



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

Functional Regression Models for Gene-based Association Studies of Complex Traits



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ABSTRACT:

By using functional data analysis techniques, fixed effect functional regression models are developed to test associations between complex traits and genetic variants, which can be rare variants, common variants, or a combination of the two, adjusting for covariates. We treat multiple genetic variants of an individual in a human population as a realization of an underlying stochastic process. The genome of an individual is viewed as a stochastic function which contains both genetic position and linkage disequilibrium (LD) information of the genetic markers. To overcome the curse of high dimensions of modern genetic data, functional regression models are developed to reduce the dimensionality. In the talk, I will show how to build test statistics for functional regression models to test association between quantitative/dichotomous/survival traits and genetic variants. Results of extensive simulation analysis and real data analysis will be shown to demonstrate the performance of the proposed models and tests. A comparison with existing popular procedure of sequence kernel association test (SKAT) and its optimal unified test (SKAT-O) will be made to facilitate an understanding of the proposed methods, and to answer whether fixed or mixed models should be used in association analysis of complex disorders.

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