Rare Variant Analysis Based on Joint Models of Multiple Traits

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September 8, 2015
2:00 - 3:00 pm
HH 3017

Abstract

In recent years, the further development of high-throughput technologies has allowed genetic associations to be investigated in more depth. Rare variants in whole genome sequence data are being analyzed with the hope of explaining more of the heritable variation in complex traits unexplained by common variants. However, the results of recent studies seem to suggest that the success herein has been limited despite the development and use of new gene-based multi-marker rare variant tests. This issue may be due to low power to detect associations between genetic variants and traits under the association models considered and the test statistics used. More informative statistical models can be considered by incorporating the dependence structure between multiple traits or multi-level biological measures. I will discuss the gain in power by using such joint models of multiple traits. A whole genome sequence data set will be used to illustrate the modeling approach.