# Bioinformatics package for population genetics

The lab of Yoram Louzoun (Mathematics and Brain research) is developing models in population dynamics and genetic data analysis for optimization of transplants.

Performing a project in computational biology can have an impact on medical studies, and provide the student with important advanced computational skills. Specifically, we propose to develop a package for the analysis of population genetics using genetic data from the MHC gene (the gene used to detect proper organ donors).

One of the most informative genetic loci in the human genome is the MHC (Major Histocompatibility Complex). This gene can be used to infer population structures, history as well as its relation to other population. We propose to develop a python package to estimate population diversity, distance between populations and population history using the HLA genetic data.

The project will require

* Implementation in Python of clustering, dimension reduction, phylogenetic analysis and machine learning to genetic data to classify populations and adapt algorithm to infer relation between populations from the genetic data.
* Visualization of results.
* Statistical analysis

The following would be an advantage (in this order), but can be learnt during the project

* Good experience in Python.
* Good Knowledge in statistics and probability theory.
* Experience in Machine learning, clustering, dimension reduction (ICA/PCA/PCOA), phylogenetics.
* Basic concepts in biology and genetics.
* Good experience in data visualization.

Applications and questions can be sent to:

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