**Seminar Series**  
**Research Frontiers in Biomathematics**

**Guest speaker**  
**Joshua Bloom**  
Research Scientist in the Kruglyak lab  
Human Genetics | UCLA

**Fall Calendar 2019**
- 9/26 Matteo Pellegrini
- 10/3 Wenyi Wang
- 10/10 Jason Ernst
- 10/17 Davide Maestrini
- 10/24 Sriram Sankararaman
- 10/31 Joshua Bloom
- 11/7 Chris Rackauckas
- 11/14 Johannes Reiter
- 11/21 Eran Halperin
- 12/5 Dino Di Carlo

**Thursday, October 31, 2019**  
4:00 to 5:00 pm  
Moss Auditorium  
A2-342 MDCC | UCLA

**Insights from mapping fitness and single-cell gene expression in large yeast populations**

**Abstract**

Here we use yeast as a model system to understand the genetic basis of complex traits, focusing on fitness and gene expression. First we generated ~14,000 progeny from crosses among 16 diverse yeast strains and identified thousands of quantitative trait loci (QTLs) that explain most of the heritable variation in 38 traits. We combined our results with sequencing data for 1,011 yeast isolates to decouple variant effect size estimation from allele frequency and showed that rare variants make a disproportionate contribution to trait variation. Evolutionary analyses revealed that this contribution is driven by rare variants that arose recently, that such variants are more likely to decrease fitness, and that negative selection has shaped the relationship between variant frequency and effect size. Additionally, we performed single-cell RNA-sequencing on tens of thousands of progeny in a one-pot experiment and developed methods to identify cis and trans-eQTL. These results refine our understanding of trait variation at the population level and suggest that studies of rare variants are a fertile ground for discovery of genetic effects.

1. Article  2. Article

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To meet with the guest speaker contact the organizer Mary E. Sehl msehl@mednet.ucla.edu