

MAPPING GENES FOR QUANTITATIVE TRAITS USING SELECTED SAMPLES OF SIBLING PAIRS

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Abstract:

One of the most important research areas in human genetics is the effort to map genes associated with complex diseases such as cancer, heart disease, and diabetes. Gene mapping will bring an understanding of genetic risk and protective factors, and a description of the interaction between environment and genetic variation. In the last ten years there has been a dramatic increase in the number of studies seeking to map genes for quantitative traits. This has caused an explosion of new work on statistical methods for human quantitative trait locus (QTL) mapping. However, little of that work has dealt with selected samples, which are more common than population samples for human studies. My research focuses on sibling pairs and considers the most common types of selected sampling. I surveyed most QTL mapping linkage methods in the literature to evaluate which are appropriate for selected samples, and also developed new statistics for selected samples. Using simulation and analytical approaches, I identified the most powerful statistics for each type of sampling considered. I then compared various sampling designs using the best statistic for each and gave guidelines for choosing appropriate and powerful designs under different scenarios.