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Uncertainty Analysis of Phenotype Prediction Problems. The Finisterrae project

a cargo de

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RESUMEN: Genomic phenotype prediction is predicated on finding a set of genes that prospectively distinguishes a given phenotype. This kind of problem has a high under-determined character since the number of monitored genetic probes markedly exceeds the number of collected samples (patients). This imbalance creates uncertainty as, potentially, there exist many equivalent genetic networks that could predict the phenotype with a similar accuracy, a feature that creates ambiguity in the characterization of the biological pathways since many genes are highly discriminatory. In top of that, a significant obstacle in the analysis of genetic data is the absence of a conceptual model that relates the different genes/probes to the class prediction between the set of genetic signatures and the set of classes in which the phenotype is divided.

In this talk I will show how we solve this interesting problems and some applications in cancer, rare and neurodegenerative diseases (FINISTERRAE PROJECT).

Día y hora: viernes, 25 de octubre de 2019, a las 12h30'.

Lugar: Sala académica *Prof. Antonio Aizpuru*. Facultad de Ciencias, torre centro, segunda planta. Puerto Real.

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