



BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

September 20, 2024
8:30am-6:30pm

11th Annual BICB Industry Symposium:

	Activity	Location
6:30 am – 6:45 am	Bus Boarding	University of Minnesota, Rochester on S. Broadway
6:45 am – 8:30 am	Bus Travel (from Rochester)	ROCH □ UMTC
8:30 am – 9:00 am	Registration and Welcome Reception	CCRB Atrium
9:00 am – 9:05 am	Opening Remarks: Paul Hanstedt (Vice Chancellor for Academic Affairs and Innovation)	CCRB 1-125
9:05 am – 9:10 am	Welcome: Chad Myers, PhD BICB Director of Graduate Studies	CCRB 1-125
	Session Chair: Yuk Sham	
9:10 am – 9:45 am	Jean-Pierre Kocher (Professor of Biomedical Informatics - Mayo Clinic)	CCRB 1-125
9:45 am – 10:20 am	Candice Hirsch (Department of Agronomy and Plant Genetics - University of Minnesota)	CCRB 1-125
10:20 am – 10:35 am	Taylor Harrison (Advisor: Hongfang Liu - Mayo Clinic)	CCRB 1-125
10:35 am-10:45 am	Break	
10:45 am – 11:05 am	Sean Larson - MinneAnalytics	CCRB 1-125
11:05 am – 12:30 pm	Poster Presentations	CCRB Atrium
12:30 pm – 1:30 pm	Lunch and Networking	CCRB Atrium
	Session Chair: Chad Myers	
1:30 pm – 2:05 pm	Benjamin Kipp (Professor of Laboratory Medicine and Pathology - Mayo Clinic)	CCRB 1-125
2:05 pm - 2:20 pm	Natalie Bennett (Advisor: Trevor Wardill - University of Minnesota)	CCRB 1-125
2:20 pm – 2:55 pm	Constantin Aliferis (Director of the Institute for Health Informatics - University of Minnesota)	CCRB 1-125



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Time	Activity	Location
2:55 pm - 3:30 pm	Matthew Moscou (USDA-ARS Research Plant Pathologist/Adjunct Assistant Professor)	CCRB 1-125
3:30 pm - 3:40 pm	Break	CCRB 1-125
3:40 pm - 4:25 pm	BICB Faculty & Student Group Meeting	
4:25 pm - 4:30 pm	Closing Remarks Yuk Sham, PhD BICB Director of Graduate Studies	CCRB 1-125
4:30 pm - 6:30 pm	Social Event	CCRB Green Rooftop
6:30 pm - 6:45 pm	Bus Boarding	
6:45 pm - 8:30 pm	Bus Travel to Rochester	UMTC □ ROCH

Thank you to our BICB partners:

University of Minnesota

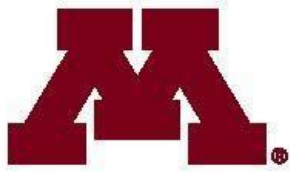
The Hormel Institute

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Candice Hirsch - Department of Agronomy Plant Genetics, University of Minnesota, St Paul, MN.

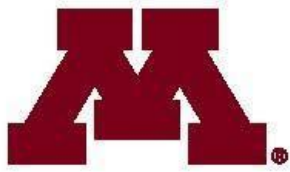
From Genome to Phenome: Understanding the Diversity of Maize

Maize is an extraordinarily diverse species. At the genome level we have demonstrated extensive structural variation in the maize pan-genome beginning with early pan-transcriptomics studies. Recent advances in sequencing technologies and assembly algorithms have allowed us, for the first time, to characterize this variation across the entirety of the genome. Pacbio-based assemblies of the 26 NAM founder lines are allowing comparative genomic analyses typically conducted across species to be applied to characterize the extensive variation within maize with regards to both genes and transposable elements. This variation in genome content is able to explain phenotypic variation in the maize NAM population that is not captured by SNP variation alone and to provide insights into genome variation that has facilitated local adaptation of the species. We have also shown these structural variants drive dynamic gene expression patterns in inbreds and expression complementation in hybrids. This variation in the maize pan-genome also drives the variation in plasticity and environmental responsiveness that is observed within the species. This talk will discuss our current understanding of variation in the maize pan-genome and the extensive variation in drives in phenotypic diversity and plasticity.

[Jean-Pierre Kocher](#) (Professor of Biomedical Informatics - Mayo Clinic)

Developing a Bioinformatics Core to support Research and the Practice: a retrospective review of the challenges and successes

The Bioinformatics Core (BIC) at Mayo Clinic provides services and collaboration to researchers and clinicians across the 3 Mayo Clinic sites. The BIC was formed 20 years ago and today includes more than 65 team members, supporting more than 200 investigators. I will review the challenges, successes, and some of the strategic decisions that have shaped the BIC.



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Student Speaker: Taylor Harrison (Advisor: Hongfang Liu - Mayo Clinic)

Advancing Digital Health Equity and Inclusiveness: Leveraging Large Language Models to Accelerate Literature Review

Digital health technologies (DHTs) have revolutionized clinical trials, offering unprecedented opportunities to streamline processes, enhance patient engagement, and improve data quality. Growing technology device and broadband access are contributing to the increasing number of DHT-enabled trials. Ideally, DHTs have the potential to make clinical research more inclusive and diverse. However, while the variety in digital technologies and implementations present a strong display of healthcare innovation, major challenges arise concerning DHT generalizability and translation into real-world medical practice. Here, we leverage large language models (LLMs), identified in existing task evaluations as possible tools supporting evidence harvesting scalability, to accelerate the literature review process related to the use of DHTs in randomized controlled trials (RCTs). LLM assisted title screening, text processing, Social Determinants of Health data (SDoH: commonly reported in Table 1) evaluation, and information extraction, yield promising results towards conducting large scale literature review. Combined with natural language processing techniques, our unique literature mining methodologies generate insights from thousands of RCTs to produce guidelines toward reporting standardization and participant inclusiveness in DHT-enabled RCTs.

Student Speaker : Natalie Bennett (Advisor: Trevor Wardill - University of Minnesota)

"Tales from the Deep: Exploring Visual Self-Recognition and Social Behaviors in Cephalopods through Deep Learning and Two-Way Mirrors"

Visual self-recognition is the ability to distinguish visually the self/viewer from another of the same species as has been shown in vertebrates, yet no invertebrates have passed the Mirror Self Recognition (MSR) test. The MSR test determines self-recognition by using a mirror to reveal a mark on the body that can only be seen via reflection. Of the invertebrates, octopuses are the most likely to pass the MSR test, as they have the largest invertebrate brain relative to body size and are capable of learning and using spatial memory. Despite octopuses' complex camouflage and signaling capabilities most authors describe them as lacking any social behaviors, even though their squid relatives have social dominance hierarchies. Thus, it remains a mystery how octopuses mate successfully if they lack any social communication. Social cues would likely help improve the outcome of mating interactions by reducing cannibalism or potentially enabling spermatophore selection. Sociality and problem solving in vertebrates is associated with large brain size, yet whether invertebrates with large brains have similar traits is unclear. By quantifying octopus behavior via two-way mirrors, high-resolution (HR) cameras, and machine learning classification tools, I will elucidate whether octopus have visual self-recognition and express social behaviors that may improve mating outcomes. Understanding such complex motor control, cognitive mechanisms, and potential social behaviors in cephalopods will increase our understanding of how diverse brains operate while also giving insights for soft robotic and prosthesis systems.