On the Power for Linkage Detection
Using Tests Based on Scan Statistics

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Abstract: We analyze some aspects of Scan statistics, which have been proposed to help detect weak signals in linkage analysis. For dense markers we derive approximations for the thresholds to control the genome wide false positive rate and for the power of a test based on moving averages of the identity-by-descent (IBD) allele sharing proportions for pairs of relatives at several contiguous markers. We use these results, which we confirm by simulation, to show that when there is a single trait gene on a chromosome this scan statistic is generally slightly less powerful than the customary allele sharing statistic, but if two genes having a moderate affect on the same trait lie close to each other on the same chromosome, this test can be more powerful than that based on the original statistic.

Keywords: Scan statistics, Genetic linkage, Complex traits.

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