



Genetics, Bioinformatics, & Systems Biology Colloquium

presents

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 **THURSDAY**
OCT 26TH

 **12PM**

 **LEICHTAG AUDITORIUM**

 **ZOOM**



BUILDING THE DRAFT HUMAN PANGENOME AND MAKING IT USEFUL FOR BIOMEDICAL RESEARCH

Human genomics has relied on a single reference genome for the last twenty years. This reference genome is a cornerstone of much of what we do in genomics but it can not, by definition, represent the variation present in the human population, and as a reference introduces a pervasive bias into genomic analyses. I will survey our recent efforts, through the Human Pangenome Reference Consortium, to build and use a reference pangenome - a collection of extremely high-quality reference genomes related together by a consensus genome alignment that we intend as a replacement for the reference genome. I will also discuss our progress in building and making tools generally useful with the pangenome, focusing on our efforts to build reliable tools for genotyping of both large and small variations.

PRESENTED BY:



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