Universitat Pompeu Fabra Barcelona | Master in Bioinformatics for Health Sciences

Master project 2020-2021

Personal Information

Supervisor	David Comas
Email	david.comas@upf.edu
Institution	Universitat Pompeu Fabra (UPF)
Website	http://www.biologiaevolutiva.org/dcomas/
Group	Human Genome Diversity Group

Project

Computational genomics

Project Title:

Human genome diversity: demography and adaptation

Keywords:

Human genome, genome diversity, demography, adaptation

Summary:

Our research is focused on the understanding of the current genomic diversity in human populations in order to establish the mechanisms, causes and consequences of this genetic variation. We are mainly focused on trying to disentangle two types of processes: - Demographic processes. Population history, such as migrations, expansions, bottlenecks and admixtures have modelled the extant genome diversity of humans. Using several genetic markers, such as mitochondrial or Y-chromosome lineages as well as high-throughput SNP coverage of several human populations, we have addressed some demographic questions, from regional aspects such as the genetic impact of the Bantu expansion in Central Africa to more global issues such as the colonization of whole continents. - Selective processes. The human genome as also been modelled by selective processes as a result of adaptations during the species history. We have analyzed parts of our genome in order to detect genetic signals yield by selective processes, such as adaptation to different environments and its relationship with human diseases. Disentangle both types of processes is not an easy task and our research deals with the analysis of the diversity of the human genome at a population level in order to detect demographic and selective processes.

Expected skills::

Basic bioinformatic skills in genome data analysis

Possibility of funding::

To be discussed

Possible continuity with PhD: :

To be discussed