Speaker Series

Guest Speaker

"Rapid Adaptation in Natural Populations: Lessons from Drosophila and the Human Microbiome"

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The availability of whole genome data from natural populations has challenged many longstanding assumptions about molecular evolution. For example, it has long been assumed that natural selection is typically slow and infrequent. Using whole-genome data from both Drosophila and the human microbiome, I found evidence that rapid adaptation is much more pervasive than previously thought. In my talk, I will first describe a method I developed to detect soft sweeps, a signature of rapid adaptation, and its application to Drosophila and other, non-model organism data. Next, I will show that selective sweeps of genes and SNPs in bacteria in the human microbiome are common on 6-month time scales, and that these sweeps likely originate in adaptive introgression from other species and strains in the microbiome. This suggests that complex ecological communities can play an important role in shaping evolution on short time scales. In sum, I will describe how we can leverage whole genome data and novel statistics for uncovering the mode and tempo of adaptation in natural populations.

Monday, October 7, 2019
11:00am – 12:00pm
Gonda Building 1st Floor Conference Room, 1357
Light snack will be provided