



École Pratique  
des Hautes Études



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## Post-doctoral position

### Development of a new method to study the distribution of the effect sizes of QTL

ERC-funded 2-years position, ISYEB, Paris, France

#### Offer Description

##### Summary

We offer a 2-years position, working as post-doctoral fellow to improve our ability to study the genetic architecture of complex traits, by developing a new method to study the distribution of the effect sizes of Quantitative Trait Loci (QTL). The job will be mostly computational, based on statistical modelling and development, as well as assessing the performance of the method using simulated data. The candidate will work for the [École Pratique des Hautes Études](#) (PSL University), joining [Pierre de Villemereuil](#)'s team, at the [Institute for Systematics, Evolution, Biodiversity](#) (ISYEB), located within the [Muséum National d'Histoire Naturelle](#) (MNHN) in Paris. This position is funded as part of the EvoGenArch ERC Starting Grant. The position starts on 2024-09-16.

##### Scientific context

Most traits of ecological and evolutionary relevance are *complex traits*, i.e. influenced by a large number of loci (named Quantitative Trait Loci, or QTL) in the genomes. The features of the QTL are often referred to as the *genetic architecture* of the trait. One of the most important collective feature to characterise such architecture is the distribution of the effect sizes (i.e. the phenotypic impact of replacing one allele for the other) of QTL. Current methods allowing for the study of such distribution of effect sizes make the same core assumption: all QTL are a subset of the genetic markers (generally SNPs) available in the genome. However, QTL should come in all possible variety of genetic variants. This distinction between markers and QTL is generally not prob-

lematic if the aim is to locate a region of interest in the genome, or perform genomic predictions. However, if the goal is to infer the distribution of effect sizes from an evolutionary perspective, this distinction between markers and QTL becomes highly important. Indeed, if many, or most, markers are only linked to causal QTL, then the amount of linkage disequilibrium between each QTL and the markers will distort the inferred distribution of effect sizes. If we want to have a chance to empirically test the evolutionary predictions from the theoretical models, it is thus necessary to develop new methods that are focused on the inference of the distribution of QTL. The aim of this post-doctoral project is thus to develop such a new method, using the relation between linkage disequilibrium among markers nearby a QTL and the trait variance each of them “explain”, which is linked to the effect size of the QTL.

## Job description

The job will be mostly computational, heavily based on statistical modelling and development, as well as assessing the performance of the method using simulated data. Under the supervision of Pierre de Villemereuil, in remote collaboration with Olivier François et Bertrand Servin, the candidate will:

- Develop the statistical method (including implementation, either as a package or as a compiled software) to infer the distribution of the effect sizes of QTL, using phenotypic and genomic data on a set of individuals. As a first approach, the method will follow the principles described in the EvoGenArch project, but the candidate will be at full liberty to put forward original ideas relevant to the project aim.
- Test the performance of the method, compared to existing state-of-the-art methods that are not distinguishing between markers and QTL, using phenotypic and genomic data simulated according to a set of scenarios.
- Empirically test the relevance of the new method by re-analysing a published dataset.

## Hosting lab & team

Pierre de Villemereuil’s research focuses on the genetics of adaptation, trying to understand how the levels of the genotype, phenotype and environment interacts to drive evolution in wild populations, notably in response to anthropic pressures. A combination of evolutionary ecology, quantitative genetics, population genomics and statistical modelling is necessary to unveil the patterns and processes of adaptation in the wild. The Institute for Systematics, Evolution, Biodiversity (ISYEB), located in the beautiful *Jardin des Plantes* of the *Muséum National d’Histoire Naturelle* in Paris, is one of the largest labs studying evolution in the city. ISYEB hosts worldwide leading science in evolution, systematics, phylogeny, genomics and ecology.

## Requirements

- PhD in statistical genetics, genomics, bioinformatics or related fields.
- Track record of research activity and academic output (publications, conference communications, etc.).
- Demonstrated ability to work as part of a scientific team, take on research tasks.
- Experience in and interest for statistical genetics and/or statistical development.
- Technical skills in a programming language, preferably compiled, as well as a data analysis language (R/Python/Julia...) are a requirement.

- Background in even basic quantitative genetics will be highly appreciated.

## **Selection process**

Please send (1) a CV/résumé; (2) a short (max. 2 pages) letter of application highlighting past research experience and accomplishment, your fit to the profile and your motivation for the position; and (3) a letter of recommendation or contact details of past supervisors (PhD or Post-doc) to the address [pierre.devillemereuil@ephe.psl.eu](mailto:pierre.devillemereuil@ephe.psl.eu). Selected candidates will be auditioned by a committee of two to three persons, including the PI, starting from May 15<sup>th</sup>, for as long as the position is not filled. Candidates are not discriminated against based on their gender, ethnicity or sexual orientation, please all feel welcome to apply!