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### Statistical Methods in Bioinformatics - An Introduction

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.

### Statistical methods in bioinformatics

Slide 23/57 | Statistical methods in bioinformatics. university of copenhagen april 8th, 2019 Resampling methods Computerintensive methods Permutation methods. Simulate data under  $H_0$ , compute test statistic and compare to test statistic from original data. Bootstrap. \Simulate data under  $H_A$ .

### Statistical methods in bioinformatics

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### (PDF) Statistical tools in bioinformatics

statistical methods in bioinformatics. UToledo course #: BTPG 5200/7200 - 3 cr. Prerequisites: PUBH532 - Statistical Methods I (or equivalent, or permission of course director) Offered: Fall Semester, Tuesdays/Thursdays. Lectures posted online/Blackboard. Course director: Dr. Sadik Khuder, Department of Medicine, (419) 383-6244, Sadik.Khuder@utoledo.edu.

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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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