

First Journée Darwin

Institut Henri Poincaré

November 18, 2011

Amphi Darboux



Program

- 9:45 Welcome
- 10:00 **Mathieu Joron** (MNHN): Tropical butterflies as models for the genetics of adaptation
- 11:00 **Frédéric Austerlitz** (MNHN and Paris-Diderot): Impact of demographic, cultural and selective processes on genetic diversity: a modelling approach
- 12:00 Lunch break
- 14:00 **Dominique Schneider** (Université Joseph Fourier, Grenoble): Phenotypic and genomic evolution during a long-term experiment with *Escherichia coli*
- 15:00 Coffee break
- 15:30 **Éric Brunet** (ENS): Ancestor tree in a branching random walk with simple selection
- 16:30 **Gilles Fischer** (UPMC): The impact of DNA replication on mutational patterns and genome evolution
- 17:30 Discussion
- 18:00 End of the session



N.B.: Participants are expected to organize freely for the lunch. The coffee break is offered by the IHP.



Abstracts

Mathieu Joron (MNHN): Tropical butterflies as models for the genetics of adaptation

Wing patterns in butterflies have been instrumental in the development of evolutionary thinking, as icons of natural selection in action and prime examples for ecological and biogeographic variation. I will present our research on the evolution of mimicry in tropical butterflies, from the ecology of selection to identifying the genes underlying adaptation. We will see how those genomic regions have acted as important hotspots of adaptive evolution, underlying diversification at various taxonomic scales.

Frédéric Austerlitz (MNHN and Paris-Diderot): Impact of demographic, cultural and selective processes on genetic diversity: a modelling approach

Genetic polymorphism within a species is shaped by demographic, cultural and selective mechanisms. I am interested in particular in understanding how these mechanisms, which act at the level of the individual or the population, impact the diversity of genes that are either involved in these mechanisms or just purely neutral genes. This is a quite important question in biology, as for instance natural selection occurs on the phenotype, while only the genes that code for these phenotypes are transmitted to the next generation. Thus the action of selection on these genes is only indirect. In this talk, I will present several examples in which we have investigated this issue through a modelling approach. As the development, the parameterisation and the validation of these models requires extensive experimental data, I will also present the statistical methods we developed to infer the relevant processes and parameters.

Dominique Schneider (Université Joseph Fourier, Grenoble): Phenotypic and genomic evolution during a long-term experiment with *Escherichia coli*

Evolution is inherently complex owing to the high dimensionality of genomes and the multitude of interactions between genes, gene products, metabolites, and environmental factors including resources. Historically, most studies have focused on components or subsets of complex biological systems. However, to understand many adaptations, one must investigate changes in entire genomes and examine their consequences for global expression and organismal performance. To achieve this goal, the molecular-genetic and phenotypic bases of adaptation are investigated in a bacterial model where twelve independent populations have been propagated in the same environment from a common *Escherichia coli* ancestor for 50,000 generations. Major evolutionary processes are investigated including i) the link between phenotypic and genetic changes and ii) the dynamics of regulatory networks and of genomes.

Éric Brunet (ENS): Ancestor tree in a branching random walk with simple selection

A branching random walk can be seen as the simplest model of evolution with mutation: each individual at each generation has a certain number of offspring, and each of these offspring inherits the fitness of its parent plus a random number representing the mutation. If, at each generation, the population is kept at a fixed size by choosing N surviving individuals at random (no selection), we recover a Wright-Fisher model with an ancestor tree described by the Kingman coalescent. I will discuss in this talk the radical changes in the ancestor tree when a simple scheme of selection is added.

Gilles Fischer (UPMC): The impact of DNA replication on mutational patterns and genome evolution

Evolutionary changes result from the combined action of the mutational forces that are at the origin of the genetic diversity and the natural selection/genetic drift that act as the evolutionary filter that sort the different genotypes. The genetic diversity between genomes of different individuals, populations and species is composed of single nucleotide polymorphisms and large structural variations of chromosomes. In this talk, I will present numerous evidences showing that DNA replication is one the main mutational force which is at the origin of the genetic diversity.

