COEVOL MULTI-SCALE COEVOLUTION

THE COCOON GROUP
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Research interests

I am an evolutionary biologist using and developing bioinformatics tools to explore various macro-evolutionary questions. My main projects at the moment are listed below.

Exploring the impact of ghost lineages on evolutionary studies

"To a first approximation, all species are extinct. " And most of those that are not are still unknown! When we study evolutionary processes, like introgression, horizontal gene transfer or endosymbiosis, we hope that (and do as if) all this unknown can be neglected. We explore with simulations the effect that ghost lineages (extinct species, unknown extant species and known discarded species) can have on horizontal gene flow detection and characterization.

See these papers (from Théo Tricou's thesis) for recent publications:

T Tricou, E Tannier and DM de Vienne. 2022. Ghost lineages highly influence the interpretation of introgression tests. *Systematic Biology*. In press ↗

T Tricou, E Tannier and DM de Vienne. 2022. Ghost lineages invalidate or reverse several results on gene flow. BiorXiv. ↗

Detecting extinct and unknown lineages thanks to horizontal gene transfers

If most species are extinct or unknown, any gene in a genome acquired through horizontal gene transfer may have originated and/or evolved for some time in species that are now extinct or still unknown. With new methods aiming at detecting horizontally acquired genes in genomes, we explore the possibility to predict *where* in the tree of life some species or clades are missing. This project (and the one briefly described above) has been funded by the French National Research Agency (ANR STHORIZ - 2018-2022).

URL of the page: https://lbbe.univ-lyon1.fr/en/annuaires-des-membres/de-vienne-damien

Developping tools for Phylogenomics

In the past, I developed differents tools for comparing trees (the Icong index) or for exploring forests of gene trees (Phylo-MCOA). Currently, and in collaboration with colleagues from Lyon and Montpellier, I develop Phylter, a new tool for identifying outlier sequences in phylogenomics datasets. This (still under-development) tool is available here : https://github.com/damiendevienne/phylter ⤢

Visualizing phylogenetic trees, pairs of trees, large trees and giant trees

I am intested in new ways of visualiazing evolutionary relationships between species. My main project on this topic is**Lifemap** (http://lifemap.univ-lyon1.fr ⤢
), a popular tool to explore in a single map the complete Tree of Life (more than 1.4 Million species). This popular tool, also available as a mobile app for Android and Apple, has now been downloaded more than 100,000 times. It is presented in the new Science Museum in Moscow and is (or has been) presented in various exhibitions around the world. Many variations of the tool exist (R package,...) or are under construction (html widget, ...).