# Thibault Latrille


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github.com/ThibaultLatrille
scholar.google.com/citations?user=6HlrDNgAAAAJ


## Curriculum Vitae

### Employments

2021-now **Postdoctoral researcher**, *Université de Lausanne, Department of Computational Biology*, advisor Nicolas Salamin.

2020-2021 **Temporary Research and Teaching Attaché**, *Université de Lyon, Biometry and Evolutionary Biology laboratory (LBBE).*

2017-2020 **PhD, October 1, 2017 – November 30, 2020**, *Université de Lyon, Biometry and Evolutionary Biology laboratory (LBBE)*, under the supervision of Nicolas Lartillot, Modelling the interplay between selective and neutral mechanisms in the evolution of protein-coding DNA sequences.
tel.archives-ouvertes.fr/tel-03405159/

### Education

2016-2017 **Master 2 in complex systems**, *Ecole Normale Supérieure de Lyon (ENS), Lyon.*

2013-2014 **Master 1 in biology**, *Ecole Normale Supérieure de Lyon (ENS), Lyon.*

2012-2013 **Erasmus in mathematics**, *University of Uppsala, Sweden.*

2011-2012 **Bachelor in biology**, *Ecole Normale Supérieure de Lyon (ENS), Lyon.*

2009-2011 **Classes Préparatoires aux Grandes Ecoles (CPGE)**, *Lycée Joffre, Montpellier.*
Post-secondary preparatory classes in Biology, Physics, Chemistry and Earth Sciences (BCPST).

### Personal information

Children **One child**, *Born June 11, 2023.*

French Native tongue.

English Fluent.

Spanish Conversational.

**Python & C++**, proficient use and extensive schooling.

**Snakemake**, proficient use and teaching.

**Rust, R, Scilab & Matlab**, understand and have written small programs.

**Web development**, front and back-end development.
Developped website ControverSciences.org, MonPotager and WhereToPublish.

**Versionning**, experimented user with git on collaborative projects.

**Machine learning**, Pytorch for training small ($\leq$ 32Gb) models.

**Adobe creative suite, Affinity suite**, experimented user.

**Office, LaTeX.**

**Ubuntu, MacOS and Windows.**

## Projects and responsibilities

2025, 6 months — **Advisor for master student**, *Léo Besançon*
Are signatures of selection consistent across different evolutionary scales?

2021-2026 — **Workshop organizer**, *Faculty of Biology and Medicine, Lausanne.*
I am currently organizing several workshops on reproducible science at the university, github.com/ThibaultLatrille/workshop-snakemake-unil2023.

2025-2026 — **Co-creator, Developer, and Designer**, WhereToPublish
WhereToPublish is a website providing information on the ownership of scientific journals and publishers across different fields of biology.

2021-2026 — **Project funding**, *Department of Computational Biology, Lausanne.*
I participated in writing a grant proposal for the Swiss National Science Foundation (SNSF) on evolutionary modelling across scales which was awarded to Nicolas Salamin data.snf.ch/grants/grant/219757. This grant is currently funding my salary, but it could only be deposited by the principal investigator under his sole name (Nicolas Salamin).

2023-2024 — **Guest Editor**, *Journal of Evolutionary Biology.*
Editor on a Special Issue on the integration of micro- and macro-evolution, five of the manuscripts that have handled as a Guest Editor have now been published (December 2024 volume of the journal, academic.oup.com/jeb/issue/37/12).

2023, 6 months — **Advisor for master student**, *Theo Schneider*
Are fitness landscapes stable through time?

2015-2026 — **Creator, Developer, and Designer**, ControverSciences.org
ControverSciences.org is a website where contributors collaboratively publish summaries of scientific controversies, based on and analyzing scientific publications. The site has been used as a teaching tool in the Master's program at the University of Montpellier, in a course led by Catherine Moulia.

2020-2026 — **Creator, Developer, and Designer**, MonPotager
MonPotager is an application that simulates a vegetable garden by allowing users to insert various species of fruits and vegetables, and determine whether their interactions will be favorable or unfavorable. The site is used as a teaching tool in the Bachelor's program at INSA Lyon, in a course led by Christophe Rigotti.

2019 — **Project funding**, *Université de Lyon.*
Participated in designing and writing a grant proposal (Community Garden Book) for Action Exploratoire (AEx) that was awarded to Eric Tannier.

2012 — **Laboratoire Junior**, *Ecole Normale Supérieure de Lyon (ENS).*
ENS promotes and helps projects built by students at their own initiative. Our project was to write a software able to produce 3D map of the drosophila's composed eye, based on pictures that cover a small part of the eye (picture matching).

## Teaching and scientific outreach

I have extensive experience in various teaching classes (bachelor, master, private sector) and science outreach programs (e.g., Fête de la Science, Egalité des Sciences) and communicating research results to different target audiences.

2025-2026 **Artificial Intelligence**, *lecturer*, Massive Open Online Courses (MOOC) on generative artificial intelligence for undergraduates, University of Lausanne.

2024 **Evolution**, *lecturer, 4h*, lectures on population genetics for undergraduates, University of Lausanne.

2021-2026 **Reproducible Science with Snakemake**, *organizer, 2×4h*, workshop for PhD students, University of Lausanne.

2021-2026 **Phylogeny and Comparative Methods**, *teaching assistant, 14h/year*, practical sessions for master students, University of Lausanne.

2021-2026 **Advanced Python Programming**, *teaching assistant, 12h/year*, practical sessions for master students, University of Lausanne.

2021-2026 **Introduction to Programming**, *teaching assistant, 12h/year*, practical sessions for undergraduates, University of Lausanne.

2024 **Modeling in Biology and Bioinformatics**, *teaching assistant, 32h/year*, practical sessions for master students, University of Lausanne.

2021 & 2022 **Scientific Methodology**, *lecturer, 2×3h*, lectures and practical sessions for master students, University of Montpellier.

2020-2021 **Bioinformatics**, *teaching assistant, 24h/year*, practical sessions for master students, University of Lyon.

2020-2021 **Genetics**, *teaching assistant, 22h/year*, practical sessions for undergraduates, University of Lyon.

2020-2021 **Population Genetics**, *teaching assistant, 18h/year*, practical sessions for undergraduates, University of Lyon.

2018 & 2019 **Bioinformatics for Sequencing Data Analysis**, *organizer, 2×12h*, course and practical sessions for professionals, Laboratory of Biometry and Evolutionary Biology (LBBE).

2017-2021 **Bioinformatics & Statistics**, *teaching assistant, 32h/year*, practical sessions for undergraduates, University of Lyon.

2017-2020 **Next-Generation Sequencing**, *teaching assistant, 20h/year*, reproducible science for master students, École Normale Supérieure de Lyon (ENS).

2017-2019 **Library Research**, *teaching assistant, 18h/year*, practical sessions for undergraduates, University of Lyon.

## Collective engagements

2025-2026 **PhD committee**, *Université de Montpellier.*
I have been part of the PhD committee of Emeline Esnouf.

2025 **Symposium organization**, *ESEB 2025, Barcelona.*
Co-organizer of the symposium Microevolutionary processes and Macroevolutionary patterns (S36).

2024-2025 **Conference organization**, *Department of Ecology and Evolution, Lausanne.*
Part of the scientific committee for the conference Biology 2025, held February 13-14, 2025 at the University of Lausanne.

2022-2026 **Department committee**, *Department of Computational Biology, Lausanne.*
I have been part of the assistant committee. I also organized a workshop to strengthen connection between labs, thibaultlatrille.github.io/DBCNet. I organized a workshops to collaboratively write a internal wiki for the department.

2021-2024 **PhD committee**, *Laboratoire de Biométrie et Biologie Évolutive (LBBE), Lyon.*
I have been part of the PhD committee of Melodie Bastian, who defended her thesis in 2024.

2019-2020 **President**, *Les pinsons migRateurs.*
I have co-founded the association and was president for its first term, the association goal is to maintain and improve scientific animation, cohesion activities and participate in professional integration within the Laboratoire de Biométrie et Biologie Évolutive (LBBE). We created "Le guide de doctorants", an informal guide to help navigate administrative mazes and share our best practices as researchers and teachers.

2017-2020 **Expert.**
Participation in the AREN (e-fran.education.gouv.fr/aren) project: ARgumentation et Numérique as a provider of content to be debated by high school students (github.com/ThibaultLatrille/AREN-corpus).

2015-2020 **Jury**, *One week per year.*
Expert as founder of the ControverSciences.org platform used in the teaching of 'Scientific controversies' in master 2 at the University of Montpellier in a course led by Catherine Moulia.

## Publication strategy

I am an advocate for reproducible science and I stand firmly on the ground that data, code and scripts should be rendered open access for any published and peer reviewed paper. The code that I write is git versioned and available online at the time of publication, for all my manuscripts. Nonetheless, code availability is necessary, but not the sole requirement of reproducible research, hence the documentation is available as a README with the necessary instructions. Finally, analyses are shared as Snakemake pipelines, allowing anyone to reproduce analysis on the original data or on their specific dataset.

From a publishing perspective, I have strongly favored submitting manuscript to journals that are owned by scientific societies. If I am the lead author, I now systematically refuse to submit to for-profit publishers. If I am a co-author, the choice is not mine but I propose journals owned by scientific societies. I have also stopped reviewing for for-profit publishers. To help guide these decisions and help raise awareness on journal's ownership, I actually co-created the project WhereToPublish that aims at providing information on the ownership of scientific journals and publishers across different fields of biology, where I am maintaining the repository.

## Publication list

Publication List which includes (i) peer-reviewed articles, (ii) preprints and articles without peer review, (iii) invited talks, and (iv) conference talks. Publications are ordered from most recent to oldest, with full references, working links, and clear indication of co-first authors (†) and PhD advisor (N. Lartillot).

## (i) Peer-reviewed publications

1. E. Trucchi, P. Massa, F. Giannelli, **T. Latrille**, M. Gargano, F. A. N. Fernandes, L. Ancona, N. C. Stenseth, J. F. Obiol, J. Paris, G. Bertorelle, and C. L. Bohec. High gene expression predicts extremely low segregation of deleterious mutations in large penguin populations. *Molecular Biology and Evolution*, 42(6):msaf146, 2025. doi.org/10.1093/molbev/msaf146.

2. **T. Latrille**†, J. Joseph†, D. A. Hartasánchez, and N. Salamin. Estimating the proportion of beneficial mutations that are not adaptive in mammals. *PLOS Genetics*, 20(12):e1011536, Dec. 2024. doi.org/10.1371/journal.pgen.1011536.

3. M. Tsuboi, T. Gaboriau, and **T. Latrille**. An introduction to the special issue: inferring macroevolutionary patterns and processes from microevolutionary mechanisms *Journal of Evolutionary Biology*, 37(12):1395–1401, Dec. 2024. doi.org/10.1093/jeb/voae132.

4. **T. Latrille**, M. Bastian, T. Gaboriau, and N. Salamin. Detecting diversifying selection for a trait from within and between-species genotypes and phenotypes. *Journal of Evolutionary Biology*, 37(12):1538–1550, Dec. 2024. doi.org/10.1093/jeb/voae084.

5. D. Silvestro, **T. Latrille**, and N. Salamin. Toward a Semi-Supervised Learning Approach to Phylogenetic Estimation. *Systematic Biology*, page syae029, June 2024. doi.org/10.1093/sysbio/syae029.

6. **T. Latrille**, N. Rodrigue, and N. Lartillot. Genes and sites under adaptation at the phylogenetic scale also exhibit adaptation at the population-genetic scale. *Proceedings of the National Academy of Sciences of the United States of America*, 120(11):e2214977120, 2023. doi.org/10.1073/pnas.2214977120.

7. D. A. Hartasánchez†, **T. Latrille**†, M. Brasó-Vives, and A. Navarro. Bridging Time Scales in Evolutionary Biology. *Mathematics Online First Collections*, pages 1–23. Springer International Publishing, Cham, 2022. doi.org/10.1007/16618_2022_37.

8. **T. Latrille** and N. Lartillot. An Improved Codon Modeling Approach for Accurate Estimation of the Mutation Bias. *Molecular Biology and Evolution*, 39(2):msac005, Feb. 2022. doi.org/10.1093/molbev/msac005.

9. **T. Latrille**, V. Lanore, and N. Lartillot. Inferring long-term effective population size with mutation–selection models. *Molecular Biology and Evolution*, 38(10):4573–4587, Oct. 2021. doi.org/10.1093/molbev/msab160.

10. **T. Latrille** and N. Lartillot. Quantifying the impact of changes in effective population size and expression level on the rate of coding sequence evolution. *Theoretical Population Biology*, 142:57–66, Dec. 2021. doi.org/10.1016/j.tpb.2021.09.005.

11. N. Rodrigue, **T. Latrille**, and N. Lartillot. A Bayesian mutation-selection framework for detecting site-specific adaptive evolution in protein-coding genes. *Molecular Biology and Evolution*, 38(3):1199–1208, Mar. 2021. doi.org/10.1093/molbev/msaa265.

12. **T. Latrille**. Modelling the Articulation of Selective and Neutral Mechanisms in the Evolution of Protein-Coding DNA Sequences. PhD thesis, *Université de Lyon*, Nov. 2020. tel.archives-ouvertes.fr/tel-03405159.

13. **T. Latrille**, L. Duret, and N. Lartillot. The Red Queen model of recombination hot-spot evolution: A theoretical investigation. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences*, 372(1736):20160463, Dec. 2017. doi.org/10.1098/rstb.2016.0463.

† Authors contributed equally to this work.
N. Lartillot is the PhD advisor.

## (ii) Publications without peer review

1. A. Laverré, **T. Latrille**, and M. Robinson-Rechavi. RegEvol: detection of directional selection in regulatory sequences through phenotypic predictions and phenotype-to-fitness functions. *bioRxiv*, 2025.11.26.690685, Nov. 2025. doi.org/10.1101/2025.11.26.690685.

2. **T. Latrille**, T. Gaboriau, and N. Salamin. Phylogram instead of chronogram when assessing the neutral evolution of a trait. *bioRxiv*, 2025.06.16.659089, June 2025. doi.org/10.1101/2025.06.16.659089.

3. L. M. Fitzgerald, **T. Latrille**, A. Marcionetti, T. Gaboriau, D. A. Hartasánchez, and N. Salamin. Genetic basis of the evolution of vertical bars in clownfishes. *bioRxiv*, 2025.03.14.643259, Mar. 2025. doi.org/10.1101/2025.03.14.643259.

4. B. M. Farina, **T. Latrille**, N. Salamin, D. Silvestro, and S. Faurby. Widespread selection relaxation in aquatic mammals, Sept. 2024. doi.org/10.1101/2024.09.18.613479.

## (iii) Invited talks

October 3, 2024 — **External Seminar, Department of Ecology and Evolution**, *Lausanne.*
ecoevo.social/@dee_unil/113204416662399007
Predicting Selection on Traits and Sequences: Contrast Across Evolutionary Scales.

April 17-21, 2023 — **Biological Evolution Across Scales**, *Lausanne.*
bevas-epfl.github.io
A phylogenetic mutation-selection model predicts fitness effects of mutations in extant mammals.

## (iv) Conference talks

September 18–19, 2025 — **Computational Biology Symposium**, *Lausanne.*
cbiosymposium.unil.ch
Between and within species variation to detect selection on gene expression level in mammals.

August 17–22, 2025 — **European Society for Evolutionary Biology**, *Barcelona.*
eseb.org
Measuring morphological changes in unit of nucleotide changes to disentangle neutral and adaptive processes.

July 26–30, 2024 — **Evolution, Third Joint Congress on Evolutionary Biology**, *Montreal.*
youtu.be/lXyhTDWSVfg?feature=shared&t=4240
Detecting diversifying selection for a trait from within and between-species genotypes and phenotypes.

July 12–16, 2024 — **Intelligent Systems for Molecular Biology**, *Montreal.*
iscb.org/ismb2024
A phylogenetic mutation-selection model predicts fitness effects of mutations in extant mammals.

February 16–17, 2023 **Biology 2023**, *Geneve.*
biology23.unige.ch
Up to 25% of beneficial mutations in protein sequences are not adaptive innovations in mammals.

January 23–25, 2023 **Interdisciplinary Approaches for Molecular Evolution**, *Grenoble.*
alphy-aiem-2023.sciencesconf.org
Up to 25% of beneficial mutations in protein sequences are not adaptive innovations in mammals.

August 14–19, 2022 **European Society for Evolutionary Biology**, *Prague.*
Empirical evidence for positive selection that is not adaptive evolution.

June 26–30, 2022 **Mathematical & Computational Evolutionary Biology**, *Chateau d'Oex.*
mceb2022.sciencesconf.org
Empirical evidence for positive selection that is not adaptive evolution.

June 29, 2020 **Society for Molecular Biology & Evolution**, *Quebec [cancelled].*
Reconstructing changes in population size at the phylogenetic scale from the pattern of substitutions.

July 21-25, 2019 **Society for Molecular Biology & Evolution**, *Manchester.*
smbe.org/smbe/SMBE2019Meeting/www.smbe2019.org/index.html
Inferring fluctuating population size and selection with phylogenetic codon models.

July 16-19, 2019 **Mathematical Models in Ecology & Evolution**, *Lyon.*
mmee2019lyon.sciencesconf.org
Inferring fluctuating population size and selection with phylogenetic codon models.

August 21, 2018 **Evolution, Second Joint Congress on Evolutionary Biology**, *Montpellier.*
programme.europa-organisation.com/slides/programme_jointCongressEvolBiology-2018/webconf/862_21082018_1120_rabelais_Thibault_Latrille_697/index.html
The Red-Queen model of recombination hotspots evolution.

November 8-9, 2017 **Interdisciplinary Approaches for Molecular Evolution**, *Lyon.*
project.inria.fr/aiem2017
Application of mean-field theory in red-queen dynamics.

November 2-3, 2016 **Blend Web Mix**, *Lyon.*
youtube.com/watch?v=oH_-9-z-o_c
Le web & internet ont-ils changé notre pratique de la science ? Mariages, infidélités et divorces entre la science et le numérique.

June 6-7, 2016 **Modèles en Ecologie Evolutive**, *Montpellier.*
La reine rouge au royaume des recombinaisons.

June 3-4, 2014 **Modèles en Ecologie Evolutive**, *Montpellier.*
Robust estimation of phylogenetic diversity: steer clear of rare species.

May 27-28, 2014 **Bioinformatics for Environmental Genomics**, *Lyon.*
ge-lyon2014.sciencesconf.org
Robust estimation of phylogenetic diversity: steer clear of rare species.