Human genomes exhibit variation at multiple levels of biological organization. I will discuss my lab’s work using computational and statistical methods to better understand the “mosaic” nature of human genomes. This includes our research into the prevalence, causes, and consequences of mosaic aneuploidy, whereby different embryonic cells possess different numbers of chromosomes. I will also discuss our research on the mosaic ancestry of human genomes and the functional implications of persisting Neanderthal DNA acquired via ancient hybridization.

Noon, Monday, October 7, 2019
Auditorium, Life Sciences Building,
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