

Statistics Seminar

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Monday, October 27, 2014

1:00 - 2:00 p.m., HH-3017

Bivariate genetic association analysis of systolic and diastolic blood pressure

Abstract:

We conduct genetic association analysis in the subset of unrelated individuals from the San Antonio Family Studies pedigrees, applying a two-stage approach to take account of the dependence between systolic and diastolic blood pressure (SBP and DBP). In the first stage, we adjust blood pressure for the effects of age, sex, smoking, and use of antihypertensive medication based on a novel modification of censored regression. In the second stage, we model the bivariate distribution of the adjusted SBP and DBP phenotypes by a copula function with interpretable SBP-DBP correlation parameters. This allows us to identify genetic variants associated with each of the adjusted blood pressures, as well as variants that explain the association between the two phenotypes.

Within this framework, we define a pleiotropic variant as one that reduces the SBP-DBP correlation. Our results for whole genome sequence variants in the gene *ULK4* on chromosome 3 suggest that inference obtained from a copula model can be more informative than findings from the SBP-specific and DBP-specific univariate models alone.