GECO Evolutionary and Computational Genomics

The main goal of the GECO department is to foster integration and synergies between theoretical and methodological research relevant for the analysis of genomes (computational genomics) and empirical analysis of genomic and multi-omic data (evolutionary and functional genomics). The department is structured in two teams, BAOBAB and BPGE:

BAOBAB is deeply rooted in computer science. Its strengths are in algorithms, models, and mathematical analysis of graphs and networks, with applications to transcriptomics and metabolic networks.

BPGE is oriented towards bioinformatics, phylogenetics and evolutionary genomics. Its research projects cover a broad range of subjects, such as methodological developments for phylogenetic inference, their applications to the reconstruction of the evolutionary history of bacteria and archaea, the role of mobile genetic elements in the evolution of bacteria and of antibioresistance, or the role of recombination, of genomic rearrangements and of transposable elements in the evolution of eukaryotic genomes.

As detailed on their pages, the research conducted in both teams integrates deep and long-ranging theoretical and methodological (algorithmic and computational) developments with data analysis driven by empirical questions. This integration is bi-directional: methodological developments are guided by empirical questions and then used in empirical applications, while theoretical modeling helps clarify the conceptual basis of subsequent empirical analyses.

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