A geometric interpretation of the permutation p-value and its application in eQTL studies

by

Wei Sun Department of Biostatistics, University of North Carolina Chapel Hill, NC, 27599, USA wsun@bios.unc.edu

Abstract

Permutation p-values have been widely used to assess the significance of linkage or association in genetic studies. However, the application in large-scale studies is hindered by a heavy computational burden. We propose a geometric interpretation of permutation p-values, and based on this geometric interpretation, we develop an efficient permutation p-value estimation method in the context of regression with binary predictors. An application to a study of gene expression quantitative trait loci (eQTL) shows that our method provides reliable estimates of permutation p-values while requiring less than 5% of the computational time compared with direct permutations. In fact, our method takes a constant time to estimate permutation p-values, no matter how small the p-value. Our approach enables a study of the relationship between nominal p-values and permutation p-values, and provides a geometric perspective on the effective number of independent tests.

This is joint work with Fred A. Wright, Department of Biostatistics, University of North Carolina.