



Department of Biomathematics Seminar Series:
Frontiers in Systems and Integrative Biology

BIO
MATH

Integrative Statistical Approaches to Find Causal Variants in Post-GWAS Studies



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Thursday, October 23, 2014

4:00 PM

13-105 Center for the Health Sciences (CHS)

ABSTRACT:

Genome-wide association studies (GWAS) have successfully identified numerous regions in the genome that harbor genetic variants that increase risk for various complex traits and diseases. However, it is generally the case that GWAS risk variants are not themselves causally affecting the trait, but rather, are correlated to the true causal variant through linkage disequilibrium (LD). Plausible causal variants are identified in fine-mapping studies through targeted sequencing followed by prioritization of variants for functional validation. In this work, we propose methods that leverage two sources of independent information, the association strength and genomic functional location, to prioritize causal variants. We demonstrate in simulations and empirical data that our approach reduces the number of SNPs that need to be selected for follow-up to identify the true causal variants at GWAS risk loci.

Host: Janet Sinsheimer, Ph.D.

To receive e-mail seminar notices, contact David Tomita (dtomita@biomath.ucla.edu)