



Seminar

Thematic Line BioMathematics - CIDMA

27 de março de 2019, 15h00

Departamento de Matemática, Universidade de Aveiro
Sala 11.3.21

Genomics Big Data: when Mathematics meets Biology

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Abstract

The Human Genome Project was completed in 2003 and for the first time we look beyond single genes in to the entire human genome sequence, that has approximately 3 billion base pairs and more than 20,000 genes. The advancement of the DNA sequencing technology, the so-called Next-Generation Sequencing (NGS), decreased exponentially the costs and the time to sequence and analyse an entire genome (in a few hours for less than a thousand dollars) and originated an explosion of biomedical data. These large data sets with different layers of information and complexity (genomics, transcriptomics, proteomics and metabolomics) require powerful computational infrastructures and bioinformaticians to do an integrative analysis to shed light on the underlying biological mechanisms. In the genomics facility of iBiMED -iBiGEN, we use bioinformatics tools to address biomedical and clinical questions, mainly related with healthy aging and age-related diseases. With this presentation we aim at showing some of the computational and statistical methodologies we apply to biological data analysis, while highlighting their major advantages and limitations, and why do we need new tools to work with such big-data projects.

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