

Biology Seminar



Western
UNIVERSITY · CANADA

12:30 - 1:30 pm
Friday, February 16 2024
BGS 0165 & Zoom



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Population and Quantitative Genomics of Deer

Genomic data has allowed for reconstructing speciation history and characterizing the genetic health of small populations. Summary statistics derived from the genome, however, are fraught with nuance and impacted by the demographic history of focal population. Using North American deer (*Odocoileus*), I present their dynamic history that shows no ancestral gene flow despite contemporary history. I then show the apparent impact of human intervention and overharvest on deer genomic diversity. Using white-tailed deer mainland and Island population samples, I show how Tajima's D, mutational load, and FROH metrics collectively shed light on historical and contemporary processes reflective of population health. We also use the unique sampling design to identify patterns recessive deleterious mutations underlying key traits in deer.