

Colloquium
Michigan State University
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Some useful permutation methods you've probably never used

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10:20 a.m. - 11:10 am
Refreshments 10:00 am
C405 Wells Hall

Abstract:

We describe several methods that involve resampling (primarily permutation), or analytic approximations to these methods, that are useful for large-scale multiple testing problems. 1) We describe the moment-corrected correlation (MCC) approximation to permutation-based association methods. MCC is very fast, and especially useful in testing of individual rare variants in genotype-phenotype association studies. 2) Next we describe safeExpress, an approach and software package for gene-set enrichment testing that provides fast approximations to permutation, for both so-called self-contained and competitive testing. Simulations and real data support the accuracy and power of the approach. 3) Finally, we describe the DiNAMIC approach to identify recurrent features in genomic data. The data structure involves a comparison of rows of a matrix, for which coincident occurrence of high or low values is indicative of a region of interest. Previous work has been somewhat unclear on the nature of the hypothesis to be tested. Using simple stationarity arguments, we provide support for the use of cyclic shift permutation in this context, with high-dimension, low sample size convergence results.

(Joint work with Yi-Hui Zhou, Bill Barry, Vonn Walter, and Andrew Nobel)

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