COEVOL COÉVOLUTION MULTI-ECHELLES

EQUIPE LE COCON

DE VIENNE Damien

CHARGÉ DE RECHERCHE

CNRS

⊙ 43 bd du 11 novembre 1918
69622 VILLEURBANNE cedex (http://maps.google.com/maps?q=43%20bd%20du%2011%20novembre%201918+69622+%20VILLEURBANNE%20cedex)

☎ 04 72 43 29 09

@ Courriel

🐦 Twitter (https://twitter.com/damdevienne)

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:

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 de la page : https://lbbe.univ-lyon1.fr/fr/annuaires-des-membres/de-vienne-damien

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).

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). Recently, in collaboration with colleagues from Lyon and Montpellier, I develop Phylter, a new tool for identifying outlier sequences in phylogenomics datasets, or 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. ↗

Davín 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 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, 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, Etc). 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. ↗