COLLOQUIUM

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Gene-Centric Gene-Gene Interactions: A Model-Based Kernel Machine Method

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Refreshments: 10:00 a.m.

Abstract

Much of the natural variation for a complex trait can be explained by the structural variation in DNA sequences. As part of the sequence variation, gene-gene interaction or epistasis has been ubiquitously observed in nature where its role in shaping an organisms development has been broadly recognized. Driven by its importance, the identification of genetic epistasis has been progressively pursued via statistical or machine learning approaches. A large body of currently adopted methods, either parametrically or non-parametrically, predominantly focus on pairwise single marker interaction analysis. As genes are the functional units in living organisms, analysis by focusing gene as a unit or system could potentially yield more biologically meaningful results. In this work, we conceptually propose a gene-centric gene-gene interaction framework for genome-wide epistasis detection. We treat each gene as a testing unit and derive a model-based kernel machine method for two-dimensional genome-wide scanning gene-gene interactions. In addition to the biological advantage, our method is statistically appealing by reducing the genome-wide multiple testing burdens. Extensive simulation studies are conducted to evaluate the performance of the method. The utility of the method is demonstrated with applications to real data sets. Our gene-centric gene-gene interaction analysis provides a conceptual platform for epistasis identification.

This talk is based on joint work with Yuehua Cui.

To request an interpretor or other accomodations for people with disabilities, please call the Department of Statistics and Probability at 517-355-9589.