FUZZY P-VALUES AND PERMUTATION TESTS FOR GENETIC LINKAGE

E. A. Thompson[†1], Y. Di[1]

[1] *University of Washington, Seattle, USA*

[†] E-mail: *thompson@stat.washington.edu*

Fuzzy p-values have been recently introduced to the statistical literature. In latent variable problems they provide a way to express both strength of evidence and uncertainty as to that strength, by putting latent-variable uncertainty directly onto the p-value scale. A particular example is in robust tests for the detection of genetic linkage, where the uncertainty is that of the underlying inheritance of DNA in a set of related individuals. Alternative tests that are robust to trait and/or DNA marker model assumptions are permutation tests, developed first for designed genetic crosses in experimental organisms, and more recently in the context of data on extended pedigrees. We compare the fuzzy p-value approach with permutation approaches for quantitative trait data in designed genetic crosses, and for a binary trait observed on members of extended pedigrees.