

POWERFUL NONPARAMETRIC SIB-PAIR LINKAGE METHODS FOR QUANTITATIVE TRAITS

Y.J. Hong[†], M.K. Kim, H.H. Song

The Catholic University of Korea, Seoul, Korea

[†] E-mail: *yujin0806@catholic.ac.kr*

The Haseman-Elston (HE) regression method and extensions of it are widely used in genetic studies for detecting linkage to quantitative trait loci (QTL) using sib-pairs. The principle underlying the simple HE regression method is that the similarity in phenotypes between pairs of sibs becomes larger as they share an increasing number of alleles at a particular QTL identical by descent (IBD) from their parents. In their procedure, similarity was identified with the closeness of the mean values of squared phenotype differences among three groups of 0, 1, and 2 alleles IBD sharing. A more powerful, rank-based nonparametric, test to detect increasing similarity in sib pairs is presented by combining univariate trend statistics not only of location but also of dispersion differences of phenotypes among three groups. This trend test does not rely on the distributional assumptions, and is applicable to the skewed or leptokurtic phenotypic distributions. The performances of nonparametric trend statistics, including nonparametric regression slope, are compared with the HE regression methods as genetic linkage strategies.