

A Confidence Set Approach for Gene Mapping

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Abstract:

As more studies adopt the approach of whole-genome screening, geneticists are faced with the challenge of having to interpret results from traditional approaches that were not designed for genome-scan data. Frequently, tests are performed to search for signals of linkage throughout the genome, for each of hundreds or even thousands of genetic markers. This practice has raised the question of how to adjust the significance level for the fact of performing multiple tests with complicated dependency. In addition to the problem of multiplicity adjustment, traditional linkage analysis does not lead to confidence inference on the location of the disease gene. The asymptotic behaviors of popular linkage statistics is not desirable for fine mapping either. In this talk, I will present a new approach, based on the construction of confidence set, to disease gene mapping. Specifically, we construct a confidence set for the location of a disease locus. The confidence set is constructed in such a way that multiplicity adjustment is not needed, no matter how many markers are tested. Furthermore, our formulation enables us to localize the disease gene to a small genomic region, an attractive feature for fine mapping. We evaluate the performance of this approach for both parametric and nonparametric test statistics. Other parameters that may potentially influence the performance of this approach are also studied.