



# Genetics, Bioinformatics, & Systems Biology Colloquium

presents



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 **Thursday**  
**Jan 11, 2024**  **12PM**  **Leichtag Auditorium**  **Zoom**

**LIVE**  
**IN-PERSON**  
**with Pizza**

\*Live stream via Zoom available

## Building Ultra-Large Pangenomes

Pangenomics is an emerging field that is allowing us to accurately and comprehensively study the within-species genetic diversity and its relationship to physical traits (phenotypes) by using a collection of genomes of a species instead of a single reference genome. Future pangenomics applications would likely require analyzing ultra-large (up to millions of sequences) and ever-growing collections of genomes. While existing pangenome data formats can represent the genetic variation in a collection of genomes, they do not store their shared evolutionary and mutational histories, and are also unlikely to keep up with the speed and volume of genome sequencing data. In this talk, I will discuss the ongoing work on a novel pangenomic data representation in my lab that which would address these limitations and greatly improve the scale, speed, and resolution of pangenomic analysis and data sharing, leading to new applications and insights. This work will focus on microbial genomes and builds on top of my pandemic-related research, which was widely used for the rapid identification of new SARS-CoV-2 variants, monitoring the prevalence of circulating variants, assessing the fitness of different variants and investigating the transmission patterns of outbreaks.

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