



BIO² Symposium

Bioinformatics & Biotechnology

August 8, 2024

**Program and
Abstract Booklet**

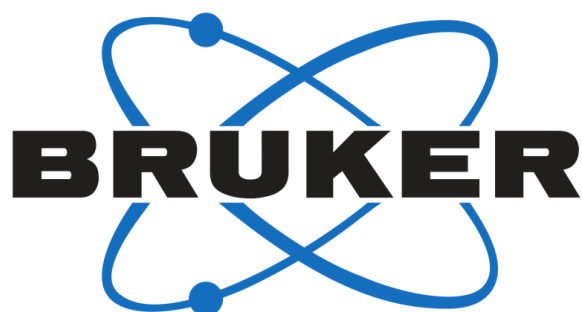
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EVENT SCHEDULE

Summerlee Science Complex Waasamowin (formerly the Atrium)

- > 8:30 – 9:00 a.m.: Registration

Alexander Hall, Room 100

- > 9:00 – 9:10 a.m.: Opening remarks
- > 9:10 – 9:50 a.m.: Keynote Speaker: Dr. Mathieu Lavallée-Adam, *Using machine learning to end brute force data acquisition in mass spectrometry-based proteomics*
- > 9:50 – 10:30 a.m.: Keynote Speaker: Dr. Asena Goren, *Computational exploration of biological systems using optimization algorithms inspired by nature*
- > 10:30 – 11:10 a.m.: Break (refreshments provided in the Summerlee Science Complex Waasamowin)
- > 11:10 a.m. – 12:20 p.m.: Presentations by current and former University of Guelph Bioinformatics and Biotechnology graduate students
 - > Carmen Machado Vides, Master of Biotechnology alumnus
 - > Maysa Niazy, PhD in Bioinformatics candidate
 - > Michael Dubé, PhD in Bioinformatics candidate
 - > Jeff Hulley, Master of Bioinformatics alumnus

Summerlee Science Complex Waasamowin (formerly the Atrium)

- > 12:30 – 1:30 p.m.: Lunch
- > 1:30 – 3:30 p.m.: Poster session with posters by our Master of Bioinformatics and Master of Biotechnology students
- > 4:00 – 4:10 p.m.: Presentation of poster awards
- > 3:00 – 5:00 p.m.: Networking with refreshments and cashless bar

KEYNOTE SPEAKERS



Dr. Mathieu Lavallée-Adam

Dr. Mathieu Lavallée-Adam is an Associate Professor at the University of Ottawa in the Department of Biochemistry, Microbiology and Immunology and is affiliated to the Ottawa Institute of Systems Biology. He obtained a B.Sc. in Computer Science and a Ph.D. in Computer Science, Bioinformatics option, from McGill University. He then performed his postdoctoral research at The Scripps Research Institute.

His research focuses on the development of statistical and machine learning algorithms for the analysis of mass spectrometry-based proteomics data and protein-protein interaction networks. He also designs computational methods mining proteomics datasets for biological information through their integration with genomics data.

Dr. Lavallée-Adam is a recipient of the John Charles Polanyi Prize in Chemistry, rewarding the impact of his bioinformatics algorithms on the mass spectrometry community. One of his publications was also recognized as the 2018 Highlight of the Year by an early career researcher at the Human Proteome Organization (HUPRO) World Congress. He was named Early Career Researcher of the Year by the Ottawa Institute for Systems Biology in 2021, and he received the New Investigator Award from the Canadian National Proteomics Network in 2023. He is also Co-Chair of the HUPRO Early Career Researcher Initiative, in which he develops training activities, advocates for junior investigators in proteomics and organizes events highlighting their research on the international stage. As VP Operations of the Canadian National Proteomics Network, Dr. Lavallée-Adam also leads and mentors the Operations Management Team, which builds a set of online activities to bring Canadian proteomics researchers together all year round.

KEYNOTE SPEAKERS



Dr. Asena Goren

Dr. Asena Goren studied Plant Science at the University of Guelph and graduated from the Bioinformatics Master's program in 2017. During her Master's degree, she developed a computational model for understanding how the interplay of enzyme activities can create the complex structure of an amylopectin molecule. Her education at the intersection of biological and computational sciences enabled her to undertake research in a broad diversity of biological systems, including endangered species conservation, plant metabolism and mycology. Her doctoral research involved exploring the spread of tick-borne disease into high latitude ecosystems using mathematical models and Bayesian statistics. Asena continues to conduct interdisciplinary research that uses computational model development to guide empirical investigations in the field and laboratory.

POSTER PRESENTATIONS

Master of Biotechnology

Alejandra Beltrán Plascencia	Uncovering a chloroplast lipase interactome in <i>Arabidopsis thaliana</i> via Bimolecular Fluorescence Complementation
Alessia Molinaro	Investigating the purpose of pharmaceutical brand promotion in healthcare
Anna Billing	Biosynthesis of prenylated and methylated hemp polyphenols
Ashitija Jasrai	Assessing the relationship between hypertension, blood-brain barrier breakdown, and neurological dysfunction
Bruke Asefa	Development of market research and analysis framework
Christian Pittao	Characterizing a succinate production pathway in <i>Lachnospiraceae</i>
Duaa Al-Majmaie	Regulation of glycogen phosphorylase under oxidative stress by S-glutathionylation
Jing Sun	Proteomics sample preparation workflow optimization
Kaine Comin	Aquatic Invasive Species Analyst
Kandice Silva	Assessing lipid traits affecting drought tolerance in Ontario-adapted commercial soybean varieties
Lazar Vujanovic	Resilience of yeast and brewing: Engaging customers during economic challenges

POSTER PRESENTATIONS

Madison Van Zyl	Optimizing protein expression and purification protocols for proteases in <i>Cryptococcus neoformans</i> and their complementary inhibitors in mollusks
Melissa Pobre	Biological mapping of a poultry processing facility
Molly Varey	Management of a case-based Systemic Lupus Erythematosus (SLE) learning activity development project
Muhammad Khalid	Driving the growth of an emerging biotech company as a Business Strategy Associate
Nicholas De Mola	Marketing PHA plastics and driving engagement to MetaCycler BioInnovations as a Business Strategy Associate
Nigel Nahous	Investigating the mechanism of action of <i>Escherichia coli</i> Glucosamine-6-Phosphate Synthase Inhibitors
Rohit Chandra	Regulation of vesicle-associated membrane protein 2 function by Cdc42
Shehla Choudhary	Cell surface MT1-MMP expression in MDA-MB-231 cells with truncated VAMP2 constructs
Taylor Howson	Investigating the ideal growth conditions of <i>Pseudomonas putida</i> for the production of Polyhydroxyalkanoate
Yuan Pei	Detection of plant pathogens in plant, soil and water samples via DNA metabarcoding

POSTER PRESENTATIONS

Master of Bioinformatics

Aania Rafi	Machine learning tracing of early warning signals for COVID-19 variant evolution in Canada
Amjad Osman	Optimizing efficiency of cultivation and harnessing machine learning to explore gut microbial dark matter
Anusha Bailoor	Impact of SARS COV-2 on pregnancy: Preterm birth risk
Arvind Srinivas	Exploring the conditions for increased viral persistence in SARS-CoV-2: An extended SIR model framework
Cassandra Drazick	Gene Detective: Uncovering top features using machine learning
Edicon Chan	Leveraging Nextflow for enhanced reproducibility and efficient RNA sequencing analysis for enzyme discovery
Jacob Hambly	High-throughput <i>in silico</i> screening of peptidase-inhibitor complexes for the discovery of novel antifungal therapeutics
Leon Edmiidz	Machine learning in multiple sequence alignment
Lina Elshurafa	De novo viral genome assembly using Oxford Nanopore long read data
Lubaina Ahmed Kothari	Inter-species and intra-population variation in <i>Amaranthus</i> species using whole genome sequencing.
Maheen Siddiqui	Ensuring accuracy in variant identification through VCF validation
Neha Patel	Impact of thermal upper limits on species range shift rates on a global scale

POSTER PRESENTATIONS

Qingyuan Pei	Exploring repetitive elements in relation to the genome size of eggplant and its wild relatives
Robin Zutshi	Forecasting COVID-19 using viral and host population factors
Simon Lim	Probing the genetic diversity of integrated mobile elements in <i>Gammaproteobacteria</i> and their role in the spread of antimicrobial resistance
Veedhi Solanki	Tracking SARS-CoV-2 evolution: Detection and phylogenetic analysis of cryptic lineages in wastewater samples
Xiao Lei Du	Automated quantification pipeline for fluorescent microscopy image analysis
Yuqi Li	Automated deep learning classification of viral genomes using Frequency Chaos Game Representation (FCGR)
Zachary Ribau	Cross sectional associations between genetically predicted sleep traits and dietary outcomes in the Guelph Family Health Study

Master of Science

Olivia Smith	Uncovering molecular mechanisms controlling cellular metabolism during heart regeneration in the gecko <i>Eublepharis macularius</i>
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PhD

Melanie Goens	Development of a Newcastle Disease Viral Vector Vaccine for Nipah Virus
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ABSTRACTS

Dr. Mathieu Lavallée-Adam

Using machine learning to end brute force data acquisition in mass spectrometry-based proteomics

Proteins are molecules that govern much of the behaviour of cells. The ability to characterize proteins is therefore crucial to provide a functional understanding of biological samples. Mass spectrometry-based proteomics is the most popular approach for the large-scale identification of proteins. Nevertheless, mass spectrometry data acquisition strategies fail to characterize all proteins in complex biological samples. These data acquisition methods require tuning many parameters for which the optimal values can vary based on the properties of the analyzed proteins. Unfortunately, mass spectrometry data acquisition techniques often select sub-optimal parameters generating low-quality data that only allow the identification of a subset of abundant proteins from samples.

Computationally optimizing data acquisition parameters in real-time during mass spectrometry experiments can improve our ability to comprehensively identify proteins in biological samples. We therefore present MealTime-MS, a novel software suite that uses machine learning algorithms to guide mass spectrometry data acquisition on the fly during mass spectrometry experiments. Our software suite uses protein properties measured by the mass spectrometer to target for data acquisition proteins that will maximize the number of protein identifications. Hence, MealTime-MS improves proteome characterization and provides a better understanding of underlying functional processes in biological samples.

ABSTRACTS

Dr. Asena Goren

*Computational exploration of biological systems
using optimization algorithms inspired by nature*

Computational biology is full of problems that are very difficult to approach using traditional analytical methods. Interpretation of large amounts of high dimensional data generated by modern laboratory technology requires the development of innovative mathematical and statistical analytical approaches. In this talk, I will introduce the utility of soft computing in bioinformatics, with an emphasis on evolutionary computation. Evolution is nature's optimization algorithm, and implementing the principles of evolution in numerical simulations yields a powerful tool for modeling biological systems. I will present some highlights of how evolutionary computation has been used to develop pattern matching and clustering algorithms, and the applications of these algorithms in genomics and other omics research. I will conclude with the presentation of a case study demonstrating the use of nature-inspired algorithms to model how the intricate structure of amylopectin, a large carbohydrate molecule, can be achieved by the coordinated actions of a suite of enzymes.

ABSTRACTS

Carmen Machado Vides

Master of Biotechnology Alumnus

Addressing coffee production challenges with biotechnology knowhow

Coffee is a vital crop globally, significantly contributing to the economies and societies of approximately 80 producing countries. In Mexico, coffee production is crucial, providing up to 500,000 jobs across 14 federal entities. However, the Mexican coffee sector has faced significant challenges over the past decade, leading to substantial yield losses.

This project aimed to explore the opportunities and challenges in the Mexican coffee industry and to propose a biotechnology innovation in the coffee space. Business approaches and methods such as market research, PESTLE (political, economic, social, technological, legal and environmental factors) analysis, SWOT (strengths, weaknesses, opportunities and threats) analysis, expert interviews, design thinking, open innovation and business model canvas were employed to accomplish the project's objectives. The project's outcome included an industry analysis, a research proposal focused on metagenomic analysis of coffee fermentation and a business plan. In conclusion, this project developed a compelling case for developing a biotechnology innovation to address a challenge in the Mexican coffee industry, emphasizing the potential benefits of metagenomics in enhancing coffee quality.

ABSTRACTS

Maysa Niazy

PhD in Bioinformatics Candidate

Towards High-Throughput Microbial Diversity Analysis: Investigating the relationship between vaginal microbiota dynamics and reproductive success in sows (Brenda Christensen, Khurram Nadeem, Lee-Anne Huber, Robert Friendship, Nicole Ricker)

The benefits of a healthy vaginal microbiome may include a fast recovery post-farrowing, resulting in a lower likelihood of urogenital infection, vaginal discharge, or prolapse. Adverse health outcomes, like vaginosis and premature birth, have been linked with increased vaginal microbial community diversity in humans. However, in sows, little is currently known about the vaginal microbiome's transition from late gestation to post-farrowing, as well as the differences in microbiome between older sows and gilts. Here, we aimed to identify 1) shifts in the vaginal microbiome as a result of farrowing, 2) whether the vaginal microbiome of the sow post-farrowing influences subsequent sow reproductive status, and 3) whether an abnormal vaginal microbiome is associated with vaginal discharge or other health issues post-farrowing.

A total of 50 primiparous (0 parity) gilts and 58 multiparous (1-6 parity) sows were chosen for the study. Vaginal swabs were collected three times: week 13 of gestation, farrowing week, and two weeks post-farrowing. The reproductive performance was determined, including the number of piglets weaned per mated sow per year (PWPMS), stillbirth occurrences, wean-to-estrus interval, and vaginal discharge (a scale of 0-2, where 0 indicates no discharge; a discharge of 1 is mild; and a discharge of 2 is severe). Microbiome composition was assessed by sequencing the V4 region of the 16S rRNA gene.

ABSTRACTS

The vaginal microbiotas of sows demonstrated noticeable variations over gestational periods for all parities, and decreased bacterial diversity was identified in the multiparous group compared to the primiparous. During the gestational period, there was an observed inverse correlation between Firmicutes and Proteobacteria, with Firmicutes increasing while Proteobacteria decreased in most animals. Based on the Bray-Curtis dissimilarity index, there was no correlation between vaginal microbiota and reproductive success when including all parities in the analysis; however, within the primiparous group, significant differences were identified in bacterial relative abundance between gilts with no discharge and those with severe discharge. Gilts with no discharge or stillbirths had lower diversity compared to those with less reproductive performance, severe discharge, and a higher stillbirth rate, as indicated by Shannon diversity ($P < 0.012$, $P < 0.022$, respectively). We confirmed that the vaginal microbiota was altered in gilts with severe vaginal discharge and stillbirth using the Latent Dirichlet Allocation model (LDA). The LDA uses mixed membership to characterize vaginal communities, addressing the sensitivity and robustness of existing clustering approaches. The LDA model identified seven subcommunities within the study population. Subcommunity 6 (*Enterococcus*, *Aerococcus*, and *Prevotella*) and Subcommunity 7 (*Pseudomonas* and *Burkholderia*) were correlated with gilts with severe discharge, while Subcommunity 1 and Subcommunity 3 had less diversity and were correlated with gilts with no stillbirth.

This study identifies the dynamics of the vaginal microbiota in sows during the gestational period, and the vaginal shifts observed point to potential directions for modifying these communities to improve the sows' performance and overall health. Our analyses using latent class models allow for the exploration of heterogeneous populations and reveal substructures in vaginal ecosystems with potential clinical and biological associations. These findings will also serve as a reference for future studies focusing on the microbiome.

ABSTRACTS

Michael Dubé

PhD in Bioinformatics Candidate

Iterating towards an evolutionary pattern search for weakly conserved biological sequences

In this talk, I outline the current progress made in my PhD towards using Evolutionary Algorithms (EAs) to locate a pattern in weakly conserved biological sequences. An EA simulates biological evolution on a population of candidate solutions to a problem. In this case, the candidate solutions are Self-Driving Automata (SDAs). Each SDA is a machine that outputs a sequence of DNA bases. The candidate solutions are subject to a number of fitness functions that evaluate the output of the SDAs. These evaluations guide evolution towards an optimal solution over successive generations of the EA. I will outline how EAs work, the SDA and progress towards using this system to locate patterns in biological sequences.

ABSTRACTS

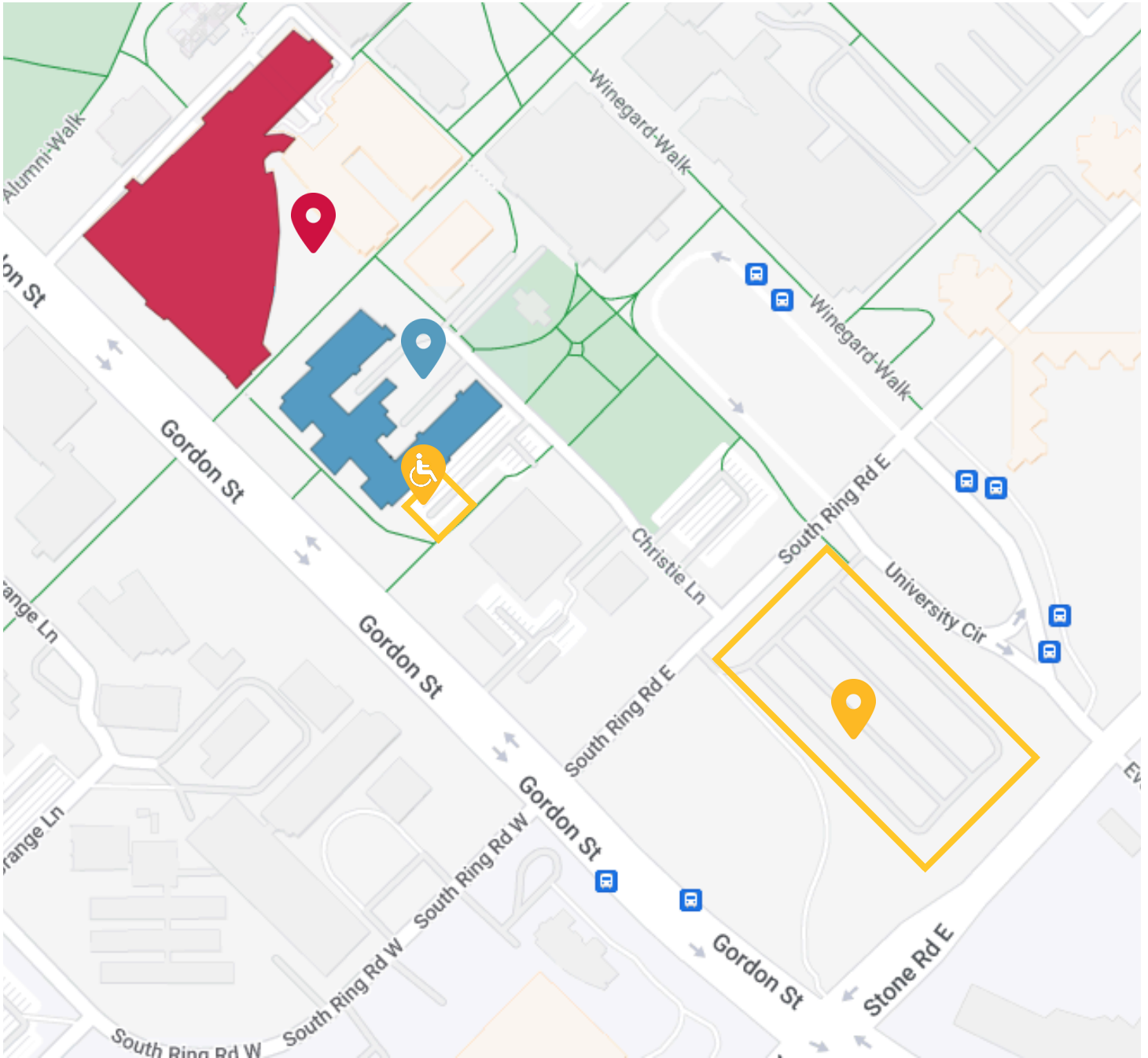
Jeff Hulley

Master of Bioinformatics Alumnus

World Wide Bioinformatics Web

Digital marketing requires knowledge from multiple disciplines, including data analytics, content creation, search engine optimization, social media management and consumer psychology. Digital marketing and bioinformatics intersect through the use of advanced data analytics and personalized strategies, leveraging large datasets to tailor specific health-related content and resources to target audiences effectively. Let me walk you through how my bioinformatics background landed me in the digital marketing space.

EVENT MAP



Summerlee Science Complex



Alexander Hall



Parking (P31)



Accessible Parking (P1)