Universitat Pompeu Fabra Barcelona

Master in Bioinformatics for Health Sciences

Master project 2020-2021

Personal Information	
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Group	Comparative Genomics

Project

Computational genomics

Project Title:

Evolution of hybrid genomes

Keywords:

Hybridization, genome evolution, phylogenomics, pathogens

Summary:

Evolution of eukaryotic species and their genomes has been traditionally understood as a vertical process in which genetic material is transmitted from parents to offspring along a lineage, and in which genetic exchange is restricted within species boundaries. However, mounting evidence coming from comparative genomic studies indicates that this paradigm is often violated. Horizontal gene transfer and mating between diverged lineages blur species boundaries and complicates the reconstruction of evolutionary histories of species and their genomes. Non-vertical evolution might be more restricted in eukaryotes as compared to prokaryotes, yet it is not negligible and can be common in certain groups. Recognition of such processes brings about the need to incorporate this complexity in our tools and models, as well as to conceptually re-frame eukaryotic diversity and evolution. In this project you will work on several hybrid genomes, including those of some pathogenic species, using comparative genomics and populations genomics tools.

References:

https://www.ncbi.nlm.nih.gov/pubmed/28681409

Expected skills::

Python, Phylogenetics, Variant calling analysis,

Possibility of funding::

Yes

Possible continuity with PhD: :

Yes

Comments:

Alternative projects, within the scope of interests of the group (see publications and webpage) can be discussed.