



## GECO GÉNOMIQUE COMPUTATIONNELLE ET EVOLUTIVE

EQUIPE BAOBAB

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I am generally interested in developing statistical and machine learning methods to solve problems in molecular biology. In particular, I have ongoing projects on :

- > GWAS for bacterial genomes and metagenomes, with collaborators at [Pendulum](#) and UC Berkeley.
- > Improving the inference of phylogenetic trees, with local collaborators at LBBE.
- > Predicting phenotypes from sequences using sparse learning and convolutional networks, with collaborators at [Inria](#).