Universitat
Pompeu Fabra
Barcelona

Master in
Bioinformatics for
Health Sciences

Master project 2024-2025

Personal Information

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Group	Human Genome Diversity Group

Project

Computational genomics

Project Title:

Analysis of the human genome diversity in order to unravel demographic and genomic processes

Keywords:

Genome diversity, human populations, adaptation, demography

Summary:

The interests of our research are focused on the human genome diversity analysis in order to infer the (genomic and population) processes responsible for this diversity and try to establish the (population and epidemiological) consequences of the human genetic variability. Thus, our main research lines are focused on aspects of human genome diversity, population genetics, genome variation and disease susceptibility, and genome evolution and disease. 1. Population processes Concerning population processes that have modeled the human genetic diversity, we have focused our research on the use of molecular tools to reconstruct the human population history through the phylogeny of genetic markers. Our interest has been focused on the genetic consequences at population level of human migrations and admixtures. The use of well-established phylogenies in the mitochondrial and Y-chromosome human genomes allowed us to unravel the population history of several populations. Nonetheless, we have recently used whole genome variation in the autosomes in order to establish the structure of human populations. 2. Genomic processes Concerning genomic processes that have modeled the human genetic diversity, our research has been focused on the relationship between human diversity and complex traits, including complex diseases. The genetic analysis in human populations of genes of biomedical interest might shed light on the evolution of these genes. In this context, we have focused our research in the analysis of genes that have been previously associated to complex diseases, such as psychiatric and immunological diseases. The analysis of these genes has allowed us to conclude that some of the failures in replicating genetic associations are due to extreme genetic differences between populations. In addition, we are also interested in other complex traits, such as height, not directly related to disease.

Expected skills:

We are looking for a highly motivated candidate with interest in population genetics, bioinformatics skills to manage large genomic datasets, as well as writing and oral skills.

Possibility of funding:

To be discussed

Possible continuity with PhD:

Yes