Processus évolutifs et patrons de biodiversité

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Résumé

Lecture 1. Genealogy of one or many genes

In this lecture, we explain how the genetic diversity of a sample of individuals can be characterized and scales with the size of the population where it is taken from, via the study of gene genealogies and Kingman's coalescent. Next, we display tools describing how genealogies of different genes are coupled by the effect of recombination. We apply these tools to a practical problem (how to infer past demography given a handful of genomes) and to a theoretical question (if ancestral genomes were all painted in distinct colors, how would the mosaic of colors on the genome look like in the long run?).

Lecture 2. The formation of new species

The evolutionary history of species can be represented by a tree called phylogeny. We explain how birth-death processes are standardly used to model the diversification of species (speciation, extinction) and how their parameters can be inferred from the phylogeny, notably via the so-called coalescent point process. We then expose the species paradox and explain how to model the formation of new species from first principles. We apply these models to an empirical question (why are species phylogenies imbalanced?) and to a theoretical question (how does the graph describing the ability to interbreed look like?).

Lecture 3. Coevolving genes and species

Due to recombination and to hybridization between species, the genealogies of genes, even sampled from distantly related species, are usually different at different genes, and (so) distinct from the species tree. We review models coupling gene trees and species tree, including the popular multispecies coalescent. We apply these models to a practical problem (how to cluster a sample of genomes into putative species) and to a theoretical question (characterization of nested coalescents describing jointly gene trees and species tree and study of their behavior close to the present).

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