

BERKELEY-STANFORD COLLOQUIUM

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At Berkeley

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Mapping Quantitative Trait Loci

The goal of genetic mapping is to locate genes that affect particular traits, especially genes that affect human susceptibility to particular diseases and related quantitative traits, e.g., blood pressure and cholesterol level. Testing markers throughout the genome to identify the relevant genes leads to a class of irregular statistical problems, where standard large sample theory does not apply. In this talk I will describe the general problem of genetic mapping with special attention to mapping quantitative trait loci (QTL).

(A) Goals

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

(i) clarifies the similarities and differences between QTL mapping in experimental genetics and in humans,

(ii) treats issues of study design of recent interest, e.g., (a) the comparative value of large pedigrees versus sib pairs, (b) genotyping only selected pedigrees,

and

(iii) provides a framework to study gene \times gene and gene \times environment interaction.

(B) Methods

Use (i) the standard components of variance model and a parameterization of the genetic effects that makes “linkage parameters” orthogonal to “segregation parameters” in conjunction with (ii) the framework of local alternatives employed in large sample statistical theory, in order to obtain explicit expressions for score statistics and for asymptotic noncentrality parameters, which can be used to compare the power of different strategies.

This is joint research with Hsiu-Khuern Tang.