



Interaction between migration and adaptation: what can we learn from genomes?

Vítor Sousa

EG-cE3c

Currently, due to next generation sequencing (NGS) technologies, evolutionary biology and ecology are entering the genomics era. Today, we can obtain data not only from present-day samples from different geographic regions but also from ancient DNA at different time points. Such spatio-temporal data hold the potential to quantify the importance of different evolutionary processes shaping the current genomic diversity, which can help us predict how species will respond to future environmental and climatic changes. We are developing flexible methods to analyse genome-wide data to test alternative hypothesis and infer relevant parameters, such as historical migration rates, past population sizes and times of divergence. I will focus on quantifying past gene flow levels due to migration and dispersal events, and on the interaction of gene flow with natural selection. I will exemplify how models and simulations offer us the possibility to interpret genome-wide patterns, and learn about the roles of demography and natural selection in the structuring of natural populations. I will discuss the application of these methods to different fundamental questions in evolutionary biology, ranging from population divergence in agro-forestry pest insects, to inferring human demographic history with modern and ancient DNA.

Thursday, December 12, 2019

FCUL (Building C2), 12h00-13h00, room **2.2.21**