RESEARCH SEMINAR
“Understanding genomic variation using high throughput sequencing”

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Genomic variations are the basis for phenotypic variations among individuals and species. Recent developments in high throughput sequencing technologies dramatically reduced the cost of acquiring genetic data, providing new opportunities for studying genomic variation. The long-term research goal of my lab is to understand the mechanisms and consequences of genomic variation. Overall my research addresses three fundamental questions in genomics: 1. How does genomic variation lead to diseases? 2. What are the functional roles of the “dark matter” of the genome (e.g., mobile elements, non-coding genes)? 3. How does genome evolve? In this talk, I will present some of our recent projects under these directions and discuss the challenges and opportunities of using high throughput sequencing data.

Noon, Monday, September 19, 2022
Auditorium, Life Sciences Building
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Zoom Registration Link | Meeting ID: 963 3843 9086 | Passcode: Genetics
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