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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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