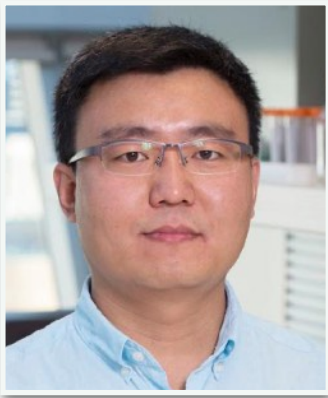


CIRC Symposium Series 2025-2026

Large-Scale Multiomic Integration Links 'Junk' DNA to Age-Related Chronic Disease

Hongbo Liu, PhD | Department of Biomedical Genetics



Genome-wide association studies have identified numerous DNA sequence variants associated with complex human diseases. However, over 90% of disease-associated variants reside in noncoding genome regions, and their functions in complex diseases remain largely unknown. To address this, we integrated various genomic and epigenomic datasets to identify the regulatory variants by developing several computational strategies, and developed a statistical model, Open4Gene, to link non-coding variants to their target genes using single cell multiome data. Open4Gene identified 1,351 target genes of genetic variants located within open chromatin regions. By integrating these GWAS and multiome datasets (total 32 types), we found over 24,000 regulatory variants targeting more than 1,000 genes, with over 600 genes also targeted by coding variants. In particular, we discovered the convergence of coding and regulatory variants on 161 key disease genes, critical cell types (including proximal tubules), transcriptional regulators (including HNF4A), and potential drug targets for kidney disease, providing an integrative strategy for functional annotation of noncoding variants in complex human diseases.

Machine Learning Optimization of Photonic Crystal Nanocavities

Christer Everly | The Institute of Optics

Photonic crystal cavity design can be an exceptionally complex and computationally expensive endeavor. This talk examines the use of data driven approaches toward optimization of dual photonic crystal nanobeam cavities for optomechanics applications. We explore the use of hybrid deep learning and genetic algorithm optimization to create novel designs.

Friday, November 21, 2025

11:30 am - 1 pm

Wegmans Hall 1400



**University
of Rochester**