

Mapping Quantitative Traits

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I describe a unified model for the statistical foundations of population based association mapping and family based linkage mapping of quantitative traits in humans. Analysis of the model involves the efficient score statistic for the conditional likelihood, given the phenotypes. Analytic expressions for noncentrality parameters give qualitative insight into the relative power of different statistics and the loss of power that occurs if the scientist's assumed genetic model differs from nature's "true" genetic model. The multiple comparisons problem of genome scans to search for anonymous genes is discussed.

References

Dupuis, J., Siegmund, D. and Yakir, B.(2007). *PNAS*, **104** 20210-20215.