

COEVOL MULTI-SCALE COEVOLUTION

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My past research has been focused on extracting information from genomes to better understand how they encode phenotypes. Extant living organisms are the result of an historical process that has unfolded over billions of years. Their genomes have accumulated footprints of past episodes of selection in response to interactions with their environment or with other species. I have developed computational methods based on probabilistic models to detect these footprints and interpret genomic data on a large scale.

In particular, I have used ancestral sequence reconstruction to study the lifestyles of organisms that lived billions of years ago, I have developed methods for reconstructing gene trees and species trees to better understand genome evolution, and I have developed and assessed methods to find examples of convergent genomic evolution.

My research in genomics these days mainly focuses on

> exploiting information from horizontal gene transfers to date species phylogenies (e.g. see

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this manuscript 🗗
and the
associated recommendation 🖓
by
PCI Evol Biol 🖓
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> detecting directional selection at the sequence level, notably to study convergent genomic evolution (collaboration with Louis Duchemin

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and
<u>Philippe Veber</u>
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I have recently broadened my interests in a variety of directions, which led me to study

> wheat yields, and how they depend on meteorological conditions (collaboration with

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Louis Duchemin
and
<u>Philippe Veber</u>
)
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> the occurrence of massive synchronized fruiting in oak trees, known as masting, and how this phenomenon depends on meteorological conditions (collaboration with

Emilie Fleurot, Marie-Claude et Samuel Venner de l'équipe "Ecologie Quantitative et Evolutive des Communautés")

> how aphids, their predators, sugar beets and viruses interact, with the hope that a better understanding of this ecological network might help us avoid pesticides when growing sugar beets (collaboration with <u>Baptiste Maucourt</u>

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Eric Tannier
and
Léo Girardin ☑
)
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> whether machine learning approaches can help in the fields of phylogenetic reconstruction and molecular evolution (collaboration with Johanna Trost,

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Luca Nesterenko
,
Philippe Veber
and
Laurent Jacob
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URL of the page: https://lbbe.univ-lyon1.fr/en/annuaire-des-membres/boussau-
bastien
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In terms of teaching, I have been involved in teaching Bayesian statistics, Computational Molecular Evolution, Genomics.

I also taught about the environmental footprint of our food systems as part of the <u>course "Climat et transitions"</u> taught at Université Lyon 1.