

The Institute of Evolutionary Biology seeks a PhD Student in Human Population Genomics

The Institute of Evolutionary Biology (IBE) is a joint Institute of the Spanish National Research Council (CSIC) and the Pompeu Fabra University (UPF) located in Barcelona city. IBE research is focused on the processes and mechanisms that generate biodiversity and on understanding the genetic basis of evolution. The IBE is a center member of the Barcelona Biomedical Research Park (PRBB).

The Human Population Genomics Group

Join a 4-year PhD project on population genomics, focussed on human isolated populations! The PhD work will be carried out within the Elena Bosch and Francesc Calafell research groups at the Medicine and Life Science (MELIS) Department of the Universitat Pompeu Fabra (UPF) and the Institute of Evolutionary Biology (CSIC-UPF). We offer an exciting job in a stimulating and international research working environment, excellent research facilities and a lively and social working place.

More information about us, please visit our group webpages:

<https://www.upf.edu/web/evolutionary-population-genetics/> and

<https://www.upf.edu/web/genomics-of-individuality/>

Project description

We offer a research position to work on deciphering demographic history and phenotypes in isolated human populations. The successful applicant will analyze SNP genotyping data and whole genome sequences to understand how the genetic and phenotypic variation of particular human groups has been shaped by i) their own demographic history, ii) their corresponding patterns of migration and admixture, and iii) natural selection. Next generation sequencing of human genomes provides an affordable, complete description of the genome sequence of every individual. Beyond the allelic states at single, predefined loci (such as SNPs), genome sequences preserve the rare variants and the linkage disequilibrium structure throughout the genome. Thus, by comparing genomes, shared chunks (haplotypes) can be easily identified, both within (known as runs of homozygosity, ROHs) and among different individuals. While the number and length of ROHs are quite informative about the inbreeding patterns within a population, shared haplotypes among populations provide a faithful record of the gene flow among populations and allow us to characterize each population as the sum of all its external contributions. In turn, the patterns of genomic variation will be used to infer the demographic history of these two populations, in terms of changes in effective population size through time, as well as to unravel the footprints of natural selection under different adaptive scenarios (hard and soft sweeps, polygenic selection, and adaptive introgression). However, since the effective population size is expected to

be reduced in some of these populations, the random effects of genetic drift could have easily outweighed the directional effect of natural selection preventing the elimination of deleterious alleles and increasing their mutation burden. Thus, the complete description of the genetic variation provided by whole genome sequencing will also help to unveil pathogenic mutations allowing an invaluable resource in the management of genetic diseases within these human population groups.

Candidate requisites

Requirements are a Master's or a degree in Bioinformatics/Biostatistics or Genomics/Genetics, strong computational skills, English fluency, and proficiency in Spanish or Catalan.

Assessment criteria: We welcome applications from candidates who have experience in bioinformatics and work with large genomic datasets (SNP, whole genomes), have a background in population genomics, and strong statistical skills. A good conceptual understanding of population genetics and/or evolutionary theory is advantageous. We welcome highly motivated candidates, with strong passion and motivation for science, and willing to collaborate with a variety of international people. In the appointment process, special attention will be given to research skills in bioinformatic analysis and population genomics, and a strong commitment to research excellence is desired.

What do we offer?

The position is for full-time, in-person work, and it also involves teaching up to 60 hours per year of undergrad practical classes.

Gross salary (annually/monthly): ~1,515.04€/18,180.48€ (1st and 2nd year); ~1,623.26€/19,479.14€ (3rd year); ~2,029.07€/24,348.78€ (4th year).

Application process

Please, send your CV, copy of your master's and bachelor's degree academic transcripts as well as your recommendation and motivation letters to elena.bosch@upf.edu and francesc.calafell@upf.edu

The deadline for applications is the **31st of August 2025**.