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The statistical methods required by bioinformatics present many new and difficult problems for the research community. This book provides an introduction to some of these new methods. The main biological topics treated include sequence analysis, BLAST, microarray analysis, gene finding, and the analysis of evolutionary processes. The main statistical techniques covered include hypothesis testing and estimation, Poisson processes, Markov models and Hidden Markov models, and multiple testing ...

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Bioinformatics is concerned with the study of inherent structure of biological information and statistical methods are the workhorses in many of these studies. Some of this inherent structure is very obvious and can be observed directly through correlations of patterns in high-dimensional data, while other patterns arise through more complicated underlying relationships.

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Several statistical methods for association mapping, including LR as well as other generalised linear models, require the specification of a genetic model of inheritance. For instance, in a CA test, or score statistics from logistic regression, an additive model can be imposed by giving genotype weights 0, 1 and 2, depending on the number of copies of the minor allele.

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