



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 and Enzo Marsot theses) for recent publications and preprints:

[Tannier E., Tricou T., Benali S., de Vienne D.M. HGTs are not SPRs: In the presence of ghost lineages, series of Horizontal Gene Transfers do not result in series of Subtree Pruning and Regrafting. BiorXiv.](#) ↗

[Tricou T., Tannier E., de Vienne D.M. 2024. Response to "On the impact of incomplete taxon sampling on the relative timing of gene transfer events". Plos Biology. 22:e3002557.](#) ↗

[Tricou T., Tannier E., de Vienne D.M. 2022a. Ghost lineages highly influence the interpretation of introgression tests. Systematic Biology. 71:1147-1158.](#) ↗

[Tricou T., Tannier E., de Vienne D.M. 2022b. Ghost lineages can invalidate or even reverse findings regarding gene flow. Plos Biology. 20:e3001776.](#) ↗

Detecting extinct and unknown lineages thanks to horizontal gene transfers

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

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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. Multiple approaches for this purpose are explored. This project (and the one briefly described above) has been funded by the French National Research Agency (ANR STHORIZ - 2018-2022). A recent preprint explains the rationale behind this idea:

[Tricou T., Marsot M., Boussau B., Tannier T., de Vienne D.M. 2025. Gene flow can reveal ghost lineages. BiorXiv.](#)

Developping tools for Phylogenomics

In the past, I developed different tools for comparing trees (the Icong index) or for exploring forests of gene trees (Phylo-MCOA). Recently, in collaboration with colleagues from Lyon and Montpellier, I developed Phylter, a new tool for identifying outlier sequences in phylogenomics datasets, and Zombi, a tool for simulating the evolution of genomes along the branches of a species tree, that accounts for ghost lineages.

[Comte A., Tricou T., Tannier E., Joseph J., Siberchicot A., Penel S., Allio R., Delsuc F., Dray S., de Vienne D.M. 2023. PhylteR: Efficient Identification of Outlier Sequences in Phylogenomic Datasets. Molecular Biology and Evolution. 40:msad234.](#)

[Davin A.A., Tricou T., Tannier E., de Vienne D.M.*, Szöllhosi G.J.* 2019. Zombi: a phylogenetic simulator of trees, genomes and sequences that accounts for dead lineages. Bioinformatics. 36\(4\): 1286–1288.](#)

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

I am interested in new ways of visualizing evolutionary relationships between species. My main project on this topic is **Lifemap** (<https://lifemap.cnrs.fr>), a popular tool to explore in a single map the complete Tree of Life (more than 2.1 Million species from the NCBI taxonomy). This popular, used by ~20,000 users every month is present in some exhibitions, and used for teaching at all levels. Other visualization-related publications are given below.

[de Vienne D.M. 2019b. Tanglegrams are misleading for visual evaluation of tree congruence. Molecular Biology and Evolution. 36:174–176.](#)

[Penel S., de Vienne D.M. 2022. tidy tree: a new layout for phylogenetic trees. Molecular Biology and Evolution. 39:msac204.](#)

[de Vienne D.M. 2016. Lifemap: exploring the entire tree of life. PLoS biology. 14:e2001624.](#)