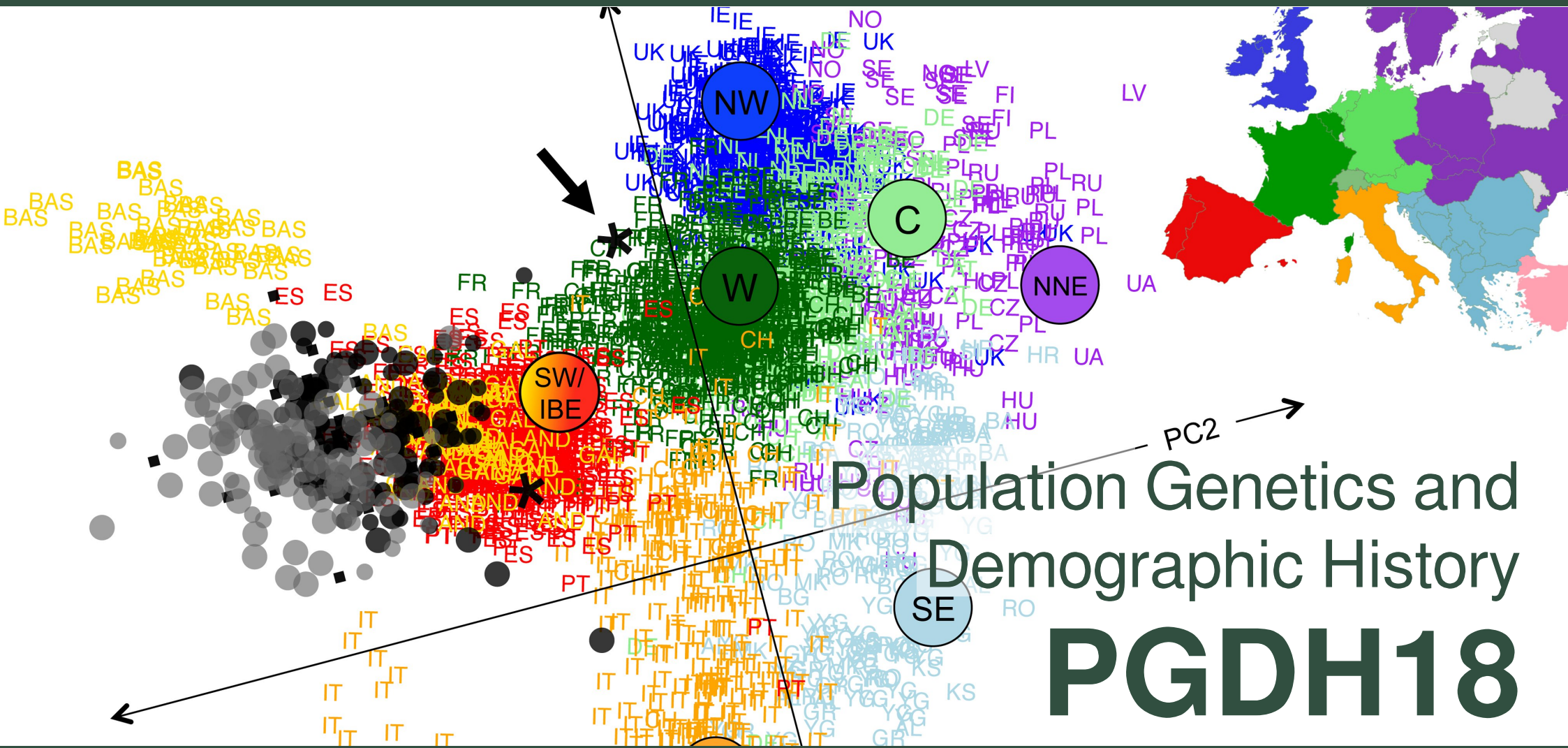


The Gulbenkian Training Programme in Bioinformatics



May 14th - May 18th 2018

Genetic and genomic data has become important for many biologists with different levels of experience to produce and analyse genetic (and genomic) data.

In this course we will take a practical approach to the analysis of genetic and genomic data, with some of the theoretical background required to understand the outputs of the software used. This course will be organised so as to mix lectures where important notions are introduced with practicals where freely available software will be used.

We will go through the basic notions that are central to population genetics, insisting particularly on the statistics used to measure genetic diversity and population differentiation. The course will also cover a short introduction to coalescent theory, Bayesian inference in population genetics and data simulation. We will also introduce two methods that have been recently developed to analyse genomic data. The PSMC of Li and Durbin reconstructs the demographic history of a species or population with the genome of a single individual. The Rehh package is an R implementation of the Extended Haplotype Homozygosity (EHH) test for selective sweeps and looks for signals of selection based on the analysis of genomic regions. Altogether this will allow to discuss the potentialities and limitations of the tools available to the community.

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