Limits of prediction in Biology
Laboratory of Logic of Genomic Systems, CNB-CSIC

How can we predict the behavior of an individual from its genome? Are there specific DNA sequences for each behavior? Or is it the whole genome that defines us? Whether one hypothesis or the other is correct will also mark the strategy that we define to develop the so-called personalized medicine. Our laboratory has been interested in recent years in understanding how we can predict the functioning of biological systems (the "phenotype") from their genome (the "genotype").

We propose two possible final master's projects in this context

• Use of metabolic models to examine when "statistical" predictions of phenotype differ from individualized predictions.

• Use of computational genetic network models to understand how the structure of these networks, and their robustness, influences the prediction of the phenotype.

For those interested in combining theory and experiments, a third work related to the prediction of the behavior of the nematode *Caenorhabditis elegans* would be available.

Requirements: Quantitative training (Physics, Mathematics, ...). Programming knowledge (Python, R, ...). Interest in Biology and solving biological problems with a quantitative approach.

Contact. Juan F Poyatos (jpoyatos at cnb.csic.es)
Laboratory information: http://wwwuser.cnb.csic.es/~jpoyatos/