



## GECO EVOLUTIONARY AND COMPUTATIONAL GENOMICS

### BIOINFORMATICS, PHYLOGENY AND EVOLUTIONARY GENOMICS GROUP

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My research focusses on the general question of modeling the evolution of genetic sequences and genomes, with applications to phylogenetic inference and molecular evolution more generally.

For phylogenetic inference, my work is mostly based on Bayesian inference: once we have defined a stochastic model of genetic sequence evolution, we develop and implement algorithms for inferring probable values for the parameters of the model (including the phylogeny itself) which best explain the data. The phylogenetic models that we have developed, through multiple collaborations and with several PhD students, are then used for inferring the evolutionary history of living species (i.e. reconstructing the tree of life), but also for characterizing the adaptive regimes experienced by protein coding genes. Of particular interest is to understand which genes are under strong adaptive pressures, such as typically induced by evolutionary arms races between hosts and pathogens.

More recently, I got interested in confronting approaches working within and between species. Thus, on one side, phylogenetic analysis compares genomes of different species, whose genetic differences have accumulated over millions of years. Population genetics, on the other hand, focus on the genetic variation within species, which typically builds up over much shorter evolutionary time scales (for humans, of the order of a few 100,000 years). With increasing genomic sequences now available, it now becomes possible to integrate those two time scales and investigate to what extent the methods developed for each of them are congruent between each other — and ultimately, how to directly integrate these macro- and micro-evolutionary perspectives in one single model. See the work of

[Latrille et al, 2023](#)

and

[Bastian et al, 2025](#)

on this subject.

Finally, I am also engaged in the development of theoretical and simulation-based models of genome evolution. Unlike those mentioned above, these models are not meant to be directly fitted to the currently available empirical genetic data. Instead, they can be used to explore and better understand the evolutionary phenomena that can spontaneously emerge from various aspects of the mechanisms of reproduction, mutation and recombination. In this direction, see the work of

[Luiselli et al, 2024](#)

, et

[Genestier et al, 2024](#)

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