pairs instead of individual samples increases the number of effective training examples, enhancing robustness—especially at the extremes of the age distribution. Our training pipeline consisted of three steps: (i) Training a ConvNeXt-based model from scratch on UK Biobank (UKBB) data (31,331 training images, 3,916 validation images), (ii) Fine-tuning the best-performing model for one epoch on Mayo Clinic Study of Aging (MCSA) data (908 training images, 101 validation images), and (iii) Mapping the predicted rank-based scores to brain age using linear regression (fitted on 76 images, validated on 25).

Results:

We evaluated our model on healthy brain scans from the Alzheimer's Disease Neuroimaging Initiative (ADNI)—an independent dataset with a different age distribution and not seen during training or validation. The model successfully predicted brain ages beyond 88 years and reduced the correlation between brain age gap and chronological age to 0.024, indicating a substantial reduction in regression toward the mean bias. These results demonstrate improved generalizability and reliability, particularly in older populations.

# MODELLING THE RELATIONSHIP BETWEEN BUBBLE CPAP PRESSURE, FLOW, AND CANISTER BUBBLING SOUNDS

**Emily Campbell**[1], Amanda Gross[2], Guilherme Sant'Anna[3], Wissam Shalish[3], Robert E Kearney[1]

1 McGill University, Department of Biomedical Engineering
2 McGill University, Department of Experimental Medicine
3 Montreal Children's Hospital, Department of Neonatology

Bubble continuous positive airway pressure (bCPAP) supports neonatal respiration through a closed system interfaced with the infant's upper airways. Air flows through a tubing system, going from the inspiratory to the expiratory arm, which ends submerged in a water canister, generating a pressure equivalent to the length of tube inserted into the water. The air escapes into the water creating pressure oscillations at a high frequency, which helps lung expansion and gas exchange. Assurance that the bCPAP system is working properly is typically assessed by the presence of bubbling sounds at the water canister and patient's lungs. This work describes the bCPAP canister bubbling sounds and develops a linear regression model relating the sounds at specific frequencies to system pressure and flow rate.

The bCPAP system was interfaced to a term or pre-term manikin in a quiet room. The water canister sound and system pressure were recorded for 3 minutes for combinations of different pressures (5,6,7,8 cmH2O) and flows (6,8,10 L/min), which are used clinically. The power spectra of the processed sound recordings were analyzed and used along with the pressure data to develop a linear regression model.

Bubbling sounds were found to have lower spectra consistently ranging from 100–10,000 Hz, with 90% of the power below 3 kHz. When pressure or flow was increased independently, the power in all frequency bands increased, but maintained similar minima and maxima. The regression model relating bCPAP pressure and flow to bubbling sounds within 1700-2600 Hz, which is distinct from most NICU noise, accounted for more than 81% of variance for both the term and pre-term manikin experiments. This data-driven approach provides the basis for the development of real-time feedback tools to assess bubbling quality, enhancing the consistency and precision of this specific neonatal respiratory support.

# DESIGN, FABRICATION AND OPTIMIZATION OF VERSATILE VASCULARIZED CANCER-ON-CHIP PLATFORMS FOR ANTICANCER DRUG SCREENING

**Amir Aidun**[1,2], Prof. Noël J-M Raynal[1,2], Prof. Houman Savoji[1,2],

1 Département de pharmacologie et physiologie, Faculté de médecine, Université de Montréal

2 Centre de recherche Azrieli du CHU Sainte Justine

Introduction: Tumor-on-a-Chip offers a promising alternative to traditional animal testing. It addresses the important need for more accurate and predictive drug evaluations. Our novel platform, featuring five connected wells of a 96-well plate, aims to simulate the tumor environment better, improving drug discovery and testing.

Materials and Methods: The Tumor-on-a-Chip platform consists of four different types of platforms, each featuring five connected wells together by a central microchannel. The microchannels are fabricated using DLP 3D printing with GelMa hydrogel. Extracellular matrix is used in wells two and four for the co-culture of fibroblasts and cancer cells (MDA-MB-231-GFP and A549-GFP). Besides, HUVEC cells are seeded into the microchannel lumen to model vascularization. Permeability was assessed using FITC-dextran diffusion across the ECM. Flow rate and shear stress calculations were performed. Preclinical evaluation involved the perfusion of Panobinostat. Immunofluorescence, Western blot, and confocal microscopy were used to evaluate cellular responses. Also, we ran a pilot test in the MiniFOR bioreactor using 1.5 L to grow bacteria for collagen extraction for use in the platform as ECM.

Results: We did live/dead staining at 24, 48, and 72 hours on the Combination of GelMa hydrogel. The results showed that cell viability stayed high over time and reached more than 96% after 72 hours. The flow rate was at 300µl/min, and the shear stress was around 60 Pa.

Anticipated results: This study investigates four tumor-on-a-chip platforms with five interconnected wells, designed to simulate lung and breast tumors. We will assess cellular behavior and evaluate the anti-metastatic and angiogenic potential of therapeutic agents introduced into the microchannels. We will measure cell proliferation, migration, and angiogenesis, immunohistochemistry, and ELISA tests.

Conclusion: The Cancer-on-a-Chip platform successfully supports 3D-tumor growth, maintains high cell viability, and allows for controlled flow conditions that mimic real tumor environments.

# POSTER PRESENTATIONS

## MAY 6
## 2:30 PM - 3:30 PM

Biomedical sensors, diagnostics, and therapeutics

T02, T03, T05, T10, T24, T26, T33, T41

Microscopy, imaging, and neuroimaging

T07, T12, T13, T16, T22

Bioinformatics, modelling, and computational biology

T21, T31, T37

Tissue engineering and regenerative medicine

T18, T23, T35, T42, T43

Other

T04, T14, T32, T39

# EXPLORING THE CONTRIBUTION OF FIBROBLAST GROWTH FACTOR-21 (FGF-21) TO MYALGIC ENCEPHALOMYELITIS PATHOGENESIS

**Ghazaleh Azimi**[1,2,3,4], Wesam Elremaly[2,3,4], Marie-Yvonne Akoume[2,4,5], Anita Franco[2,3,4], Alain Moreau[1,2,3,4,6]

1 Department of Biochemistry and Molecular Medicine, Faculty of Medicine, Université de Montréal

2 Viscogliosi Laboratory in Molecular Genetics of Musculoskeletal Diseases, CHU Sainte-Justine, Azrieli Research Center

3 Open Medicine Foundation ME/CFS Collaborative Center at CHU Sainte-Justine/Université de Montreal

4 ICanCME Research Network, CHU Sainte-Justine Azrieli Research Center

5 Département de pharmacologie et toxicologie, Faculté de médecine, Université des Sciences de la Santé (USS) de Libreville, Libreville, Gabon

6 Department of Stomatology, Faculty of Dentistry, Université de Montréal

**Background:** Myalgic Encephalomyelitis (ME) is a multisystemic disease characterized by persistent fatigue, post-exertional malaise (PEM), cognitive impairments, and sleep disturbances. Fibroblast Growth Factor-21 (FGF-21), involved in carbohydrate and lipid metabolism as well as cellular stress responses, has emerged as a potential biomarker and therapeutic target. Metabolic abnormalities and mitochondrial dysfunction frequently observed in ME suggest a role for FGF-21 in disease progression.

**Methodology:** This cross-sectional study recruited 251 ME patients meeting the Canadian Consensus Criteria and 58 age- and sex-matched controls. All participants completed SF-36, DSQ, and MFI-20 questionnaires to assess health status and symptom severity. Plasma FGF-21 levels were measured by ELISA and correlated with clinical severity and key symptoms, including fatigue and PEM. Statistical analyses, including Pearson correlation and multivariate regression, were conducted to evaluate the utility of FGF-21 as a reliable biomarker for disease severity.

**Results:** ME patients exhibited significantly higher plasma FGF-21 levels than controls, although not all individuals showed elevated levels. To clarify this heterogeneity, we classified patients into low (0–50 pg/ml), normal (51–300 pg/ml), and high (>300 pg/ml) FGF-21 groups. Those in the high group presented more pronounced physical, cognitive, and sleep-related symptoms. Furthermore, variations in circulating FGF-21 correlated with specific metabolomic changes in plasma and urine, suggesting potential metabolic signatures linked to disease severity.

**Conclusion:** Our findings highlight FGF-21's importance in ME, indicating its potential as both a biomarker for disease severity and a therapeutic target. By elucidating the relationship between FGF-21, mitochondrial dysfunction, and immune responses, this research may facilitate earlier diagnosis and personalized treatment strategies. Targeting FGF-21 could help address underlying metabolic and immune dysregulation, ultimately improving patients' quality of life. Further investigation into FGF-21-mediated pathways may also shed light on novel interventions for this complex and debilitating condition. Hence, identifying further FGF-21-related mechanisms can significantly broaden our understanding of ME pathophysiology.

# EXPERIMENTAL DEMONSTRATION OF MICROWAVE BLADDER FULLNESS DETECTION WITH 3D PELVIC MODEL

**Fadilah Khan**[1], Yunxiao Zhang[1], Ali Farshkaran[2], Emily Porter[1], Eleonora Razzicchia[1]

1 McGill University

2 University of Texas at Austin

Urinary incontinence (UI) is the involuntary discharge of urine in any quantity, which affects millions of people around the globe. This condition affects people in different age brackets and can be caused by a variety of different factors such as aging, pregnancy, irritable bowel syndrome (IBS), diabetes, and various neurological diseases such as Parkinson's Disease (PD) and Multiple Sclerosis (MS), among some. Non-invasive microwave (MW) bladder state detection has potential as a support tool for individuals with UI, to alert when the bladder is full and provide information on bladder volume. Microwave methods allow non-ionizing, continuous and safe sensing, with devices that can be wearable or portable.

In this work, an experimental demonstration of MW differentiation of full and empty bladder is investigated. A realistic and anatomically accurate model of the pelvic region was 3-D printed and filled with a homogeneous tissue-mimicking background. Two flexible antennas were placed on the skin, supported in place by the 3-D printed model, were used to measure S-parameters for both full and empty bladder models. Overall, this work provides a design for a life-sized pelvic phantom and demonstrates the potential for experimental testing and optimization of MW bladder sensing technologies. This work further establishes a novel experimental testbed to evaluate the viability of MW sensing of the bladder to support patients with urinary incontinence.

T04

# MICROFLUIDIC PHAGE DISPLAY PLATFORM FOR CANCER SPECIFIC PEPTIDE IDENTIFICATION AND TARGETED PHAGE DRUG CONJUGATE

**Jiarui Shen**[1], Maryam Tabrizian[1]

1 McGill University

Cancer remains one of the most fatal diseases globally, with 10 million deaths each year. In Canada alone, 45% of Canadians will be diagnosed with cancer in their lifetime, and 22% of Canadians will die from cancer. The high incidence and mortality rates of cancer underscore the urgency of improving diagnostic and therapeutic strategies.

Despite advances in targeted therapies, tumour heterogeneity and their ability to develop resistance continue to limit treatment efficacy. Phage display technology offers a powerful approach to identifying cancer-specific peptides, yet traditional methods often lack precision in recapitulating tumour microenvironments. To address this, we propose a Phage Display Microfluidics Chip (PDMC) platform to screen tumour spheroid targeting peptides and develop phage-based drug conjugates for precision therapy.

Our platform integrates a microfluidic chip capable of capturing 3D cancer tumoroids, mimicking in vivo conditions more accurately than conventional culture models. The chip enables phage display screening within a controlled microenvironment, identifying specific peptides targeting tumoroid. To validate the PDMC, we employ cultured melanoma tumoroids and patient-derived xenografts, ensuring physiologically relevant biopanning. In the future, identified peptides will be conjugated to therapeutic phages, enabling precise drug delivery while minimizing off-target effects.

The PDMC was designed in Fusion 360, and fluid dynamics were simulated using COMSOL Multiphysics. The device has been fabricated using SU-8 photolithography and PDMS moulding, and initial experiments with B16F10 melanoma spheroids confirm successful tumoroid capture. This work presents a scalable, high-throughput approach for personalized cancer therapy, offering a novel integration of microfluidics and phage display to improve cancer-specific targeting.

# LUNG-TARGETED LIPID NANOPARTICLES FOR ANTI-VIRUS THERAPY

**Yueyang Deng**[1], Mo Chen[1], Zhenlong Liu[1], Rongtuan Lin[1], Guojun Chen[1]

1 McGill University

Despite the encouraging clinical outcomes of lipid nanoparticles (LNP) for RNA delivery, several limitations associated with LNP remain. First, current LNP formulations lack good stability during lyophilization and storage, and thus require cold-chain storage and transportation, which significantly hinders the wide distribution and applications. Second, current LNP formulations exhibit insufficient in vivo stability, due to the fact that LNPs are formed by self-assembly of multiple molecules through weak interactions, such as hydrophobic and electrostatic interactions, which can be easily disrupted by many factors in vivo, including dilution, interactions with biomolecules, and physical changes (pH, ionic strength) in surrounding environments. Third, there is no active mechanism in the current LNP formulations to release cargos to function. Therefore, strategies to enhance the stability of LNP while promoting cargo release are heavily needed.

Here, we report an advanced LNP formulation with enhanced stability and responsive cargo release for gene delivery (Fig. 1). Specifically, lipid X is included for polymer incorporation (denoted as pLNP), increasing the LNP structure rigidity. Of note, the pLNP does not hinder the release of cargos because the polymer can be easily detached in endosomes (pH 5.5-6.5). Importantly, bio-responsive ionizable lipids are also incorporated in the pLNP, which can facilitate the degradation of pLNPs in the cytosol to release cargos. Our results showed that pLNPs displayed delayed clearance and excellent lung specific transfection capability after intravenous administration, which resulted in a remarkable anti-virus effect in virus-infected mice model with 5'pppRNA loading.

# HEAD CIRCUMFERENCE AND GROWTH OF THE HUMAN CEREBRAL CORTEX IN INFANCY : A NEUROIMAGING APPROACH

**Paula Toaca**[1,2], James Hengenius[1], Tomas Paus[1,3]

1 Centre Hospitalier Universitaire (CHU) Sainte-Justine

2 Department of Neuroscience, Faculty of Medicine of the University of Montreal

3 Department of Neuroscience and Psychiatry, Faculty of Medicine of the University of Montreal

During the first two years of life, the human brain undergoes rapid cortical expansion, reaching approximately 80% of its adult size. Brain growth is tightly associated with head growth, which follows non-linear and sex-dependant growth trajectories. Cross-sectionally, head circumference (HC) correlates strongly with brain size. However, the relationship between the trajectories of head growth and cortical growth is unknown. We analyzed 230 magnetic resonance imaging (MRI) scans from the NIH Pediatric Database (NIHPD), collected from birth to two years of age, across 90 infants. Maximum HC was manually measured on 1.5T MRI scans, and cortical surface area was extracted using neuroimaging tools to examine inter- and intra- subject trajectories. Additionally, we will ask whether trajectories of head growth during infancy predict cortical surface area in childhood. To answer this question, we have selected 3,257 participants from the Generation R Study, a Rotterdam-based longitudinal cohort. HC was measured at five time points between 2 and 13 months, with at least one MRI scan obtained at ~10 and/or ~15 years. In both samples, we will assess cortical surface area in 11 cortical regions, associated with genetic data, including unimodal (e.g., primary visual and motor cortices) and multi-modal (e.g., prefrontal cortex) areas. We hypothesize that overall growth relates differently to cortical growth in uni-modal versus multi-modal regions due to the different timing of their post-natal development (e.g., the temporal sequence of experience-driven dendritic growth). This study may provide new knowledge about early brain development and determine whether HC provides insights beyond global brain growth during infancy.

# NANOPARTICLES-MEDIATED INTRATUMORAL GENE EDITING TARGETING PD-L1 AND GALECTIN-9 FOR IMPROVED CANCER IMMUNOTHERAPY

**Tianxu Fang**[1], Yueyang Deng[1], Mo Chen[1], Tianwen Luo[1], Tianqin Ning[1], Guojun Chen[1]

1 McGill University

PD-L1, a typical immune checkpoint expressed on tumor cells, reduces the effectiveness of T cell-mediated killing, which is further aggravated by Galectin-9 (Gal-9) co-expression through the TIM3/Gal-9 pathway. Although immune checkpoint inhibitors have shown promise in cancer therapy, limitations remain including low response rate, systemic toxicities, and the need of frequent treatments. Here, we described a dual knockout approach targeting PD-L1 and Gal-9 in tumor cells, achieved by nanoparticle-assisted CRISPR-Cas9 delivery, aimed at improved cancer immunotherapy. A calcium phosphate nanoparticle (CaP NP) was engineered for co-delivery of CRISPR-Cas9/sgRNA ribonucleoprotein (RNP) and initiation of anti-tumor immunity. Intratumoral administration of RNP-loaded CaP NPs effectively knocked out PD-L1 and Gal-9 in tumor cells, evoking robust anti-tumor immunity. Additionally, Ca2+ overload due to the degradation of CaP NPs led to release of damage-associated molecular patterns (DAMPs) signals, further enhancing T-cell-mediated antitumor immune responses. Our results demonstrated that this treatment effectively evoked both local and systemic anti-tumor immune responses, significantly inhibiting the growth of primary and distant tumors in mouse models. Importantly, local treatment also altered the phenotypes of circulating tumor cells, as a substantial of circulating tumor cells originated from RNP-CaP-treated primary tumors and exhibited dual knockouts, which led to reduced lung metastasis.

# CELLULAR STRESS AND POLYGLUTAMINE EXPANSIONS DISRUPT HUNTINGTIN MEDIATED AXONAL TRANSPORT

**Lale Gursu**[1], Adam Hendricks[1]

1 McGill University

Defective axonal transport is a key feature of Huntington's disease, where polyglutamine expansions in huntingtin (HTT) alter interactions between cargoes, motor proteins, and adaptors. Neuroinflammatory stress, particularly through interferon gamma (IFN-γ), may further disrupt these interactions, but how they change at the single-cargo level remains unclear. Here, we use DNA-PAINT super-resolution microscopy to quantify the recruitment of transport machinery to axonal cargoes in fixed neurons differentiated from embryonic stem cells (ESCs).

Neurons expressing 30Q or 81Q HTT were treated with IFN-γ or vehicle and fixed. BDNF-coated quantum dots were used to pulse-label internalized cargoes prior to fixation. We performed DNA-PAINT against multiple transport-related proteins and applied localization-based fluorescence correlation spectroscopy (lbFCS) to measure protein copy numbers on individual axonal cargoes.

Preliminary results suggest that IFN-γ treatment increases the number of dyneins associated with cargoes, with distinct patterns observed between 30Q and 81Q neurons. These findings support a model in which inflammatory stress alters cargo composition in a polyQ-dependent manner, potentially contributing to transport dysregulation in Huntington's disease. This approach allows direct visualization and quantification of transport protein organization at the single-cargo level in neurons.

# SIMULATION-DRIVEN OPTIMIZATION OF SPIRAL NAVIGATOR TRAJECTORIES FOR ENHANCED MRI MOTION CORRECTION

**Benjamin Beggs**[1,2], Christine Lucas Tardif[2,3,4]

1 Department of Biological and Biomedical Engineering, McGill University, Montreal, Canada
2 McConnell Brain Imaging Centre, Montreal Neurological Institute, Montreal, Canada
3 Department of Biomedical Engineering, McGill University, Montreal, Canada
4 Department of Neurology and Neurosurgery, McGill University, Montreal, Canada

Magnetic resonance imaging (MRI) is widely used in clinical and research settings, but patient motion can degrade image quality, impair quantitative analysis, and necessitate costly rescans. Correcting for patient motion typically requires continuous tracking of subject motion throughout a scan. Navigators—periodic, sparsely sampled MRI acquisitions during an imaging protocol—enable subject motion tracking without external equipment, which can be cumbersome to set up and integrate into the MRI workflow. However, navigators may require extending overall scan time, increasing the window for patient motion. Thus, efficient navigators that maximize motion tracking accuracy while minimizing acquisition times are highly desirable. Navigator acquisition time is largely determined by its k-space trajectory, the 'path' taken through the frequency-space MRI data is acquired in. Spiral trajectories are attractive as they efficiently utilize the MRI system's gradient hardware to maximize sampling coverage, although they are typically tuned using heuristic methods rather than systematic optimization approaches. This work presents a simulation-driven method to optimize spiral navigator trajectories to allow for more time-efficient navigators with greater motion tracking accuracy. The approach was applied to 3D brain imaging and can be easily adapted for other MRI applications. Trajectories were tested under controlled motion scenarios—encompassing translation-only, rotation-only, and combined movements. Simulations were based on open access patient head motion data measured during MRI scans to replicate realistic ranges and types of head motion. The Colin 27 brain volume was used as a digital phantom for simulations. Navigator-derived motion estimates were quantitatively assessed by evaluating metrics such as mean error, error variance, and confidence intervals across different motion profiles and noise levels. An optimized 3-4ms spiral navigator trajectory for 3D brain imaging is presented. It demonstrates superior motion characterization performance to spiral trajectories of similar duration parameterized through heuristic methods.

T14

# RSL3-LOADED NANOPARTICLES AMPLIFY THE THERAPEUTIC POTENTIAL OF COLD ATMOSPHERIC PLASMA

**Tianwen Luo**[1], Mo Chen[1], Yueyang Deng[1], Tianxu Fang[1], Guojun Chen[1]

1 Department of Biomedical Engineering, Rosalind & Morris Goodman Cancer Institute, McGill university

Cold atmospheric plasma (CAP) has exhibited exciting potential for cancer treatment. Reactive oxygen and nitrogen species (RONS), the primary constituents in CAP, contribute to cancer cell death by elevating oxidative stress in cells. However, several intrinsic cellular antioxidant defense systems exist, such as the glutathione peroxidase 4 (GPX4) enzyme, which dampens the cell-killing efficacy of CAP. RAS-selective lethal 3 (RSL3), also known as a ferroptosis inducer, is a synthetic GPX4 inhibitor. Therefore, we hypothesized that RSL3 can amplify CAP-induced cell death by inhibition of GPX4. In this study, we showed that RSL3 loaded in poly (ethylene glycol)-block-poly(lactide-co-glycolide) (PLGA-PEG) nanoparticles can enhance CAP-induced cell deaths in 4T1 tumor cells. Furthermore, the combination of CAP and RSL3 also promoted cancer immunogenic cell death (ICD), induced dendritic cell (DC) maturation, and macrophage polarization, initiating tumor-specific T-cell mediated immune responses against tumors. For in vivo application, RSL3@NP was co-delivered with CAP via injectable Pluronic hydrogel. In 4T1-bearing mice, hydrogel-mediated delivery of CAP and RSL3-loaded nanoparticles can effectively elicit potent anti-tumor immune responses and inhibit tumor growth.

# UNDERSTANDING THE ROLE OF KINESIN-3 MOTORS USING OPTOGENETIC INHIBITORS

**Sahil Nagpal**[1], Maud Verdier[2], Adam Hendricks[1]

1 Department of Bioengineering, McGill University Canada

2 Department of Biomedical Engineering and Health, Episen, Universite´ Paris-Est Creteil, France

Each cargo in a cell employs a unique set of motor proteins for its transport. In our previous work, we developed optogenetic inhibitors for kinesins-1, -2, and -3 and dynein motors and looked at the effect of inhibition on Rab5-positive early endosomes, Rab7-positive late endosomes, and lysotracker-positive lysosomes. We found that the directionality of transport is controlled through regulating kinesin-1 and dynein activity. On vesicles transported by several kinesin and dynein motors, motility can be directed by modulating the activity of a single type of motor on the cargo. In this work, we specifically focus on the role of kinesin-3 motors in transport. There are multiple types of kinesin-3 motors in a cell, but not much is known about their function. We developed optogenetic inhibitors targeting different types of kinesin-3 motors, namely KIF1B, KIF13B and KIF16B motors and looked at the effect of this inhibition on Rab11-positive recycling vesicles, Rab6-positive secretory vesicles and lysotracker-positive lysosomes. We found that that there was a strong decrease in the motility of Rab6 vesicles with a shift towards peripheral localization of cargoes in cells upon inhibition of any of the kinesin-3 motors. For Rab11 vesicles, there was no change in motility upon KIF1B and KIF13B inhibition, and a decrease in motility with KIF16B inhibition with a subsequent inward shift in cargoes for all the conditions. For lysosomes, we saw a decrease in motility with an inward shift upon inhibition of KIF1B and KIF13B inhibition, and no change in motility in case of KIF16B inhibition. Overall, our new data reveals that kinesin-3 has varied roles for different cargoes in cells and plays an integral role in regulation of intracellular transport.

T18

# INVESTIGATING THE IMPACT OF AIR POLLUTANTS ON MUCUS PROPERTIES AND MUCOCILIARY CLEARANCE USING AN AIRWAY-ON-A-CHIP MODEL

**Shu Yuan Zhang**[1], Jeremy Newton[2], Edmond W. K. Young[2], Caroline E. Wagner[1],

1 Department of Bioengineering, McGill University

2 Department of Mechanical & Industrial Engineering, University of Toronto

Air pollution is a major global health concern associated with acute and chronic respiratory diseases, with preliminary evidence suggesting that pollutant exposure can exacerbate the severity of respiratory diseases and viral infections by compromising airway defense mechanisms. The respiratory mucus barrier, whose primary polymer components are mucin glycoproteins, plays a critical role in trapping and clearing pathogens via mucociliary clearance (MCC). This study aims to investigate whether common air pollutants, including ozone ($O_3$), nitrogen dioxide ($NO_2$), and particulate matter ($PM_{2.5}$), compromise mucus barrier integrity through altering mucin secretion, MCC function, and/or mucus rheology. Using an airway-on-a-chip (AoC) model, we cultured Calu-3 airway epithelial cells under static air-liquid interface (ALI) conditions to optimize cell growth and validate differentiation into mucin-producing goblet cell and ciliated cell phenotypes. Immunofluorescence microscopy results confirmed the formation of an intact epithelial barrier with mucus production. As future steps, we will evaluate the impact of pollutant exposure on mucin production and MCC efficiency within the AoCs using an integrated airflow system. Additionally, micro- and macro-rheological techniques, including single-particle tracking (SPT) and small-amplitude oscillatory shear (SAOS), will be employed to evaluate potential changes in mucus rheology upon cell exposure to pollutants. The findings from this study will advance our understanding of the biophysical mechanisms through which air pollutants interact with airway mucosal barriers. We expect that this will offer insight into the kinetics of the early stages of respiratory infection, and guide public health recommendations for mitigating the impact of air pollution on respiratory health.

T21

# A DIGITAL TWIN TECHNIQUE USING EXTERNAL OBSERVATIONAL DATA TO REDUCE SAMPLE SIZES IN CLINICAL TRIALS ON ALZHEIMER'S DISEASE

**Daniel Andrews**[1,2], D. Louis Collins[1,2,3]

1 Department of Biomedical Engineering, McGill University, Montreal, QC, Canada

2 McConnell Brain Imaging Centre, Montreal Neurological Institute, McGill University, Montreal, QC, Canada

3 Department of Neurology and Neurosurgery, McGill University, Montreal, QC, Canada

Background: Randomized placebo-controlled trials (RCTs) are the gold standard to evaluate efficacy of new treatments for Alzheimer's disease (AD). For example, the FDA approved the anti-amyloid drug lecanemab following CLARITY AD, Eisai's positive Phase 3 RCT. However, recruiting enough trial participants is difficult and expensive. Fortunately, historical patient data from external studies of a disease can help populate RCTs. We propose a trial framework that, for each participant, sources "digital twins" from an external study. Using computer-simulated trials mimicking CLARITY AD design parameters, we show that our digital twin trial (DTT) has higher power than a conventional RCT.

Methods: A continuous time linear mixed model mapped CDRSB change-from-baseline (CDRSBΔbl) trajectories in 670 ADNI participants satisfying CLARITY AD inclusion criteria. To simulate trial "recruits", we resampled and added noise to participants' data, generating a sample of recruits who we randomized to "drug" and "placebo" groups. We calculated recruits' CDRSBΔbl scores at 18 months and simulated the drug effect as a 25% reduction in CDRSBΔbl. For each recruit in our DTT, we used Gower's distance on demographic and clinical baseline variables to identify 20 most-similar ADNI participants (digital twins) from our 670. Each ADNI participant's 18-month CDRSBΔbl was calculated using the model. A z-score was then calculated for each DTT recruit's 18-month CDRSBΔbl relative to their digital twins. T-tests evaluated DTT drug vs. placebo group difference in mean z-score and, separately, RCT group difference in mean 18-month CDRSBΔbl. Power is the percentage of 1,000 trial simulations with a statistically significant group difference.

Results: 90% power was reached with ~500 fewer recruits in simulated DTTs (~1,600 recruits) compared to RCTs (~2,100 recruits).

Conclusions: DTTs might require substantially fewer recruits than conventional RCTs, accelerating trials in AD and rare diseases.

T22

# MAKING THE INVISIBLE VISIBLE: REVERTING CLEARED LIGHT-SHEET FLUORESCENT MICROSCOPY SAMPLES FOR MULTI-DIMENSIONAL TISSUE ANALYSIS

**Leonor Simoes**[1,2,3], Nika Gvazava[2], Iran Augusto[2], Valeriia Skoryk[2], John Stegmayr[2], Darcy Wagner[1,2,3]

1 McGill University RI-MUHC, Meakins-Christie Laboratories, Block E, RI-MUHC, EM3.2219, 1001 Bd Décarie, Montréal, QC H4A 3J1

2 Lund University, Biomedicinskt centrum, Sölvegatan 17, 223 62 Lund.

3 Universidad Francisco de Vitoria, Carretera Pozuelo a, Av de Majadahonda, Km 1.800, 28223 Madrid.

Whole-organ and tissue imaging at high cellular and molecular resolution is possible with light-sheet fluorescence microscopy (LSFM) following optical clearing (OC). While this technique overcomes challenges of traditional histology by providing true 3D data, it is limited by the number of phenotypic markers available due to the use of hydrophobic refractive index-matching solutions needed for imaging (e.g., ethyl cinnamate). As a result, techniques requiring aqueous environments, such as antibody multiplexing or RNA-based analyses, are not feasible. Samples are typically discarded following imaging due to the absence of protocols to reverse OC. Furthermore, current OC protocols use organic solvents that fail to preserve endogenous fluorescent protein signals (e.g. GFP) due to their denaturing effects. This project aimed to identify more suitable chemicals that preserve endogenous fluorescent proteins and reverse OC to enable additional analyses of previously imaged tissues.

We used the methanol-based iDISCO+ protocol to clear mouse lungs, followed by LSFM imaging. The lungs were segmented, and a chemical screen of organic solvents was conducted to identify compounds capable of removing ethyl cinnamate while preserving tissue architecture and epitopes for antibody staining. Samples later underwent standard tissue processing and paraffin embedding for histological scoring and immunofluorescence qualification. Alcohol-based solvents best preserved tissue structure compared to polar aprotic solvents, though epitope preservation varied with methanol-based reverse OC.

Building on these findings and existing evidence that iDISCO+ does not preserve endogenous fluorescence, we developed a new OC protocol, isoDISCO. Using a simplified system with recombinant GFP embedded in agarose, we tested the top-performing chemicals screened above. Isopropanol emerged as the most effective substitute solvent and was validated in mouse models across various tissues, including lung, brain, and embryos. isoDISCO effectively preserves fluorescence and enables tissue clearing for LSFM.

Future work will integrate spatial transcriptomics and multiplexed staining for multidimensional analysis of LSFM-imaged tissues.

T23

# NANOGHOSTS: NOVEL TOOLS FOR BONE TISSUE ENGINEERING

**Antoine Karoichan**[1,2], Celine Agnes[2,3], Ling Li[3], Bettina Willie[1,2], Maryam Tabrizian[1,3]

1 Faculty of Dental Medicine and Oral Health Sciences, McGill University, Montreal, QC, Canada
2 Shriners Hospital for Children, Montreal, QC, Canada
3 Department of Biomedical Engineering, McGill University, Montreal, QC, Canada

Mesenchymal stem cell-derived extracellular vesicles (MSC-EVs) hold promise for bone tissue engineering due to their regenerative, immunomodulatory, and anti-inflammatory properties. However, clinical translation is hampered by challenges such as low yield, high heterogeneity, and lack of standardization. Recently, nanoghosts (NGs) have emerged as bioactive EV mimetics derived from downsizing ghost cells. NGs retain the surface functionalities of parent cells while offering more standardized production and higher yield than EVs. This study explores the osteogenic potential of NGs synthesized from MSCs (MSC-NGs) for bone tissue engineering. MSC-NGs were produced by hypotonic lysis of MSCs followed by sonication to form EV-like nanoparticles. Characterization via nanoparticle tracking analysis, zeta potential, electron microscopy, and protein assays confirmed that MSC-NGs share colloidal and vesicular properties with MSC-EVs. In vitro, MSCs treated with MSC-NGs under osteogenic conditions exhibited significantly enhanced osteogenic differentiation and mineralization compared to MSC-EVs, as demonstrated by ALP activity, osteogenic marker qPCR, and alizarin red staining. The current work also consists of assessing the effects of MSC-NGs in vivo. The study investigates the hypothesized outcomes that the administration of MSC-NGs at the site of a bone fracture in mice models will lead to faster bone healing and bridging compared to controls.

# CLASSIFICATION OF SINGLE EXTRACELLULAR VESICLE PROFILES IN BRAIN CANCER USING RAMAN SPECTROSCOPY COUPLED WITH MACHINE LEARNING AND DEEP LEARNING

**Carolina del Real Mata**[1],Yao Lu[1], Mahsa Jalali[1], Marjan Khatami [2], Laura Montermini[2], Nada Jabado[2], Januzs Rak[2], Livia Garzia[2], Danilo Bzdok[3], Sara Mahshid[1]

1 Dept. of Bioengineering, McGill University, Montreal, QC. Canada.
2 Research Institute of the McGill University Health Centre, Montreal, QC. Canada.
3 Dept. of Biomedical Engineering, McGill University, Montreal, QC. Canada.

The rapid growth of complex biological data are a results of the constant innovations in biosensing technologies. Surface-enhanced Raman spectroscopy (SERS)-based optical sensors enable the generation of molecular fingerprints from samples like extracellular vesicles (EVs)—nanoscale vesicles shed by cells, including cancerous ones. EVs carry molecular cargo reflective of their cellular origin, making them promising biomarkers for non-invasive diagnostics such as liquid biopsy. However, analyzing single-EV SERS fingerprints is challenging due to data complexity.

To address this, we apply machine learning (ML) and deep learning (DL) techniques. Computational models now enable researchers to handle large, complex biological datasets and have shown promise in cancer detection and monitoring. In this study, we compare the performance of ML/DL models—random forests, support vector machines, and convolutional neural networks—for two cancer detection tasks using EV data: (i) multi-cell line classification and (ii) binary classification of cancerous vs. non-cancerous samples.

We use a rich SERS dataset of EVs collected on a nanostructured platform with single-EV resolution, covering 7 cell lines, 10 healthy controls, and 10 cancer patient samples. Medulloblastoma and Glioblastoma serves as cancer models. Hyperparameters were optimized, and cross-validation applied to reduce overfitting. We evaluated performance based on accuracy as sample size increased and receiver operating characteristic (ROC) curves. Data preprocessing and augmentation techniques, such as smoothing, were also tested to enhance model performance. The application of ML models in diagnostics has immense potential for overcoming the challenges posed by the analysis of complex biological data, like EV populations, which could be pivotal on advancing personalized medicine technologies.

# MULTIPHASE RESERVOIR SUBCIRCUIT FOR MICROFLUIDIC CHAIN REACTION OF IMMISCIBLE AND MISCIBLE MULTIPHASE LIQUIDS IN CAPILLARIC CIRCUITS

**Geunyong Kim**[1,2], Molly L. Shen[1,2], Andy Ng[1,2], David Juncker[1,2]

1 Biomedical Engineering Department, McGill University, Montreal, Quebec, Canada

2 Victor Phillip Dahdaleh Institute of Genomic Medicine, McGill University, Montreal, Quebec, Canada

Capillaric circuits (CCs) recently enabled scalable autonomous liquid delivery on a 3D-printed chip by microfluidic chain reaction (MCR), automating assays for bacterial and viral pathogens, and blood coagulation. However, the CCs were unable to work with low-surface-tension liquids (LSLs) due to their low contact angles ($\theta < 30°$) on the CCs that were specifically treated for handling water. Multiphase control is often required in biochemical applications such as DNA extraction and droplet microfluidics, necessitating a new liquid controlling approach. Here, we present multiphase stop valve (MSV), that exploits the immiscibility of LSLs (oil) with water for multiphase fluid control in CCs. Utilizing water as a control unit based on its high surface tension (72.8 mN/m) and functional contact angle ($\sim 30° < \theta < \sim 50°$), the valve enables handling of water-immiscible LSLs on CCs having a single surface chemistry for water. Then, we introduce a multiphase reservoir subcircuit (MRS) that (i) functions for both immiscible and miscible LSLs and (ii) can be integrated into a MCR for the preprogrammed delivery of LSLs. The MRS enables the control of any LSLs by using water plugs, and an air trap that prevents a miscible LSL from leaking into the main channel, thereby keeping CCs functional. The control by the MRS is based on water plugs; therefore, multiphase controls of water and LSLs can be implemented together on CCs having a surface chemistry tuned for water. Using the MRS, we expands the MCR to a multiphase MCR with the capacity of scalable sequential delivery of water and any LSLs on a single chip. Multiphase MCRs could broaden the applications of CCs for sample preparation, assays and synthesis requiring multiple phases.

# SPATIAL TRANSCRIPTOMICS DATA ANALYSIS OF LUNG TUMOR TISSUE ACQUIRED WITH MERFISH: DEVELOPMENT OF AN INTERACTIVE PLATFORM FOR IDENTIFYING CELL TYPES AND GENE EXPRESSION PATTERNS

**Isabel Carballo Rueda**[1], Darcy Wagner[2]

1 Facultad de Ciencias Experimentales, Universidad Francisco de Vitoria, Ctra., Madrid, España.
2 Research Institute of the McGill University Health Centre, Montreal, Canada

Spatial transcriptomics enables the identification of gene expression patterns along with their spatial localization within tissues. MERFISH (Multiplexed Error-Robust Fluorescence In Situ Hybridization) stands out for achieving subcellular resolution through a robust barcoding system. This makes it effective for single-cell resolution of RNA transcripts while preserving spatial information, essential for studying tissue architecture and cell-to-cell interactions.

This project analyzes spatial transcriptomics data from lung tumor tissue to identify cell types and characterize gene expression patterns in diseased states. Given the lung's complexity, this approach allows for high-resolution mapping of its heterogeneity. It is particularly relevant for diseases such as pulmonary fibrosis and lung cancer, where understanding spatial organization of gene expression is critical to improving our understanding of disease.

To support exploration by biologists and clinicians, an interactive interface is being developed in Python using libraries such as Scanpy and Pandas. The platform enables visualization and interpretation of MERFISH data through analytical tools including UMAP for dimensionality reduction, revealing patterns and clusters of distinct cellular populations. These clusters are further analyzed using dot plots and heatmaps to explore gene expression signatures linked to specific lung regions or cell subtypes.

By centralizing these tools in an accessible interface, the platform helps generate biologically meaningful hypotheses. Cell type identification from spatial transcriptomics typically requires programming skills, knowledge of gene expression, and significant computational resources, posing barriers for many researchers. This platform addresses such challenges by providing intuitive visualizations and interactive features, allowing users to explore clusters and expression patterns without coding, thus broadening access to MERFISH data interpretation.

T32

# NUCLEAR STIFFNESS REGULATES CELLULAR SENESCENCE VIA YAP-DEPENDENT MECHANOTRANSDUCTION

**Luv Kishore Srivastava**[1], Ajinkya Ghagre[2], Allen Ehrlicher[1]

1 Department of Bioengineering, McGill university

2 Department of biomedical engineering, University of British Columbia

Alterations in nuclear mechanics are associated with aging and age-related diseases, yet the mechanistic connection between nuclear compressibility and cellular senescence remains unclear. Here, we demonstrate that nuclear compressibility modulates cellular senescence through the mechanotransduction pathway regulated by Yes-associated protein (YAP) in both 2D single-cell cultures and 3D spheroid models. By employing human dermal fibroblasts (HDF) and Hutchison-Gilford Progeria Syndrome (HGPS) cells, we found that decreased nuclear compressibility, driven by elevated lamin A/C expression or progerin presence, significantly reduces nuclear localization of YAP. This reduction subsequently diminishes human telomerase reverse transcriptase (hTERT) expression, thereby accelerating cellular senescence, quantified by increased senescence-associated β-galactosidase (SA-β-gal) activity. Conversely, enhancing nuclear compressibility through lamin A/C silencing or mechanical compression increased nuclear YAP localization, elevated hTERT expression, and delayed senescence. Pharmacological modulation further validated the critical role of YAP nuclear translocation in regulating senescence biomarkers. Our findings establish nuclear compressibility as a crucial regulator of cellular senescence via the YAP–hTERT signaling axis in both 2D single-cell and 3D spheroid environments, offering novel mechanistic insights into aging and suggesting potential therapeutic targets for age-related pathologies.

# SIZE PHOTOMETRY AND FLUORESCENCE IMAGING (SPFI) FOR THE HIGH THROUGHPUT SINGLE PARTICLE LIPID NANOPARTICLE CHARACTERISATION

**Lan Anh Huynh**[1], Andreas Wallucks[1], David Juncker[1]

1 McGill University

Lipid nanoparticles (LNPs) are synthetic nanoparticles of sizes between 50-200nm[1] with immense potential as versatile carrier vesicles of nucleic acids for vaccine development, gene therapy, and RNA therapeutics[2]. The development of new LNP formulations require optimisation of various physical and chemical critical process parameters (CPPs) to ensure a high cargo loading efficiency as well as high reproducibility of cargo delivery to recipient cells[1,3]. The current most common characterization method is dynamic light scattering (DLS)[4-6], which is a bulk measurement based on the detection of light intensity scattered by the Brownian motion of LNPs. DLS provides an average size and polydispersity index (PDI) value; however, it cannot differentiate individual LNP subpopulations and struggles with highly disperse samples. On the other hand, the gold standard for high accuracy single LNP sizing is cryo-transmission electron microscopy. While being the most accurate, this method suffers from extremely low throughput and requires extensive sample preparation. Other methods such as nanoparticle tracking analysis (NTA) and microfluidic resistive pulse sensing (MRPS) are gaining interests however none can combine high accuracy single particle sizing with high sample throughput whilst incurring a low running cost. Interferometric scattering (iSCAT) microscopy is a label-free, single particle, optical sizing technique that can be implemented on standard inverted fluorescence microscopes, and can achieve sensitivities exceeding that of MRPS and NTA, as recently shown on extracellular vesicles[7]. Here we demonstrate that iSCAT is able to characterize LNP size distributions and can be combined with a fluorescent RNA stain to determine LNP cargo loading efficiency. We show preliminary data revealing the effect of dialysis (a post processing fabrication step), total flowrate and cargo size on the size distribution. We further showcase recent progress in developing an iSCAT rapid screening platform for LNPs to systematically optimise different formulations for diverse cargos in a high throughput manner.

1 McMillan, C. et al. Tailoring lipid nanoparticle dimensions through manufacturing processes. RSC Pharm 1, 841-853 (2024). https://doi.org/10.1039/d4pm00128a

2 Hald Albertsen, C. et al. The role of lipid components in lipid nanoparticles for vaccines and gene therapy. Adv Drug Deliv Rev 188, 114416 (2022). https://doi.org/10.1016/j.addr.2022.114416

3 Shepherd, S. J. et al. Throughput-scalable manufacturing of SARS-CoV-2 mRNA lipid nanoparticle vaccines. Proc Natl Acad Sci U S A 120, e2303567120 (2023). https://doi.org/10.1073/pnas.2303567120

4 Vargas, R. et al. Dialysis is a key factor modulating interactions between critical process parameters during the microfluidic preparation of lipid nanoparticles. Colloid and Interface Science Communications 54, 100709 (2023). https://doi.org/https://doi.org/10.1016/j.colcom.2023.100709

5 Xu, Y. et al. AGILE platform: a deep learning powered approach to accelerate LNP development for mRNA delivery. Nature Communications 15, 6305 (2024). https://doi.org/10.1038/s41467-024-50619-z

6 Li, S. et al. Payload distribution and capacity of mRNA lipid nanoparticles. Nature Communications 13, 5561 (2022). https://doi.org/10.1038/s41467-022-33157-4

7 Wallucks, A., DeCorwin-Martin, P., Shen, M. L., Ng, A. & Juncker, D. Size photometry and fluorescence imaging of immobilized immersed extracellular vesicles. Journal of Extracellular Vesicles 13, e12512 (2024). https://doi.org/https://doi.org/10.1002/jev2.12512

T35

# MODULATING IONIC STRENGTH TO OPTIMIZE GELATION OF ECM-BASED HYDROGELS FOR LUNG TISSUE REGENERATION

**Lucia Pena López**[1,2], Simran Jaffer[1], Darcy Wagner[1]
1 McGill University
2 Universidad Francisco de Vitoria

Chronic obstructive pulmonary disease (COPD) poses a major global health challenge, affecting millions and ranking among the leading causes of death and disability. Characterized by chronic inflammation and irreversible damage to the lung parenchyma, COPD lacks therapies capable of reversing structural deterioration. This has driven growing interest in regenerative medicine, particularly ECM-based hydrogels that mimic the lung's biochemical environment and support tissue repair.

These hydrogels are primarily composed of structural proteins like collagen, which self-assemble into fibrillar networks under physiological conditions, forming a 3D matrix that supports cell adhesion and migration. This gelation process is highly sensitive to ionic interactions, which can be modulated by adjusting the buffer composition. While chloride ions are known to be essential for type IV collagen network formation, their role in type I collagen, responsible for fibrillar structures, is less understood.

This project focuses on optimizing ECM hydrogel gelation from decellularized porcine lung tissue, which contains both type I and IV collagen. To investigate ionic effects, we first used purified collagen type I from rat tails and varied sodium and chloride ion concentrations from 25 to 400 mM, including 137 mM as a physiological control. Two collagen concentrations were tested to assess how ionic strength affects gelation. Results showed that increasing chloride concentrations accelerated gelation and increased its magnitude. Interestingly, low salt concentrations failed to induce gelation at high collagen content but succeeded at lower concentrations.

Our next step is to apply these ionic conditions to dECM solutions. Turbidity assays will monitor gelation kinetics, rheometry will assess mechanical properties, and SEM will evaluate microstructure. Biocompatibility studies will examine cell adhesion and viability. Ultimately, this work aims to improve the consistency of ECM hydrogels and support their application in regenerative strategies for COPD.

# EVOLVING DIVERSE GENE NETWORKS

**Qichen Huang**[1], Nacer Eddine Boukacem[1], Philippe Martin[1], Paul François[1]

1 University of Montreal, Mila Quebec AI Institute

CGene regulatory networks (GRNs) underlie key developmental processes, yet the landscape of diverse network architectures capable of achieving the same function remains largely unexplored. We propose a novel approach using a Generative Flow Network (GFlowNet) to efficiently explore and evolve GRNs that fulfill specific developmental tasks. We designed the GFlowNet to perform both global search and local refinements in the space of network configurations. Initially applied to classical genetic oscillators, GFlowNet efficiently navigates the state space, where each state represents a directed network with edges corresponding to gene regulation. Our approach reveals that, for a given target function multiple distinct topological motifs can achieve the desired behavior. Moreover, even within a fixed network topology, diverse interaction strengths (weights) can yield similar developmental patterns, underscoring the inherent flexibility of GRNs. Furthermore, we extend our analysis to more complex functions in developmental patterning of somitogenesis, we uncover common core modular motifs that emerge during network evolution, and find diverse design principles and evolutionary trajectories from simple oscillator network to segmentation network. Dimensionality reduction techniques further help us visualize these evolutionary pathways, aligning our findings with the core and periphery hypothesis of network evolution. Additionally, our exploration into larger networks indicates that increased node counts contribute to enhanced robustness and diversity, as more weight configurations within a given topology can produce similar target patterns. Overall, our results demonstrate that the generative model (GFlowNet) efficiently explores GRN configurations to identify both conserved and diverse motifs, offering new insights into the evolutionary plasticity of genetic networks and paving the way for the rational design of synthetic networks with improved performance and robustness.

# POROUS POLY(ETHYLENE GLYCOL) DIACRYLATE HYDROGEL- BASED INKS FOR HIGH-RESOLUTION LOW-COST LCD 3D PRINTING OF MICROFLUIDICS

**Justin de Vries**[1], Houda Shafique[1], Emilie Johnson[1], David Juncker[1]

1 McGill University

Liquid crystal display (LCD) 3D printing has emerged as an alternative to conventional digital light processing (DLP) printing, with the benefit of low cost (~US$150-600), high pixel number (>94 M), and small pixel size (17-50 µm). However, LCD 3D printers suffer from reduced irradiance and red-shifted emission wavelengths (~405 nm), thus requiring tailored inks. Here, we optimize several poly(ethylene glycol) diacrylate (PEGDA) hydrogel-based inks, both with and without polyacrylamide (PAAm), for LCD 3D printing and benchmark them for high-resolution fabrication of microfluidics. We formulated 70% water content hydrogel inks, with 3 different photoabsorber candidates: Quinoline Yellow (QY), tartrazine, and microemulsions of water-insoluble 2-isopropylthioxanthone (ITX). The Jacobs working curve was established for each ink formulation, finding optimal penetration depths of 34 µm and 58 µm for the PEGDA and PAAm/PEGDA hydrogel inks with QY, respectively. Free-standing, single-layer membranes of ~20 µm thickness could be 3D-printed for each optimized ink formulation with mean dimensional accuracies between 74-91%. Finally, we designed a multimaterial microfluidic dialysis device and employed a print-pause-print strategy to integrate the porous hydrogel-based inks with solid inks. Selective permeability of the printed hydrogels in the dialysis device was confirmed via time-course diffusion of a small Rhodamine B tracer (479 Da) but exclusion of a large IgG antibody (~160 kDa).

# ANALOGUE BAT: A RAPID, RESOURCE-EFFICIENT PLATFORM FOR POINT-OF-CARE DIAGNOSTICS

**Breona Martin**[1], Geunyong Kim[1], Houda Shafique[1], Andy Ng[1], and David Juncker[1]

1 McGill University

Rapid biomarker detection could improve prehospital triage for traumatic brain injury (TBI). S100B, currently included in Scandinavian guidelines, supports decisions about hospital transport after head trauma. However, most point-of-care (POC) technologies either lack sensitivity or require bulky instrumentation, limiting their use in emergency and low-resource settings.

This project introduces the Analogue Brownian Affinity Trap (BAT) assay: a novel diagnostic platform that uses microchannel “traps” embedded in a solid PEGDA membrane to enhance protein capture. As reagent flows through the channels, target molecules collide with functionalized walls, improving binding via increased surface area and reduced diffusion distances compared to conventional ELISA.
The 3D-printed membrane is arranged as an array aligned to a 384-well ELISA plate. Manual dipping of the array into preloaded wells drives convective flow, enhancing transport without pumps or electronics.

The project includes: (1) membrane design and fabrication for optimal flow and capture, (2) optimization of a flow-through ELISA for S100B, and (3) plasma compatibility testing. Early results show successful membrane fabrication and initial ELISA integration. While pore geometry is not yet reproducible, initial trials confirm feasibility. BAT offers a promising path toward rapid, scalable biomarker detection for prehospital and global health applications.

T42

# DEVELOPMENT OF SPHEROID MODELS TO MIMIC THE VULNERABLE ATHEROSCLEROTIC PLAQUE MICROENVIRONMENT

**Ibukunoluwa Naiyeju**[1], Dr Stephanie Lehoux[2], Professor Maryam Tabrizian[1,3]

1 Department of Biological & Biomedical Engineering, McGill University, Montreal, Canada
2 Lady Davis Institute for Medical Research, McGill University, Montreal, Canada
3 Faculty of Oral Health & Dental Sciences, McGill University, Montreal, Canada

Atherosclerosis is a chronic, systemic, inflammatory disease associated with the build-up of fatty deposits ("plaques") in arteries when low-density lipoproteins (LDL) and cholesterol gain access into the subendothelial space due to the compromised nature of the injured arterial endothelium. There, these foreign macromolecules kickstart an inflammatory signalling cascade. In existing literature, there is a dearth of characterized co-culture spheroid (3D) models of the atherosclerotic plaque to provide insight into this inflammatory process. To address this knowledge gap, we have developed co-culture spheroid models treated with oxidized LDL as a scalable cell-based model for atherosclerosis research.

The spheroids were fabricated using THP-1-derived M0-macrophages and human coronary artery smooth muscle cells in agarose molds at a 1:1 co-culture ratio. Spheroids were treated with oxidized LDL (20-40 µg/ml) for 1 hour and 3 hours respectively, and subsequently maintained with 50%-50% RPMI & SMC media. AlamarBlue assay, confocal microscopy imaging and qT-PCR were used to assess spheroid metabolic activity, composition, and gene expression respectively over 10 days.

The lipid-treated spheroid groups show an increase in proliferation from D3 to D7 and a general upregulation of genes (fibronectin, elastin, connexin 43, ABCA-1 & CD36) associated with the microenvironment of the vulnerable atherosclerotic plaque. Confocal microscopy is expected to provide additional insights into the impact of lipid treatment on spheroid size & composition. In conclusion, this study demonstrates that spheroid models show the potential of mimicking the microenvironment of the vulnerable atherosclerotic plaque. Vital knowledge about the relevant parameters which can enhance model design efficiency and reproducibility will be gained as future investigations into protein and cytokine expression are conducted.

T43

# ENZYMATIC CROSSLINKING OF DECELLULARIZED EXTRACELLULAR MATRIX TO GENERATE MECHANICALLY TUNABLE HYDROGELS

**Omar Peza Chavez**[1], Joseph M. Kinsella[1]

1 McGill University

Decellularized extracellular matrix (dECM) has successfully translated into clinical use cases and remains an excellent candidate to develop tissue engineering matrices. dECM is compromised by detergent- and enzyme-based techniques that fragment proteins and damage tissue-specific microstructure. Supercritical carbon dioxide (scCO2) offers an alternative approach that preserves ECM bioactivity and post-translational modifications2. Here, we present a novel scCO2-based decellularization method that yields >30% scaffold in ~36 h, compared to <5% yield in >10 days with detergent-based methods, while retaining matrix integrity. The dECM is crosslinked using controlled reactions with transglutaminase-2 (TG) to form mechanically tunable hydrogels matching gastric tumor tissue moduli.

We demonstrated that scCO2-based dECM retained 39±14 ng/mg DNA and lacked visible nuclei under DAPI. LC-MS/MS identified 174 total proteins, from which 125 are unique to scCO2 dECM. Key ECM proteins such as collagens (I, II, III, IV, V, VI, VIII, XII) filamin, fibrillin, laminin, fibronectin, and elastin, were more present and prevalent in the scCO2 dECM. We formulated a reinforced hydrogel using G and TG as rheological modifiers. TG enzymatically crosslinks the hydrogel, allowing mechanical tunability at different ratios. Thermal cooling enhanced G self-organization, increasing TG crosslinking. Rheological analysis characterized viscosity, gelation, flow properties, and complex moduli for bioprinting, demonstrating that higher TG concentrations stiffened the hydrogel.

Bioprinting conditions were investigated rheologically. At 24 °C, DGTG1% and DGTG5% rapidly increased in storage modulus (G') within 40 min, plateauing at ~70 min with >50% of their final G' values: 18.93 ± 5.67 Pa (TG1%) and 322.25 ± 103.71 Pa (TG5%), denoting a 17-fold difference between a soft (TG1%) and stiffer (TG5%) conditions. After a 12 h investigation at 37 °C, G' values matched final 24 °C values, maintaining mechanical properties post-incubation.