

Master project 2020-2021

Personal Information

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Group	Comparative Genomics

Project

Computational genomics

Project Title:

Population genomics and conservation for whole genomes of 200 species of primates

Keywords:

Whole genomes DNA sequencing, Population genetics, variant calling, admixture

Summary:

Genomic diversity is at the core of many evolutionary inferences. The finer study of primates, our closest relatives, is relevant for several reasons. They are the only living organisms with whom we share a higher proportion of genetic material as we have a shared evolutionary history over time. Thus, studying the genetics of the primates is a necessary endeavour to define the similarities among primates, the uniqueness of humans, and to strengthen the foundations of primate management and conservation. The latter of which should be an international effort, as these species should be considered a treasure of humanity. In the recent years, we have shown that it is possible to study full genome information from apes (Prado-Martinez et al. Nature 2013, Xue et al. Science 2015; deManuel et al. Science 2016; Nater et al. Current Biology 2017). Considering the population decline that all primates are experiencing, it is time-sensitive to act rapidly and generate the global dataset of variation for all primates. We have generated high quality full genome information for a large panel of primates all over the world. By using samples from the wild, we will further elucidate the role of demography, admixture and selection on genome diversity. In so doing, fundamental insights will be gained into the study of primates with multiple ramifications to biology.

References:

Prado-Martinez et al. Nature 2013, Xue et al. Science 2015; deManuel et al. Science 2016; Nater et al. Current Biology 2017

Expected skills::

Programming, population genetics.

Possibility of funding::

To be discussed

Possible continuity with PhD: :

Yes
