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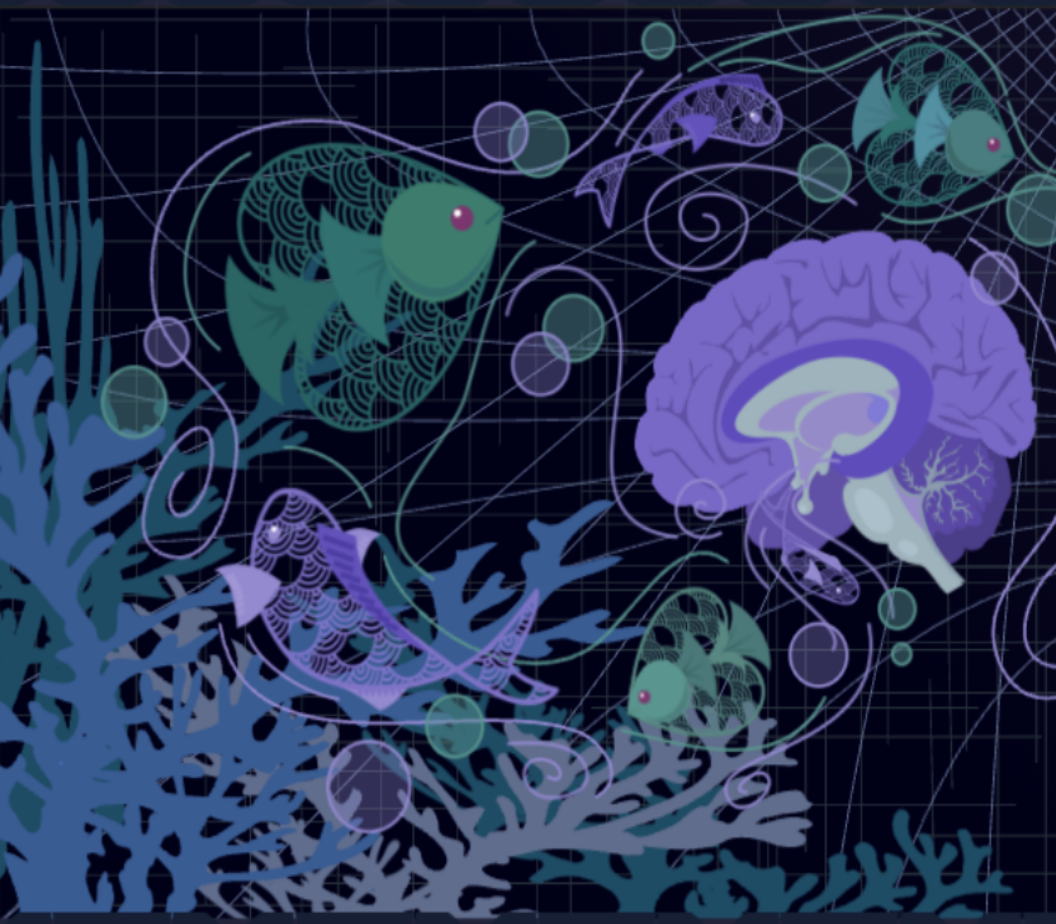
Proceedings of the 7th Annual McGill Undergraduate Science Showcase



McGill Science Undergraduate Research Journal
In collaboration with
the Office of Science Education

About the Undergraduate Science Showcase

Offered by the Office of Science Education, the Undergraduate Science Showcase is a student learning initiative that supports students in developing academic skills and culminates in a celebration of their work. At this annual, community-wide event, undergraduates share their scientific research, field work, in-class assignments, and passion projects in the form of scientific posters and creative presentations. The Office of Science Education has had the privilege of gathering the McGill community at the Undergraduate Science Showcase since 2020.

About MSURJ

The *McGill Science Undergraduate Research Journal (MSURJ)* is a student-run, peer-reviewed academic journal that publishes undergraduate science research. Established in 2005 to promote undergraduate research and provide students with publishing and peer-review experience, MSURJ serves as a platform for students to share their innovative work with the broader scientific community.

A Note from the Editors

Dear Reader,

We are delighted to present this collection of abstracts from the 2025 Undergraduate Science Showcase. The diverse range of topics demonstrates the curiosity, dedication, and scientific rigor of our undergraduate researchers. We extend our gratitude to the Office of Science Education (OSE) who makes this event possible. Each abstract represents countless hours of inquiry, experimentation, and analysis, and we invite you to explore this impressive collection of undergraduate scholarship.

MSURJ is proud to present its Special Issue: Proceedings of the 7th annual McGill Undergraduate Science Showcase. The Undergraduate Science Showcase, hosted by McGill's Office of Science Education (OSE), aims to celebrate the research conducted by undergraduate students through an annual scientific exposition. MSURJ's publication of the conference proceedings is a testament to our dedication to open science and promoting the next generation of scientific discovery. Featuring works in a range of disciplines of science and investigation, this year's proceedings challenge the boundaries in the domains of artificial intelligence, public health, ecology, neuroscience, cell biology, and more.

Through a rigorous reviewing process by our editing team, the following abstracts have been compiled in our second ever proceedings publication, Volume 21 No. 2. We hope you find something that aligns with your interests, or perhaps, sparks a new one.

Laura Zhang, Lisa Xie, and Benjamin Lévesque Kinder
On behalf of the MSURJ team

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Variation in the status of *Acropora palmata* coral in relation to environmental factors along the west coast of Barbados

Hana Kaloudis[1], *Eleanore Lukas*[1], *Faye Dryden*[1], *Lindsey Myhre*[1], *Atisha Lloyd*[1], *Virginie Millien*[1]

[1]Faculty of Science, McGill University, Montreal, QC, Canada
[2]Faculty of Science and Technology, University of the West Indies at Cave Hill, Saint Michael, Barbados

Keywords: *Acropora palmata*, Barbados, Breakwater, Coral health index, Latitude, Runoff output

Corresponding author email: hana.kaloudis@mail.mcgill.ca

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Acropora palmata is a critically endangered Caribbean coral whose decline threatens both coastal ecosystems and shoreline protection. Barbados once supported extensive *A. palmata* colonies along its west coast, yet the environmental drivers shaping current patterns of colony health and distribution remain unclear. We re-surveyed twelve sites in 2025, five of which were also assessed in 2024 and all originally mapped in 2015, to evaluate temporal changes in colony abundance, size, and condition, and to test how spatial and environmental gradients influence *A. palmata* health. Average colony height increased from 2015 to 2024, but declined sharply in 2025, consistent with fragmentation following heavy wave action and Hurricane Beryl in 2024. Despite this size reduction, health index scores improved significantly from 2024 to 2025, indicating rapid recovery in live tissue and pigmentation since the 2024 bleaching and hurricane events. Lack of pattern in count across study years suggests that varying environmental conditions across sites had different impacts on abundance. Our PCA results revealed four distinct habitat groupings across the coastline, with strong environmental gradients associated with latitude, distance to breakwaters and runoff outputs, depth, and distance from shore. Percent dead tissue was significantly related to a depth/distance to shoreline gradient, colony abundance was strongly structured by latitude, and total colony area increased significantly along the same gradient. Distances to individual anthropogenic structures were not associated with colony condition once broader spatial gradients were considered. Collectively, these results indicate that *A. palmata* conditions along Barbados's west coast are shaped primarily by latitudinal environmental variation rather than direct proximity to runoff outputs or breakwaters. These findings provide an updated baseline for restoration planning and highlight the importance of spatial context in the management of recovering *A. palmata* populations.

RainbowZero: Combining Advancements in Search and Reinforcement Learning for Complex Environments

Jonathan Lamontagne Kratz[1]
[1]Department of Computer Science, McGill University, Montreal, QC, Canada

Keywords: Reinforcement learning, Monte Carlo Tree Search, MuZero, Stochastic optimization, Artificial intelligence
Corresponding author email: jonathan.lamontagnekratz@mail.mcgill.ca
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While deep reinforcement learning has achieved superhuman performance in fully observable, zero-sum games, environments characterized by high stochasticity and complex state spaces remain a significant challenge. This ongoing research introduces "Rainbow Zero," a novel algorithmic framework that synergizes the forward-planning capabilities of search-based algorithms (such as MuZero and Muesli) with advanced value estimation techniques and world models (e.g., Dreamer and Rainbow). We utilize the board game *Settlers of Catan* as our primary testbed due to its complex mechanics, varying board layouts, and high variance. Currently, our framework is being evaluated on reduced-complexity, randomized Catan boards, alongside classic control environments and foundational games. By benchmarking against the Catantron library baselines, this project aims to isolate the impact of combining specific architectural components—such as search-based planning and distributional reinforcement learning—via planned ablation studies. Ultimately, the goal of this research extends beyond game-playing. By mastering the stochastic resource generation and long-term planning required in Catan, the Rainbow Zero architecture is being developed as a proxy for complex, real-world optimization problems, with future applications specifically targeting autonomous decision-making in mining operations and genomic sequence alignment.

Action-Based Cognitive Remediation in Bipolar Disorder: A Linear Mixed Effects Analysis of Pre-Post Clinical Symptoms

Momoko Hesketh[1], *Martin Lepage*[2,3], *Delphine Raucher-Chéné*[2,3]
[1]Department of Psychology, McGill University, Montreal, QC, Canada
[2]Douglas Research Centre, Verdun, QC, Canada
[3]Department of Psychiatry, McGill University, Montreal, QC, Canada

Keywords: Action-Based Cognitive Remediation (ABCR), Bipolar Disorder (BD), Linear Mixed-Effects Model, Clinical Symptoms, Remote Intervention

Corresponding author email: momoko.hesketh@mail.mcgill.ca

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Bipolar disorder is a chronic mental health condition defined by recurrent shifts in mood and impairment in cognitive functioning. Action-Based Cognitive Remediation (ABCR), originally developed for schizophrenia-spectrum disorders, integrates cognitive exercises with real-world application strategies. The intervention consists of four modules that focus on improving speed and attention, memory, executive functioning, and social cognition. ABCR has shown preliminary promise for improving cognitive and functional outcomes in individuals with bipolar disorder. The aim of this preliminary study is to examine the effect of ABCR intervention on clinical mood symptoms and functioning using a linear mixed-effects model. Based on prior ABCR research using Reliable Change Indices (RCI) and relative percent change, pre-post changes in clinical symptoms were expected to be small. The linear mixed effects model was expected to provide a more informative estimation of these changes by accounting for individual variability and estimating the overall direction and magnitude of group-level change in a small sample. Ten participants (eight females, two males) from the External Clinic for Bipolar Disorders at the Douglas Mental Health Institute were recruited, with seven completing the seventeen-session videoconference intervention. Results indicate small, non-significant average changes across outcomes. Trend estimates suggested modest improvement in functioning, while depressive symptoms and quality of life showed minimal change at the group level. Although limited by a sample size, these findings demonstrate the value of mixed-effects models as a preliminary tool for estimating the overall trend in small clinical samples. Future work should integrate linear mixed-effects models with other measures such as Reliable Change Indices, to better capture improved clinical symptoms and cognitive functioning in patients with bipolar disorder.

Engineering SPEF1 Fusion Proteins for Improved Microtubule Seam Alignment for Cryo-Electron Microscopy

Helena Goodey-Parfitt[1], Tina Alagha[1], Hayley Rose Blythe[1], Thibault Legal[1], Khanh Huy Bui[1]

[1]Department of Anatomy and Cell Biology, Faculty of Medicine and Health Sciences, McGill University, Montreal, QC, Canada

Keywords: Computational protein design; Cryo-electron microscopy; Fusion proteins; Microtubule seam; Microtubules; Sperm flagellar protein 1 (SPEF1)

Corresponding author email: helena.goodey-parfitt@mail.mcgill.ca

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Microtubules are dynamic polymers of - tubulin heterodimers that support cell structure and contribute to processes including cell division, intracellular transport, and cilia stability. Their functions are modulated by microtubule-associated proteins (MAPs), which regulate microtubule assembly, stability, organization, and interactions with other cellular components. Accurate identification of the microtubule seam, where heterotypic - interactions replace homotypic - and - contacts, is essential for cryo-electron microscopy (cryo-EM) reconstruction. Current seam-alignment strategies employ kinesin motor domains that generate alignment contrast but mask lattice features and limit compatibility with many MAPs. The Bui lab identified Sperm Flagellar Protein 1 (SPEF1) as a seam-binding alternative, though its small size limits reliable visualization. We hypothesised that engineering larger SPEF1 fusion proteins would improve seam contrast and alignment while preserving microtubule binding. Fusion constructs were designed using RoseTTAFold Diffusion to append structured domains to the SPEF1 microtubule-binding region while preserving predicted folding and function. Constructs were cloned, sequence-verified, and expressed in *Escherichia coli*, with several designs demonstrating strong expression and yielding soluble protein after purification. Using a microtubule co-sedimentation assay, the engineered construct SPEF1 (1-120)-300AA demonstrated effective binding to polymerized microtubules, supporting its suitability for further microtubule seam-targeting studies, although cryo-EM validation remains ongoing. These results position engineered SPEF1 fusion proteins as promising seam-alignment tools that provide a broadly compatible and experimentally validated strategy for advancing cryo-EM studies of microtubule architecture and enabling direct evaluation of seam localization without masking lattice features or disrupting lattice-binding protein interactions, thereby overcoming limitations imposed by existing seam-alignment strategies.

Impact of human-like knock-in mutation on glomerular structure in a mouse model of Sanfilippo Syndrome (MPS IIIC)

Emily Pun[1], *Lorena Carvelli*[1], *Alexey V. Pshezhetsky*[1], *Carlos R. Morales*[1]

[1]Department of Anatomy and Cell Biology, McGill University, Montreal, QC, Canada

Keywords: Heparan sulfate; Lysosomal storage disorder; Renal pathology; Sanfilippo syndrome C

Corresponding author email: emily.pun@mail.mcgill.ca

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Mucopolysaccharidosis type IIIC, also known as Sanfilippo syndrome type C, is a lysosomal storage disease caused by a deficiency of heparan sulfate acetyl-CoA: alpha glucosaminide N-acetyltransferase (HGSNAT). HGSNAT is one of the key enzymes involved in the degradation of heparan sulfate, a glycosaminoglycan present in proteoglycans and basement membranes. The absence of HGSNAT activity leads to an accumulation of heparan sulfate in lysosomes, causing cellular dysfunction and progressive neurological degeneration. This study examined the glomerular renal pathology in a CRISPR-Cas9-generated knock-in mouse model expressing the Pro304Leu HGSNAT variant, which replicates the human Pro311Leu mutation. The model showed early-onset MPS IIIC with dominant-negative effects and stress on the endoplasmic reticulum and lysosomes. Wild type (WT, n=3, 7 months old) and HGSNAT knock-in (KI, n=3, 7 months old) mice were used for each experiment. Kidneys were collected and processed for histological and ultrastructural analysis by light and electron microscopy. ImageJ was used to quantify the stained area of the mesangial matrix. Compared with WT, KI mice exhibited a more intense Periodic acid Schiff staining of the glomerular mesangial matrix, an accumulation of empty vesicles in the podocytes, distorted mesangial cells, and severely affected podocytes filled with lysosomes and enlarged pedicels. In conclusion, the increased deposition of heparan sulfate in the mesangial matrix is associated with glomerular distortion and mesangial proliferation, findings that could be consistent with the development of mesangial proliferative glomerulonephritis.

Gestational Exposure to Nanoplastics and its Effect on Maternal Behaviour, Progeny Outcome, and Sex Ratio: A Literature Review

Ella Domingo[1], *Caroline Fei*[1], *Yu Chen Nan1*[1], *Lan Yun Wu*[1]
[1]Department of Pharmacology, McGill University, Montreal, QC, Canada

Keywords: Microplastics, Plastic nanoparticles, Gestational exposure, Maternal behavior, Progeny outcome, Sex ratio

Corresponding author email: caroline.fei@mail.mcgill.ca

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Exposure to plastic nanoparticles has been investigated since the late 1980s and has become a growing public health concern over recent years. Among these concerns are their potential impact on fertility and reproduction, as the small size of plastic nanoparticles allows for their entry into the systemic circulation and translocation across the placental barrier, potentially affecting and disrupting reproductive processes. This literature review aims to examine how gestational exposure to plastic nanoparticles and the substances they carry can influence or alter maternal behaviour, progeny outcome, and sex ratio. We hypothesized that gestational exposure to plastic nanoparticles disrupts neuroendocrine pathways regulating maternal behaviour and offspring development. After synthesizing data from *in vitro* and *in vivo* studies in PubMed, a comprehensive review of the current scientific literature was conducted. Overall, study findings suggest that nanoparticle exposure during pregnancy can reduce oxytocin levels in both the plasma and the hypothalamus, correlating with decreased observable maternal behaviours in affected mice. Additionally, adverse outcomes have been reported in exposed progeny, including thinning of the cerebral cortex in Sprague Dawley rats and transgenerational changes in population fitness in *D. Magna* plankton. Specific sex-based vulnerabilities were identified, with some studies suggesting a potential skewing of the male-to-female ratio, with male embryos being more severely impacted. However, current evidence more strongly implicates general environmental pollution rather than nanoparticles specifically. Moreover, contemporary scientific information is limited by a stronger focus on oxytocin. While the link between environmental pollutants and oxytocin is well-documented, other critical regulators of maternal behaviour, such as placental lactogen and prolactin, remain understudied and yield conflicting data regarding nanoparticle interference. The importance of this investigative literature review lies in the urgency to understand the mechanisms by which nanoplastics impact reproductive health, and to prevent the adverse effects of nanoparticle exposure on our ecosystems and our future generations.

Understanding the Impact of Antigen-Specific Regulatory T cells on Anergy Induction *in vivo*

Sophie Courville[1], *Stefanie F. Valbon*[2,3], *Marilaine Fournier*[3], *Heather J. Melichar*[3,4]

[1]Department of Physiology, McGill University, Montreal, QC, Canada
[2]Department of Microbiology, Immunology and Infectious Disease, Université de Montréal, Montreal, QC, Canada
[3]Rosalind and Morris Goodman Cancer Institute, McGill University, Montreal, QC, Canada
[4]Department of Microbiology and Immunology, McGill University, Montreal, QC, Canada

Keywords: Adoptive cell transfer, Antigen-specific regulatory T cells, Peripheral tolerance, Single-cell RNA sequencing, T Cell Anergy

Corresponding author email: sophie.courville@mail.mcgill.ca

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Abstract: In order to properly function, the immune system must achieve a fine balance between attacking foreign invaders while avoiding damage to healthy (self) tissue. One way it maintains this balance is through the induction of T cell anergy. Anergy is a key tolerance mechanism that renders self-reactive T cells hyporesponsive, thereby preventing the development of autoimmune diseases. T cell anergy is typically induced under steady state conditions when antigen recognition occurs without co-stimulation, such as in the absence of inflammation. Regulatory T (Treg) cell-mediated suppression of self-reactive T cells may contribute to anergy induction, but their specific role remains poorly defined. In this study, we investigate how antigen-specific Tregs influence the generation and accumulation of anergic CD8 T cells *in vivo*. To test this, we generated Tregs *ex vivo* from OVA-specific OT-II CD4 T cells. We injected OVA-specific OT-I CD8 T cells with or without OT-II Tregs into mice expressing OVA as a model self-antigen. After fourteen days, we observed an increase in the proportion of OT-I T cells in the spleen of mice co-adoptively transferred with OT-II Tregs as compared to mice injected with OT-I T cells alone. We confirmed, via *ex vivo* re-stimulation, that OT-I T cells induced in the presence of OT-II Tregs remained anergic. Interestingly, single-cell RNA-sequencing revealed that levels of antigen-specific Tregs correlate with transcriptional heterogeneity among anergic CD8 T cells *in vivo*. These findings suggest that antigen-specific Tregs promote the accumulation of anergic CD8 T cells. This work contributes to a broader effort to define mechanisms of peripheral tolerance, providing a foundation for their potential use in therapeutic interventions to prevent autoimmune disease.

A Computational Model of the Hippocampus Supports Exploratory Behaviour in Reinforcement Learning Agents

Sabrina Du[1], Adel Halawa[1,2], Aleksei Efremov[1,2], Adrien Peyrache[1], Daniel Levenstein[3], Blake Richards[1,2,3,4,5]

[1]Montreal Neurological Institute, McGill University, Montreal, QC, Canada
[2]Mila – Quebec Artificial Intelligence Institute, Montreal, QC, Canada
[3]Department of Neuroscience, Yale School of Medicine, New Haven, CT, USA
[4]School of Computer Science, McGill University, Montreal, QC, Canada
[5]Learning in Machines and Brains Program, CIFAR, Toronto, ON, Canada

Keywords: Cognitive maps, Intrinsic reinforcement learning, Curiosity-driven exploration

Corresponding author email: sabrina.du@mail.mcgill.ca

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The hippocampus supports spatial navigation, memory, and planning through the formation of cognitive maps—structured environmental representations reflected in neural activity. These neural dynamics can be modeled computationally using recurrent neural networks (RNNs) to provide insights into how cognitive maps guide behavior. However, these RNNs are typically trained via reinforcement learning (RL) using external rewards, failing to capture the intrinsic drive of freely exploring animals in the absence of external rewards. Instead, reward-free RL models, which rely on internal environmental representations, are better candidates to study novelty-seeking and exploratory behaviour. This study aims to investigate whether an RNN exhibiting hippocampal-like activity builds spatial representations sufficient to support exploratory behavior in reward-free RL agents. We leveraged an existing RNN trained for sensory sequence prediction, which exhibits hippocampal-like activity patterns, and used its prediction error as the intrinsic reward to train an Actor-Critic agent. Performance was evaluated using a Novel Object Recognition task to quantify its preference for novel versus familiar stimuli. The RL agent occupied the region of interest (defined as a 3-unit radius around the novel object) significantly more often than a random agent across multiple episodes and novel object locations. The RL agent's performance was also measured in a multi-room environment, where its visitation frequency to novel rooms was significantly higher than a random control. This work demonstrates that hippocampal-like representations can support autonomous exploratory behaviour, and provides a framework for investigating how cognitive maps guide exploration and navigation.

Introducing Ultrasound-Guided Peripheral IV Catheter Insertion to Nursing Students Through a Student-Led Workshop

Rawane Soboh[1,2], Dohee Kim[1,2], Melanie Xie[1,2], Juan Avila Amariles[1,2], Marc-Alexandre Bourget[1,2], Mélodie Lewis[1,2], Andrea Lian[1,2], Chloe Luu[1,2], Mélanie Gauthier[1,2], Caroline Marchionni[1,2], William Landry[1,2]

[1]McGill University, Ingram School of Nursing, Mcgill, Montreal, QC, Canada
[2]McGill Vascular Access Student Club,Mcgill, Montreal, QC, Canada

Keywords: Ultrasound-guided (USG), Nursing students, Difficult Intravenous Access (DIVA), Peripheral intravenous insertion (PIV insertion)

Corresponding author email: juan.avilaamariles@mail.mcgill.ca

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Patients with difficult intravenous access (DIVA) pose a significant challenge in clinical settings, often leading to delayed care and complications such as pain, phlebitis, and increased infection risk due to multiple insertion attempts. Although evidence supports ultrasound-guided peripheral intravenous catheter (USGPIVC) insertion as a superior approach for DIVA patients, this technique remains largely absent from undergraduate nursing curricula and is typically accessed through post-registration certification, creating workflow inefficiencies and potential delays in care. To address this gap, McGill's Vascular Access Student Club (VASC) organized a workshop to introduce USGPIVC insertion to nursing students through both theoretical and hands-on learning. Participants completed pre- and post-workshop surveys assessing familiarity with USGPIVC insertions and confidence in managing DIVA patients. Among 24 Bachelor of Nursing (Integrated) (BNI) and Bachelor of Science in Nursing (BScN) participants, 66.7% were in their first year of undergraduate studies. Second- and third-year students reported low baseline confidence in IV insertion for DIVA patients, with 95.4% reporting "not confident at all" or "slightly confident." Although 36.4% had observed USGPIVC insertions, none had received formal training. Post-workshop feedback was overwhelmingly positive: 100% rated the session as beneficial, and 62.5% advocated for training prior to clinical practice. More than 90% of participants expressed interest in advanced training. This student-led initiative reveals a critical gap in undergraduate curriculum and a strong demand for structured ultrasound-guided vascular access training. Integrating these skills early may enhance nursing preparedness for DIVA patients and lead to improved patient care.

Building Confidence Through Practice: Evaluating a Student-Led Flu Vaccination Clinic Using Retractable Safety Needles

Rawane Soboh[1,2], Andrea Lian[1,2], Mélodie Lewis[1,2], Juan Avila Amariles[1,2], Marc-Alexandre Bourget[1,2], Dohee Kim[1,2], Chloe Luu[1,2], Melanie Xie[1,2], William Landry[1,2], Mélanie Gauthier[1,2], and Caroline Marchionni[1,2]

[1]McGill University, Ingram School of Nursing, Montreal, QC, Canada
[2]McGill Vascular Access Student Club, Montreal, QC, Canada

Keywords: Vaccination clinic, Nursing students, Retractable safety needles, Influenza, Nursing

Corresponding author email: juan.avilaamariles@mail.mcgill.ca

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Nursing students often graduate with limited experience vaccinating. Low-fidelity simulations using task trainers are effective for skill development, but are not realistic and, when used alone, limit engagement with the interpersonal and clinical aspects of care. The introduction of retractable safety syringes designed to minimize needlestick injuries has advanced clinical practice, yet students have limited exposure to them. McGill's Vascular Access Student Club organised a vaccination clinic at the Sakoto Shibata Clinical Nursing Laboratories to bridge this gap by assessing the impact of retractable safety syringes on patient experience and the skills and confidence of student vaccinators. Vaccinated participants included 87 nursing students and laboratory staff who completed a post-vaccination survey rating their experience. Most rated 5/5 in terms of "safety" and "comfort", with a median pain score of 1/10. Professionalism and technical skills were rated 5/5 by 89% of respondents, while 92% were "very likely" to recommend the clinic. Vaccinators were graduating students who underwent mandatory training. Of 11 student vaccinators, 80% had no prior experience vaccinating with safety needles, and 60% reported "very high confidence," up from 0% pre-event. 70% felt more comfortable using safety syringes than non-safety syringes, and 90% reported that vaccinating real patients was "different" or "very different" from simulated practice. Results showed that this student-led clinic using retractable safety syringes improved patient experiences, boosted student confidence and skills, and transferred the learning from low-fidelity training to a clinical practice.

The Bi-functional Role of BMP in *mid* Regulation in *Drosophila*

Chihao Xu[1], *Laura Nilson*[2]

[1]Department of Biochemistry, McGill University, Montreal, QC, Canada
[2]McGill University, Montreal, Quebec, Canada

Keywords: Drosophila, Embryogenesis, Genetic mosaic analysis, Intracellular signal, Transcription regulation

Corresponding author email: chihao.xu@mail.mcgill.ca

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During early embryogenesis, intracellular signals determine whether follicle cells differentiate towards anterior or posterior fate. Bone Morphogenetic Protein (BMP) is one of the regulatory proteins repressing *mid*, a transcription factor induces the posterior pattern formation in *Drosophila*. BMP regulates *mid* expression via binding to the intron segment of the *mid* gene, known as *mid*-in. Previous work using the lacZ reporter in *mid*-in has shown that *mid*-,requires BMP expression in some cases, presenting a potential bi-functional role of BMP. We hypothesize that such a property might be determined by the availability of *schnurri*, a well-known co-repressor of BMP. We examined lacZ fused with *mid*-in in three groups of *Drosophila* (over expression of BMP, knock-down of *schnurri*, and the combination of both genotypes). Each group contained 40 samples and was analyzed using genetic mosaic analysis. We found that reporter expression decreased substantially when *schnurri* was present and BMP was over expressed. In contrast, the reporter was ectopically expressed when *schnurri* was absent and BMP signalling was overactivated. However, because schnurri was only knocked down using *schnurri* RNAi in this experiment, the activation phenotype was not strong. Future experiments could repeat this analysis using *Drosophila* a with *schnurri* gene mutation instead. Overall, these results demonstrate the bifunctional property of BMP pathway in the regulation of the *mid*-in reporter. Future work may focus on identifying the locations of the BMP activation and repression motif within the *mid*-in sequence.

Automated Microtubule Detection for Subtomogram Averaging in Cryo-Electron Tomography

Molly Yu[1], *Khanh Huy Bui*[2]

[1]Department of Computer Science and Department of Biology, McGill University, Montreal, QC, Canada

[2]Department of Anatomy and Cell Biology, McGill University, Montreal, QC, Canada

Keywords: Cryo-electron tomography, Filament detection, Microtubules, Structural cell biology, Subtomogram averaging

Corresponding author email: yining.yu@mail.mcgill.ca

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Cryo-electron tomography enables three-dimensional visualization of macromolecular structures within intact cells. Filamentous structures such as microtubules are essential for intracellular transport, structural stability, and cell division. Structural analysis of microtubules often relies on subtomogram averaging, a process that requires manual or semi-manual filament picking and alignment. These steps are time-consuming, computationally demanding, and can introduce user bias, making it difficult to handle large datasets efficiently. We developed an automated pipeline for microtubule detection and particle orientation prediction to improve efficiency and consistency in subtomogram averaging workflows. The pipeline integrates filament tracing, line connection analysis, and geometric modeling to detect microtubules and predict particle angles prior to alignment. Quality control measures were incorporated to identify elliptical distortions, misaligned particles, and outliers in dense datasets. Performance was evaluated by comparing pipeline outputs with manually processed datasets, examining particle ordering, angular consistency, alignment behavior, resolution, and processing time. Automated picking preserved expected structural organization and produced angle predictions consistent with refined alignment parameters while reducing analysis time. However, performance may vary depending on tomogram quality and filament density. These findings demonstrate that automated filament detection can reduce manual effort and support efficient structural analysis in cryo-electron tomography. Further improvements may increase reliability across different cellular contexts.

Assessing the Social and Ecological Synergies of Green Alleys in Montreal

Justine Adlhoch-Mathé[1], *Nicolas Kosoy*[1]
[1]Department of Agricultural and Environmental Sciences, McGill University, Montreal, QC, Canada

Keywords: Alleyways, Community engagement, Green infrastructure, Social capital, Urban greening, Urban planning
Corresponding author email: justine.adlhoch-mathe@mail.mcgill.ca
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Urban alleyways are underexplored spaces of potential ecological and social significance. While green alleyways are promoted to improve environmental quality, their distribution relies on borough-level governance and community engagement. The extent to which structural alley availability and socioeconomic factors facilitate greening, and how greening influences social capital and inter-species connections, remains unclear. This study aims to map regular (non-green) alleys, quantify greening patterns, and provide a baseline for assessing associated social and ecological outcomes. Using QGIS, we mapped 1,348 regular alleys across four Montréal boroughs and recorded their greening status. 25 Quartiers de Référence were analyzed to examine relationships among alley quantity, density, median household income, and green alley prevalence. Analysis methods used included descriptive statistics, Pearson correlations, linear regression, and binomial regression. A follow-up cross-sectional study (REB pending) will assess bonding, bridging, and inter-species social capital among residents in green alleys, regular alleys, and non-alley areas. On average, 22% of alleys were greened (range: 0–44%). Alley counts strongly predicted green alleys ($r = 0.74$), with moderate associations for density ($r = 0.39$) and income ($r = 0.60$). Linear and binomial models confirmed that higher alley availability, density, and income increased the likelihood of greening ($p < 0.05$). Causal inference cannot be made; greening may reflect pre-existing community engagement. Social capital outcomes await REB approval. Higher number and density of regular alleys encourage alleyway greening. Future analyses will clarify whether green alleyways correlate with community cohesion or environmental engagement.

Impact of Salt Identity, Concentration, and Buffer Composition on Hierarchically Structured Protein Fibers from Recombinant Tobacco Mosaic Virus Self-Assembling Capsids

Louise Mussard[1], Guido M. Merino[2], Amy S. Blum[2]

[1]Department of Physics, McGill University, Montreal, QC, Canada
[2]Department of Chemistry, McGill University, Montreal, QC, Canada

Keywords: Tobacco Mosaic Virus, Virus-Like Particle, Self-assembly, Hierarchal Structure, Protein Fibers

Corresponding author email: louise.mussard@mail.mcgill.ca

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Biological organisms have mastered the self-assembly of proteins into multifunctional materials, achieving remarkable properties through complex molecular organization at the macroscopic scale. However, replicating this level of hierarchical organization in man-made materials remains a persistent challenge. Tobacco Mosaic Virus coat proteins (TMVcp) can self-assemble into different conformations (helical rods, disks, stacked disks) through variation of solution ionic strength and pH. Recent data from the Blum group suggests that TMVcp are able to form macroscale hierarchically structured protein fibers. The objective of this study was to investigate the effect of exogenous salt concentration and buffer identity on the hierarchical structure of the TMVcp fibers. Four salts were introduced at concentrations ranging from 1mM to 100mM and six buffer systems were evaluated, varying in both cation and anion identity. The fibers were characterized through Polarized Light Microscopy (PLM), which revealed the presence of birefringence that indicates a hierarchical structure, and Small Angle Xray Scattering (SAXS), which was used to characterize the organization and spacing between the helical rods within a fiber. Results indicate an optimal added salt concentration range which significantly enhanced birefringence and internal hierarchical order. Notably, citrate-based buffers demonstrated superior self-assembly efficiency compared to other buffer systems, as evidenced by distinct features in the SAXS spectra. Furthermore, Scherrer analysis confirmed that the rods pack into an hexagonal lattice, a consistent feature across all fibers formed with 25mM added salt, regardless of salt identity. This work highlights the influence of ionic strength and buffer composition on the hierarchical structure of the TMVcp fibers, opening new pathways for tuning the self-assembly of viral capsids via environmental control.

Development of Colorimetric Analysis Software for 2.2.2-Kryptofix Compliance Testing in [18F]FDG Production

Aude Longtin[1], L.M Alonso Martinez[1], M. Boudjemeline[1]
[1]Laboratory of Radiopharmaceutic Sciences, CHU de Québec, Université Laval, Quebec, QC, Canada

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Corresponding author email: aude.longtin@mail.mcgill.ca
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[18F]fluorodexyglucose ([18F]FDG) is a glucose analog where the hydroxyl group in the C-2 position is substituted by the cyclotron-produced [18F] radionuclide. This radiopharmaceutical is used in medical imaging, particularly in positron emission tomography (PET) scans crucial in cancer diagnoses and monitoring. 18F-FDG synthesis involves a nucleophilic substitution with 2.2.2-Kryptofix as a phase-transfer catalyst. However, Kryptofix residue quantities must be strictly regulated due to their toxicity. Current quality control processes employ spot testing where sample colors are compared to that of a standard, which is prepared at maximal Kryptofix concentration of 0.5mg/V. This project aims to build a user-friendly interface able to determine whether a 18[F]FDG sample passes the Kryptofix concentration test through image analysis techniques. A Python-based application was developed using the "Tkinter" library to create a graphical user interface, integrated with image processing features. The software employs colorimetric analysis by quantifying pixel intensity and performing statistical comparisons on user-defined cross-sections of the image. Software validation is performed using images with known sample and standard concentrations. The user-friendly interface aims to improve accessibility and limit the subjectivity of human analysis for the determination of 2.2.2-Kryptofix contents in a sample and successfully determines the pass/fail status of the sample regarding regulatory safety standards of 0.5mg/V. The software generates reports documenting the analytical process, which are required for regulatory compliance and quality assurance documentation. These reports are crucial in the case of a test failure or deviation. Further improvements can be made to the software to quantify the Kryptofix concentration in [18F]FDG samples rather than provide only pass/fail data. The basic software architecture has also been adapted and modified to conduct other quality control tests in a radiopharmaceutical laboratory, with promising preliminary testing for bacterial colony counting and environmental monitoring.

To See Behind Walls; Contrast-Enhanced Micro-CT 3D Reconstructions of Morphological Adaptations in the Fourth Digit of a Human for Tool-usage

Kate Birch[1], *Anthony Smith*[1], *Hans Larsson*[1]
[1]Department of Biology, McGill University, Montreal, QC, Canada

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Corresponding author email: kate.birch@mail.mcgill.ca
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The human hand is a pillar of the species' distinction, a crucial orchestrator of the technological and cognitive adaptive niche that has shaped the modern world. Artifacts of morphological adaptations guiding transitions in early hominin evolution are present in the hand. As early hominins shifted from suspensory arboreal regimes to bipedalism, and from occasional tool-using to tool-making, the human hand adapted morphologically, leading to its current form. Conversely, the chimpanzee hand evolved within a primarily arboreal locomotive niche at the expense of optimization for tool-usage. Comparative studies can elucidate functional relationships that have shaped these changes. In this study, we aim to visualize the morphological adaptations present in the human hand in a non-destructive manner that can be applied to rare and valuable chimpanzee specimens. Using DragonFly software, we present a 3D reconstruction of an entire human hand, contrast-enhanced with phosphotungstic-acid. Additionally, we identified and segmented four unique morphological adaptations present in the human finger for advanced manual handling ability. These include the unique morphology of the distal phalanx, a strengthened flexor digitorum profundus insertion, increased neural innervation in the distal tip, and a compartmentalized digital pulp. This study precedes our upcoming application of the above on a chimpanzee fourth digit, and a future report of comparative sensory neural innervation, which is involved in sensorimotor feedback during tool-usage in both species but may be specialised in *Homo sapiens*.

Effects of Time Pressure and Ambiguity Under Controlled Perceptual Conditions

Sacha Harmony Fontes[1]*, *Samuel Massicotte*[1]*, *Seol Han*[1]*
[1]Department of Psychology, McGill University, Montreal, QC, Canada
*All authors contributed equally

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Corresponding author email: samuel.massicotte@mail.mcgill.ca
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Decision-making under uncertainty often occurs with incomplete information and limited time for response. Prior work has highlighted two influential determinants driving choice under uncertainty: ambiguity aversion and time pressure effects. However, experimental designs are frequently confounded with perceptual difficulty, making it unclear whether observed preferences reflect true decisional bias or limitations in sensory encoding. In this study, we tested whether time pressure changes ambiguity preferences when perceptual clarity is controlled. In this within-subjects design, six undergraduate participants completed a decision task in which they chose between known probabilities and ambiguous lotteries displayed as calibrated visual grids. Ambiguity was manipulated by masking probability information while pressure varied using short and long response deadlines. A perceptual calibration procedure ensured that probability information was equally interpretable across conditions. Results showed a slight preference for ambiguous options under matched sensory conditions. Increased ambiguity shifted choices modestly towards the known option. Time pressure reduced reaction times and increased missed responses but did not amplify ambiguity aversion. These preliminary results suggest that ambiguity and time pressure may influence decision-making through distinct contributions. Increasing the sample size and extending to other sensory modalities may further clarify how uncertainty and urgency jointly shape perceptual and decisional processes under uncertain conditions.

Investigating the Role of IL-37 in Brain Endothelial Cells and Blood–Brain Barrier Regulation in Multiple Sclerosis

Londynn Ostroff[1], *Stephanie Zandee*[1]

[1]Department of Neurology and Neurosurgery, Montreal Neurological Institute, McGill University, Montreal, QC, Canada

Keywords: Blood-brain barrier, Cytokine signaling; IL-37, Multiple sclerosis, Neuroinflammation

Corresponding author email: londynn.ostroff@mail.mcgill.ca

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IL-37 is a member of the IL-1 cytokine family and functions as a broad anti-inflammatory mediator through suppression of pro-inflammatory cytokines and modulation of immune signaling pathways. Uniquely, IL-37 signals through both extracellular receptor-mediated mechanisms (IL-18R1 and IL-1R8 (SIGIRR)) and intracellular pathways (SMAD3-mediated nuclear translocation) that broadly reduce inflammatory pathway activation. The protective effects of IL-37 in EAE occur through its extracellular function, specifically binding IL-1R8, thereby inhibiting pro-inflammatory signaling cascades such as NF- B, MAP kinases, and mTOR pathways. IL-37 has been studied in cardiovascular endothelial cells, where it inhibits atherosclerosis, reduced endothelial apoptosis, and protects against coronary endothelial damage, suggesting therapeutic potential in inflammatory endothelial pathologies. However, the expression and function of IL-37 in human brain endothelial cells remains poorly characterized. These cells are implicated in Multiple sclerosis (MS), a chronic neuroinflammatory disease affecting around 2.9 million people worldwide. The disease results from immune cell infiltration across the blood-brain barrier (BBB), which disrupts neuronal signalling by promoting inflammation, demyelination, gliosis and neuroaxonal degeneration. Transgenic mouse studies that introduced IL-37 in experimental autoimmune encephalomyelitis (EAE), the standard animal model for MS, demonstrated significantly reduced clinical scores and decreased demyelination. In addition, IL-37 expression reduced immune cell accumulation in the spinal cord and shifted cytokine profiles toward a more anti-inflammatory phenotype. Because human brain endothelial cells regulate immune trafficking and inflammatory signaling at the BBB and are associated withMS pathology, this project aims to investigate IL-37 signaling in human brain endothelial cells and determine whether this pathway contributes to immune regulation at the BBB. Understanding IL-37 in this context may provide insight into mechanisms that limit neuroinflammation in MS and identify potential therapeutic targets.

Identifying Variant Surface Glycoprotein Gene Regulators in *Trypanosoma brucei*

Valeria Bernal Araujo[1], *Jade Laurent-Le Bras*[1], *Larsen Iorgovits*[1], *Igor Cestari*[1]

[1]Institute of Parasitology, McGill University, Ste Anne de Bellevue, QC,Canada

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Corresponding author email: valeria.bernalaraujo@mail.mcgill.ca

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Trypanosoma brucei is a single-celled, flagellated, extracellular protozoan parasite and the causative agent of African trypanosomiasis in humans and animals. *T. brucei* evades the host antibody responses by periodically switching its Variant Surface Glycoprotein (VSGs) coat. VSGs are highly antigenic proteins expressed in a monogenic manner from a repertoire of 2,500 genes and pseudogenes, at subtelomeric expression sites (ES). However, the mechanisms that control VSG switching remain unclear. Previously, immunoprecipitation coupled with cross-linking and mass spectrometry revealed that, as part of the phosphatidylinositol signaling pathway, phosphatidylinositol 5-phosphatase (PIP5Pase) associates with the VSG silencer repressor-activator protein 1 (RAP1) to regulate VSG expression and switching in *T. brucei.* Additionally, PIP5Pase and RAP1 strongly interact with several additional proteins, including eight candidate regulators which we hypothesize are essential genes for parasite survival and VSG expression control. Our objective is to investigate the role of these candidate regulators in antigenic variation in *T. brucei.* We constructed tetracycline-inducible RNA-interference (RNAi) cell lines in bloodstream form *T. brucei* SM427 to induce gene-specific knockdowns, followed by gene expression analysis. Five genes were cloned into the MC177VSG221RNAi vector, and two constructs were successfully transfected to generate tetracycline-inducible RNAi cell lines. RNAi-mediated knockdown of the two candidate regulators did not significantly affect parasite growth or morphology. Therefore, these two genes are unlikely to be essential for parasite viability. Gene expression analysis and VSG switching assays are in progress to determine the consequence of the knockdowns on VSG expression and better understand the host evasion mechanisms used by *T. brucei.*

Understanding the Link Between Biological Motion Processing and Social Responsiveness in Autistic and Nonautistic Persons

Mia Ginsberg[1], *Charlotte Sumpf*[1], *Luc Langille*[1], *Adina Gazith*[1], *Emily Stubbert*[1], *Armando Bertone*[1], *Jacob A. Burack*[1]

[1]Department of Educational and Counselling Psychology, McGill University, Montreal, QC, Canada

Keywords: Autism, Cognitive development, Neuropsychological assessment, Social development

Corresponding author email: mia.ginsberg@mail.mcgill.ca

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Social development in autistic persons, for whom difficulties in social functioning are the basis of a diagnosis, has been evaluated in various ways. For example, behavioral paradigms used to assess biological motion (BM) provide insight into dynamic social information processing, whereas parent-report questionnaires are used to assess broader patterns of social functioning ability in everyday contexts. We assessed score concordance on these two disparate measurements of social development among autistic and non-autistic persons. We further assessed this relationship in relation to mental age (MA). The participants included 29 autistic (five females, 24 males; mean age = 12.47 years, mean MA = 10.90 years) and 29 non-autistic (eight females, 21 males; mean age = 10.40 years, mean MA = 11.21 years) participants. These groups were subdivided into high and low MA groups based on the median MA (10.57 years). A BM task was used to assess social perceptual processing via accuracy in identifying the walking direction of a point-light figure with increasing distractor dots. Social functioning was evaluated with the Social Responsiveness Scale (SRS-2) and MA was assessed with the Wechsler Abbreviated Scale of Intelligence. The autistic group showed significantly higher SRS-2 scores than the non-autistic group ($p < .001$), reflecting greater social difficulties. However, the groups did not differ significantly in BM performance ($p = .64$). BM and SRS-2 scores were significantly correlated when accounting for the diagnostic group ($p = .048$). Further stratified by mental age group, BM was significantly associated with the SRS-2 in the higher MA group ($p = .046$) but not in the lower MA group ($p > .50$). These findings indicate that scores on perceptual and questionnaire-based measures of social functioning are linked at higher MA, indicating a role for cognition in the coherence of disparate aspects of social development.

Adapting Monotonic Subtype and Stage Inference (SuStaIn) to Model Patterns of Disease Progression for Psychiatric Disorders

Ethan Yan[1], Katie M Lavigne[2,3]

[1]Department of Psychology, McGill University, Montreal, QC, Canada
[2]Douglas Research Centre, Montreal, QC, Canada
[3]Department of Psychiatry, McGill University. Montreal, QC, Canada

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Corresponding author email: siliang.yan@mail.mcgill.ca

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Significant progress has been made in disease progression modelling, with crucial implications for understanding and managing chronic, progressive diseases, such as neurodegenerative diseases. One prominent framework is Subtype and Stage Inference (SuStaIn), an event-based machine learning model that characterizes disease progression and can reveal spatiotemporal and phenotypic heterogeneity in chronic diseases using only cross-sectional data. SuStaIn has demonstrated success across neurodegenerative, psychiatric, and pulmonary diseases. However, a key limitation of SuStaIn is its assumption of monotonic disease progression, which may be biologically implausible and clinically restrictive, particularly for diseases that commonly involve remission and recovery (e.g., psychiatric disorders). *To examine the impact of this assumption, this proof-of-concept study systematically evaluated SuStaIn's performance on non-monotonic data.* We generated both monotonic and bidirectional ground-truth disease progression datasets. The bidirectional datasets were further manipulated across sample sizes, numbers of biomarkers, and subtype proportions. Model performance was evaluated using Kendall's tau to compare the inferred event sequences with the ground-truth progression. Results show that SuStaIn performs significantly worse on datasets with bidirectional underlying disease progression than on baseline monotonic datasets. While SuStaIn reliably captures the number of subtypes and their proportions, it fails to accurately model progression within subtypes that contain switch biomarkers. Moreover, increasing the sample size and the number of biomarkers does not substantially improve performance under bidirectional conditions, in contrast to monotonic progressions. These findings provide empirical evidence that SuStaIn's monotonic assumption limits its ability to model bidirectional disease processes, as in many psychiatric disorders. More broadly, this work deepens the understanding of SuStaIn as an event-based model and informs future methodological extensions to relax the monotonic progression constraint.

Understanding How Workplace Interactions Impact Social Cognitive Performance, Self-esteem, and Self-stigma in Individuals with Bipolar Disorder

Isabella Yeghiayan [1,2],Katie M. Lavigne[1,3], Geneviève Sauvé[1,4] , Delphine Raucher-Chéné[1,3]

[1]Douglas Research Centre, Montréal, QC, Canada
[2]Department of Psychology, McGill University, Montreal, Québec, Canada
[3]Department of Psychiatry, McGill University, Montréal, QC, Canada
[4]Department of Education and Pedagogy, Université du Québec à Montréal, Montréal, QC, Canada

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Corresponding author email: isabella.yeghiayan@mail.mcgill.ca

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Individuals with bipolar disorder (BD) have low employment rates, partly due to impaired cognitive performance. However, employment plays an important role in an individual's sense of purpose and quality of life. For those with BD, employment has been associated with enhanced self-satisfaction and reduced psychiatric symptoms, which in turn are linked to increased self-esteem and improved mood, as employment can be viewed as attaining important goals. Goal attainment is also negatively correlated with self-stigma, as social cognitive performance may decline when individuals face stigmatizing scenarios in the workplace. There is a lack of understanding of the relationships among social cognition, self-esteem, and self-stigma in the context of employment. This study aims to examine these relationships in individuals with BD over a two-month period of employment-related observation. Twenty-two individuals with BD were recruited from the Douglas Institute outpatient clinic for mood disorders. Given that they were all employed, they underwent assessments measuring the quality of workplace interactions, as well as their social cognitive performance, self-esteem, and self-stigma. To test our hypotheses, a repeated-measures ANOVA will be conducted to evaluate the effect of time on social cognitive performance, self-esteem, and self-stigma. Correlation analyses and a mediation model will also be used to examine relationships between workplace interactions and these outcomes. It is hypothesized that self-stigma will decrease before there is an increase in self-esteem and social cognitive performance, along with the expectation that self-stigma and social cognition are correlated and that self-stigma will impact social cognitive performance.

Characterization of Antibiotic Combinations Against *Mycobacterium abscessus* Using Growth and Viability Assays

Zeineb Haouari[1], *Andréanne Lupien*[1,2]

[1]Department of Microbiology and Immunology, McGill University, Montreal, QC, Canada

[2]Department of Medicine, McGill University, Montreal, QC, Canada

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Corresponding author email: zeineb.haouari@mail.mcgill.ca

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The *Mycobacterium abscessus* complex is a rapidly growing group of non-tuberculous mycobacteria associated with severe pulmonary infections and intrinsic antibiotic resistance, limiting treatment options for affected patients. Thus, to maximize efficacy, combination therapy is commonly used in the clinical management of *M. abscessus* pulmonary exacerbations. However, the interactions between antibiotics are not fully characterized at the experimental level. This study evaluates the activity of selected ribosome-targeting antibiotics alone and in combination against *M. abscessus* smooth and rough morphotypes, with the hypothesis that certain combinations demonstrate enhanced activity relative to single agents. Single-drug and combination effects were first assessed using a resazurin microtiter assay (REMA). Linezolid was tested in combination with multiple macrolides with different spectra of activity against *M. abscessus*, including josamycin, tylosin tartrate, and clarithromycin. Among these combinations, only linezolid combined with clarithromycin demonstrated enhanced inhibitory activity in the *M. abscessus* smooth reference strain. To further characterize this interaction, duplicate checkerboard assays were performed, followed by colony-forming unit (CFU) enumeration to distinguish between growth inhibition and reduction in viable bacteria (cidality of the combination). Ongoing work includes extending combination testing to the rough morphotype to determine whether the observed interaction is strain-dependent. Together, these experiments aim to better define antibiotic interactions against *M. abscessus* and clarify the nature of the linezolid-clarithromycin effect.

Global Z-score Normalization Enables Training-free Automatic Detection of Punctate White Matter Lesions in Neonates

Hoi Ching Wat[1,2], Erjun Zhang[1,3], Kylie Xu[1,4], Gregory Lodygensky[1,5,6]
[1]CHU Sainte-Justine Hospital Research Center, Montreal, QC, Canada
[2]Department of Biomedical Engineering, McGill University, Montreal, QC, Canada
[3]Neuropoly Lab, Institute of Biomedical Engineering, Polytechnique Montréal, Montreal, QC, Canada
[4]Department of Medicine, University of Montréal, Montreal, QC, Canada
[5]Department of Pediatrics, University of Montréal, Montreal, QC, Canada
[6]Department of Pharmacology and Physiology, University of Montréal, Montreal, QC, Canada

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Corresponding author email: hoi.wat@mail.mcgill.ca
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Punctate white matter lesions (PWMLs) are common in preterm neonates and linked to adverse neurodevelopmental outcomes. Conventional identification relies on subjective visual contrast on MRI. We propose a global, training-free z-score normalization framework for automatic PWML detection, enabling standardized, interpretable segmentation across modalities without machine learning or subject-specific calibration. We analyzed 44 neonates from the dHCP dataset, comprising 1069 axial slices from T1w, T2w, and mean diffusivity (MD) maps. Reference masks were generated by consensus among four trained raters. Slices within each modality were standardized to a global z-score space, allowing comparable intensity distributions. For each modality, a detection threshold of z-score was swept from -3 to 3 standard deviations to construct receiver operating characteristic (ROC) curves. Lesion–white matter contrast ratios (CR) were also computed. Inter-rater reliability (Cohen's k) reached 0.88 for T1w, 0.77 for T2w, and 0.73 for MD. PWML–white matter contrast differences were statistically significant ($p < 0.01$). Contrast magnitude was greatest for T1w (CR = 0.57 ± 0.19), compared to T2w (-0.18 ± 0.08) and MD (-0.14 ± 0.12). ROC analysis revealed that T1w outperformed the other modalities, achieving an AUC of 0.98 at an optimal threshold of 0.84 (True Positive Rate = 0.90, False Positive Rate = 0.06). In contrast, T2w and MD achieved lower AUCs of 0.84 and 0.67, respectively. Global z-score normalization yields a robust, fully automatic lesion detection method. This interpretable baseline achieves high sensitivity with minimal false positives and provides a reproducible benchmark for evaluating deep-learning or quantitative MRI pipelines.

Bromodomain Mutations Confer Resistance to SWI/SNF PROTAC-Mediated ATPase Degradation

Sofia Zahariadis[1,3], *Benjamin Martin*[2,3,4]
[1]Department of Pharmacology and Therapeutics, McGill University, Montreal, Quebec, Canada
[2]Gerald Bronfman Department of Oncology, McGill University, Montreal, QC, Canada
[3]Lady Davis Institute for Medical Research, Jewish General Hospital, Montreal, QC, Canada
[4]Department of Biochemistry, McGill University, Montreal, QC, Canada

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Corresponding author email: sofia.zahariadis@mail.mcgill.ca

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The SWI/SNF (SWItch/Sucrose Non-Fermentable) chromatin-remodelling complexes regulate transcription by repositioning nucleosomes; their paralogous ATPase subunits, BRG1 and BRM, are frequently altered in human disease. Mutations in SWI/SNF subunits occur in more than 20% of human cancers, underscoring the importance of these complexes in transcriptional regulation. AU-15330 is a proteolysis-targeting chimera (PROTAC) that targets BRG1, BRM, and the PBRM1 subunit of PBAF; however, the potential for acquired resistance remains unclear. This study investigated whether two bromodomain mutations identified in AU-15330–resistant BRG1 clones are sufficient to prevent BRG1 degradation. Wild-type and mutant BRG1 constructs tagged with 3×FLAG/HiBiT were generated, expressed in cells, and treated with AU-15330. HiBiT luminescence was normalized to cell count and reported relative to DMSO-treated controls. AU-15330 caused a substantial loss of wild-type BRG1 signal, reducing normalized HiBiT luminescence by 64% compared to DMSO. In contrast, the bromodomain-mutant BRG1 construct showed only a 4% decrease in signal, demonstrating that these two mutations render BRG1 largely resistant to PROTAC-mediated degradation. Western blot analysis confirmed robust degradation of endogenous BRG1. Although exogenous mutant BRG1 expression was below the limit of detection due to low expression, its strong HiBiT signal still indicated resistance relative to exogenous wild-type BRG1. Because these residues are conserved in the bromodomains of BRM and PBRM1, analogous mutations may similarly confer resistance and warrant further investigation. In addition, this system provides a tool to selectively preserve BRG1 while selectively degrading BRM and PBRM1 thereby enabling the study of paralogue-specific SWI/SNF functions.

Grow the Glow: Design and Evolution of a Fluorescence-Based Genetically Encoded Biosensor for Glycine

Juliette Demers[1,2], Rochelin Dalangin[2], Marie-Eve Paquet[2,3,4]
[1]Department of Biochemistry, McGill University, Montreal, QC, Canada
[2]CERVO Brain Research Center, Université Laval, Quebec, QC, Canada
[3]Department of Anesthesiology and Intensive Care, Université Laval, Québec, QC, Canada
[4]Department of Microbiology, Biochemistry and Bioinformatics, Université Laval, Québec, QC, Canada

Keywords: Genetically Encoded Biosensor, Glycine, Neurotransmitter Dynamics, Protein Engineering, Structure-Guided Mutagenesis
Corresponding author email: juliette.demers@mail.mcgill.ca
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Glycine is an amino acid that plays a crucial role in the development, functioning, and regulation of the central nervous system. It acts as the major inhibitory neurotransmitter in the brainstem, cerebellum, and spinal cord by modulating chloride ion levels in neurons. Additionally, glycine is a co-agonist required for the activation of excitatory NMDA receptors. Despite the importance of glycine in neurotransmission, much remains unknown about glycine dynamics *in vivo* due to the lack of appropriate monitoring tools. Fluorescence-based genetically encoded biosensors, composed of a fluorescent protein linked to a ligand-binding domain, provide the spatial (synaptic) and temporal (millisecond) resolution needed to monitor neurotransmitter dynamics. Although some existing biosensors can bind glycine, they suffer from low affinity and preferentially bind structurally similar molecules, such as L-proline and D-serine. Using these green fluorescent protein-based scaffolds, a glycine biosensor was designed by optimizing for physiological glycine affinity while minimizing binding of other amino acids. Combining structure-guided design and random mutagenesis, libraries of glycine biosensor variants were generated. Using a bacterial system, these libraries were screened for variants with increased glycine affinity, decreased affinity for other amino acids, and greater changes in fluorescence intensity upon ligand binding. Variants displaying desirable performance across these metrics were conserved for additional rounds of mutagenesis and screening. Preliminary screenings identified key mutations near the ligand-binding site and linker region that improve the biosensor's glycine affinity and change in fluorescence intensity. However, high-affinity off-target binding to amino acids structurally similar to glycine, such as L-alanine, remains a major challenge. To minimize challenges in off-target binding, future work will focus on transferring the screening process to a mammalian cell culture system, where optimization of membrane trafficking, folding, and functional performance in a physiologically relevant environment may be achieved.

Characterizing Urotensin Receptor Ligands for Potential Signaling Bias

Candide Bazinet[1], *Jiajia Lu*[1], *Jana Schüttpelz*[1], *Terry Hébert*[1]
[1]Terry Hébert Lab, McGill University/Telescope Therapeutics, Montreal, QC, Canada

Keywords: Urotensin, Biased Agonism, Species Specific, GPCR
Corresponding author email: candide.bazinet@mail.mcgill.ca
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Urotensin receptors (UT) play a central role in cardiovascular physiology, contributing to vasoconstriction, vasodilation, fibroblast activation, angiogenesis, and cardiac hypertrophy. Expression of the endogenous ligands urotensin II (UII) and urotensin-related peptide (URP) is elevated in patients with chronic kidney and cardiovascular disease, suggesting that modulation of this pathway may hold therapeutic potential. Preclinical studies have proposed that UT inhibition could benefit conditions such as congestive heart failure, atherosclerosis, and pulmonary arterial hypertension. However, despite promising results in rodent models, UT antagonists have not translated into clinical efficacy—likely reflecting interspecies differences between human UT (hUT) and rat UT (rUT), as well as species-specific forms of UII. This work examines the hypothesis that divergent clinical outcomes stem from fundamental biological differences between hUT and rUT, which may yield distinct activation profiles for both endogenous ligands and synthetic antagonists. To address this, we aim to characterize UT signalling using BRET-based biosensors in HEK293 cells expressing either hUT or rUT. Two complementary biosensors will be used: a PKN1-RLucII system to monitor $G_{12/13}$-dependent signaling through Rho recruitment, and a PKC-based biosensor to assess G_q-mediated activation of phosphoinositide pathways, including PIP3 and DAG production. Responses to UII and URP will be compared across species-specific receptors, followed by evaluation of known antagonists. A comparative understanding of hUT and rUT responses to endogenous ligands and antagonists may clarify the reasons behind previous clinical failures and guide the development of more effective UT-targeting therapeutics capable of slowing the progression of cardiovascular disease.