We are advertising a PhD position at the interface of phylogenetics and population genetics, under the supervision of Laurent Guéguen, University of Lyon 1, France, and Carina F. Mugal, Uppsala University, Sweden. The PhD position is funded by a three-year grant from the BATantiVIr project, French Research Agency (ANR).

The selected candidate will work at the Laboratory of Biometry and Evolutionary Biology (LBBE), located in Lyon, France. The candidate will also visit the Department of Ecology and Genetics (IEG), located in Uppsala, Sweden, as part of the PhD project. Both institutions offer highly stimulating and international scientific environments. At the LBBE, the PhD student will interact with the molecular evolution team, and be part of the BATantiVIr project, involving also the "Centre International de Recherche en Infectiologie", ENS Lyon. At the EBC, the PhD student will interact with the evolutionary biology program, part of the "Department of Ecology and Genetics (IEG)", Uppsala University.

Interested students are encouraged to get in touch by email to Laurent Guéguen, Laurent.Gueguen@univ-lyon1.fr, and/or Carina F. Mugal, carina.mugal@ebc.uu.se.

Context:

The BATantiVIr project aims at studying the evolutionary history of adaptation of immune genes in bats (Chiroptera).

Bats are one of the most diverse and widespread mammalian order. They host many viruses, including high-profile zoonoses (rabies, Nipah, Ebola & Marburg filoviruses, SARS coronavirus) and viruses close to primate pathogens (poxvirus, Hepatitis B Virus). During bat evolution, lineage-specific adaptation may have occurred as a response to pathogen selective pressure, differentially shaping the innate immune repertoire in bat species. However, most of the evolutionary history and mechanism of bat antiviral immunity is still unknown.

The estimation of selection on genes frequently relies on phylogenetic methods. However, since immune genes in bats are highly polymorphic, it is crucial to incorporate polymorphism in those phylogenetic analyses.

The study of polymorphism lies at the core of population genetics theory, which focuses at the time-scale of a single species and does not explicitly extend to the inter-species scale. On the other hand, in classical phylogenetic analysis, the presence of polymorphism is ignored, and substitutions are assumed to occur instantaneously. The latter assumption biases the inference of natural selection. Typically, polymorphic sites are considered as substitutions, which results in an overestimation of the presence of positive selection.

Project:

The aim of the PhD project is to fill the gap between classical phylogenetics and population genetics, and provide a multi-scale approach for the estimation of natural selection that incorporates intra- and inter-specific data.

This work will be based on the theoretical work of Carina F. Mugal, which provides analytical solutions for the influence of polymorphism dynamics on the estimation of selection in classical phylogenetic approaches. The novel approach will implement the theory in order to compute the transition probabilities between polymorphic states and substitutions among species. For this purpose, the work also relies
on models of speciation dynamics (starting with the simplest models of speciation, so-called isolation-without-migration models).

The novel approach will be implemented in Bio++ libraries, which are a set of C++ libraries dedicated to bioinformatics, phylogenetics, and molecular evolution. Finally, building on these developments, the student will investigate the evolutionary dynamics of bat genes that lie at the core of the BATantiVIR project.

Requirements:

The ideal candidate has a good knowledge of molecular evolution, and a solid bases in mathematical modelling. She/he is familiar with bioinformatics, population genetics and phylogenetic concepts. Last, she/he is autonomous in C++ programming.

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När du har kontakt med oss på Uppsala universitet med e-post så innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gör det kan du läsa här: http://www.uu.se/om-uu/dataskydd-personuppgifter/

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