

Design and Analysis of Genetic Mapping Studies

Jurg Ott

*Rockefeller University, New York, U.S.A. and Beijing Institute of Genomics,
Chinese Academy of Sciences, P.R. China*

Several methods have been developed for the genetic mapping of disease genes, the two most important ones being linkage and association (linkage disequilibrium) analysis. The latter is likely to gain more and more importance at the expense of the former. The different methods will be compared but the focus will be on case-control association studies. Questions of heterogeneity and potential solutions will be addressed. Finally, methods for determining statistical significance (false positive rates, false discovery rates) will be mentioned and a few recent examples of successful association studies will be quoted.

[Jurg Ott, Rockefeller University, 1230 York Avenue, New York, NY 10021, U.S.A. ;
ott@rockefeller.edu]