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The CODATA-RDA Research Data Science Applied workshops on Extreme sources of data, Bioinformatics and IoT/Big-Data Analytics | (smr 3178)

Thursday 27 July 2017

Bioinformatics - Adriatico Guest House - Informatics Laboratory (09:00-15:00)

Abstract: High-throughput data sets from next-generation sequencing provide a rich but highly complex picture of the biological processes assayed. Statistical challenges abound, arising from high dimensionality, strong heterogeneity and general low replication of the data. In this talk, I will describe how techniques from machine learning and computational statistics can be effectively used to answer some of these questions. I will focus on the issues of statistical testing for epigenomic data such as ChIP- and BS-Seq, and determining isoform proportions/ splicing ratios from low coverage RNA-Seq data.

time	title	presenter
09:00	Using machine learning to address challenges in high-throughput biology	SANGUINETTI, Guido
10:30	Coffee break	
11:00	Using machine learning to address challenges in high-throughput biology	SANGUINETTI, Guido
12:30	Lunch break	
13:30	Warp up and hands out certificates	POLICRITI, Alberto SANGUINETTI, Guido