

Mapping Quantitative Trait Loci

David O. Siegmund, Ph.D.
Visiting Professor, Section on Statistical Genetics

Abstract:

(A) Goals

To give a systematic large sample theory for QTL mapping, which

1. clarifies the similarities and differences between QTL mapping in experimental genetics and in humans QTL mapping in experimental genetics and in humans
2. treats issues of study design of recent interest, e.g. (a) the comparative value of large pedigree versus sibpairs, (b) genotyping only selected pedigrees, and
3. provides a framework to study gene x gene and gene x covariate interaction

(B) Methods

Starting from the standard components of variance model and a parameterization of the genetic effects that makes “linkage parameters” orthogonal to “segregation parameters” use the framework of local alternatives employed in large sample statistical theory, in order to obtain explicit expressions for robust score statistics and for asymptotic non-centrality parameters, which can be used to compare the power of different strategies.

References

Tang and Siegmund (2001) *Biostatistics* 2, 147-162.

Tand and Siegmund (2002) *Genetic Epidemiology*, **22**, 313-327.