

Biomedical Informatics Special Seminar



Farhad Hormozdiari, PhD; postdoctoral fellow at Harvard and the Broad institute

Statistical Methods to Understand the Genetic

Architecture of Complex Traits

Tuesday, April 30th, 2019 10 am—11 am HSC L3 Classroom 155

Abstract: Although genome-wide association studies (GWAS) have successfully identified thousands of risk loci for complex traits, only a handful of the biologically causal variants have been successfully validated. Identifying causal variants can aid us to understand the biological mechanism of diseases. However, detecting the causal variants is challenging due to linkage disequilibrium (LD) and the fact that some loci contain more than one causal variant. In this talk, I will introduce CAVIAR (CAusal Variants Identification in Associated Regions) that is a new statistical method for fine mapping. Next, I aim to understand the underlying mechanisms of GWAS risk loci by integrating GWAS and expression quantitative trait loci (eQTL) signals. I will introduce eCAVIAR (eQTL and GWAS CAusal Variants Identification in Associated Regions), a statistical method to compute the probability that the same variant is causal for both GWAS and eQTL signal while accounting for complex LD structure. Lastly, I will introduce a new set of functional annotations based on causal posterior probabilities of fine-mapped molecular cis-QTLs, using data from the GTEx and BLUEPRINT consortia. We show that these annotations are more strongly enriched for heritability across 41 diseases and complex traits than annotations containing all significant molecular QTLs. eQTL annotations obtained by meta-analyzing all GTEx tissues generally performed best, whereas tissue-specific eQTL annotations produced stronger enrichments for blood-and brain-related diseases and traits.

Bio: Farhad Hormozdiari obtained his bachelor's degree in computer science from Tehran University. Later, Farhad moved to Vancouver where he obtained his master's degree in computer science at Simon Fraser University under the supervision of Cenk Sahinalp. Farhad obtained his PhD in computer science at UCLA under the supervision of Eleazar Eskin. Now, Farhad is a postdoctoral fellow at Harvard and Broad institute under the supervision of Alkes Price. Farhad has won various awards including the Ian Lawson Van Toch Memorial Award for Outstanding Paper at ISMB 2015. Farhad's research involves developing computational and machine learning methods to understand the genetic architecture of human disease.

Questions? Please call the Biomedical Informatics Department at 631-638-2590.