

Statistical methods in bioinformatics

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Abstract

This session is devoted to novel contributions and new insights into statistical methodology in Bioinformatics. The advent of the genomic age, where human and other genomes has been deciphered, has raised new challenges for statistics. These come from the fact that huge quantity of data that are being generated by technologies such as microarrays, or the more recent ultra deep sequencing, and from the need to integrate these data in a systems biology approach that yields a better understanding of the underlying biological processes. The appearance of these high throughput data has led to many applications of statistics as well as to development of new methods tailored to the new problems. Jointly with probabilistic modelling, or multiple testing, multivariate statistics is one of the fields where most of this activity has happened, due to the high dimensionality of these type of data.