Mapping Quantitative Traits in Humans

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1 Overview of the Field

Genetic mapping of quantitative traits attempts to determine locations in the genome contributing to quantitative traits, e.g., blood pressure, serum cholesterol, serum insulin, and if possible any gene-gene and gene-environment interactions that may be involved. Because inheritance involves a random selection of genetic materials that is passed down to each succeeding generation, gene mapping necessary involves statistical analysis of genetic data. Controlled breeding experiments play a considerable role in simplifying the problem of gene mapping in plants and animals, but gene mapping in humans involves special complications because of one's inability to perform suitable breeding experiments.

There are two general approaches to gene mapping in humans: linkage, which is based on (close) relationships in families, and association, which is based on the (distant) relationships in populations.

2 Outcome of the Meeting

The main outcome of the meeting was a paper giving a unified foundation to the statistical problem of mapping quantitative traits by either family based or association based methods. This paper was published in *Proc Natl Acad Sci U S A*. A second manuscript that builds on the foundation in the first paper and provides relevant statistical software has now been submitted for publication.

References

[1] Dupuis J, Siegmund DO, Yakir B. 2007 A unified framework for linkage and association analysis of quantitative traits. *Proc Natl Acad Sci U S A*, **104**, 20210-5.