

Tree Models in Genetic Epidemiology

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Abstract:

With discovery of an increasing number of candidate genes that may affect inter-individual variability in response to drugs, the design of drug trials that incorporate their study has become relevant. We discuss the determination of sample size for such studies when the number of tests to perform is given, or, alternatively, the number of tests to perform when the sample size is given. In many cases, a uniformly most powerful test does not exist and normal approximations are not sufficiently accurate to determine sample size. We discuss briefly various tests of interest and we give simple examples to illustrate some of the problems that arise.