



Ciências
ULisboa

Ciclo de Seminários em Biologia Humana e Ambiente

Mestrado em Biologia Humana e Ambiente . Departamento de Biologia Animal

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Reconstructing past gene flow from ancient human genomes.

Currently, due to next generation sequencing (NGS) technologies, the study of human genetic and evolution 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 human genomic diversity. 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. I will exemplify how models and simulations offer us the possibility to interpret genome-wide patterns and learn about the roles of demography (gene flow) in the structuring of natural populations. Specifically, I will illustrate how ancient human genomes can help us reconstruct scenarios of the population replacement and colonization, as well as the relationship between modern humans and Neanderthal.

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