Thibault Latrille

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G **scholar.google.com/citations?user=6HlrDNgAAAAJ**

Education

2017-2020	**PhD, november 30, 2020**, *Université de Lyon*, 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
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.* University-level institution training teachers and researchers, which entrance to is based on a competitive exam.
2009-2011	**Classes Préparatoires aux Grandes Ecoles (CPGE)**, *Lycée Joffre, Montpellier.* Post-secondary preparatory classes in Biology, Physics, Chemistry and Earth Sciences (BCPST) for competitive exam to the French leading institutions of higher education, such as veterinary schools, engineer schools and the ENS.

Employment history

2021-now	**Postdoctoral researcher**, *Université de Lausanne*, advisor Nicolas Salamin.
2020-2021	**Temporary Research and Teaching Attaché**, *Université de Lyon*, under the supervision of Nicolas Lartillot.
2012-2017	**Elève normalien stagiaire**, *Ecole Normale Supérieure de Lyon (ENS)*, Students who succeed in the entrance examinations are considered trainee public servants, and receive a salary for their studies during 4 years.
2017	**5 months internship**, *Laboratoire de Biométrie et Biologie Évolutive (LBBE)*, under the supervision of Nicolas Lartillot.
2016	**6 months internship**, *Laboratoire de Biométrie et Biologie Évolutive (LBBE)*, under the supervision of Nicolas Lartillot.
2014	**6 months internship**, *Institut des Sciences de l'Evolution de Montpellier*, under the supervision of Francois Rousset.
2013	**2 months internship**, *Laboratoire de Biotechnologie de l'Environnement*, under the supervision of Jérôme Hamelin.

Teaching activities

2024	**Evolution**, *lecturer, 4h*, lectures on population genetics for undergraduates, University of Lausanne.
2024	**Modeling in Biology and Bioinformatics**, *teaching assistant, 32h/year*, practical sessions for master students, University of Lausanne.
2021 & 2023	**Reproducible Science with Snakemake**, *organizer, 2×4h*, workshop for PhD students, University of Lausanne.
2021-2024	**Phylogeny and Comparative Methods**, *teaching assistant, 14h/year*, practical sessions for master students, University of Lausanne.
2021-2024	**Advanced Python Programming**, *teaching assistant, 12h/year*, practical sessions for master students, University of Lausanne.
2021-2024	**Introduction to Programming**, *teaching assistant, 12h/year*, practical sessions for undergraduates, 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.

Institutional responsibilities

2023-2024	**Guest Editor**, *Journal of Evolutionary Biology.*
	Editor on a Special Issue on the integration of micro- and macro-evolution (December 2024 volume of the journal, academic.oup.com/jeb/issue/37/12).
2019-2020	**President**, *Les pinsons migRateurs.*
	Association to maintain and improve scientific animation, cohesion activities and participate in professional integration within the Laboratoire de Biométrie et Biologie Évolutive (LBBE).

Reviewer

Genome Biology and Evolution (GBE), PLOS Genetics, Molecular Phylogenetics and Evolution, BMC evolutionary biology.

Personal projects

2015-2024 **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.

2020-2024 **Creator, Developer, and Designer**, MonPotager.

Mon Potager 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.

2015-2016 **Co-founder and Developer**, Symbiosis-Technologies

Symbiosis-Technologies developed Lab-A, a software that allows scientists to track laboratory inventory, share protocols, and monitor ongoing experiments. Today, Symbiosis-Technologies employs one additional engineer alongside the co-founders, while I left the company in 2016 to continue my studies.

Approved research projects

2023 **Evolutionary modelling across scales**, *Department of Computational Biology, Lausanne.*

Participated in designing and writing a grant proposal for the Swiss National Science Foundation (SNSF) which was awarded to Nicolas Salamin data.snf.ch/grants/grant/219757.

2019 **Community Garden Book (Réseaux et communautés agroécologiques)**, *Université de Lyon.*

Participated in designing and writing a grant proposal for Action Exploratoire (AEx) that was awarded to Eric Tannier.

2017 **PhD scholarship**, *Université de Lyon.*

3 years scholarship grant awarded by ENS de Lyon based on the candidate PhD project and his results during master studies.

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).

Conference talks

October 3, 2024 **External Seminar, Department of Ecology and Evolution**, *Lausanne.*
Predicting Selection on Traits and Sequences: Contrast Across Evolutionary Scales.

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.

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 mammal.

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.

Peer-reviewed publications

1. **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.

2. 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.

3. **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.

4. 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.

5. E. Trucchi, P. Massa, F. Giannelli, **T. Latrille**, F. A. N. Fernandes, L. Ancona, N. C. Stenseth, J. F. Obiol, J. Paris, G. Bertorelle, and C. L. Bohec. Gene expression is the main driver of purifying selection in large penguin populations, *Peer Community in Evolutionary Biology, 100705*, Mar. 2024. doi.org/10.24072/pci.evolbiol.100705.

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.

Personal skills

French	Native tongue
English	Fluent
Spanish	Conversational

- **PYTHON & C++**, proficient use and extensive schooling.
- **Snakemake**, proficient use and teaching.
- **Web development**, front and back-end development
  Used web languages (Ruby on Rails framework, Javascript, jQuery, D3.js, HTML5 & CSS3), to design website ControverSciences.org, MonPotager.org and co-create Lab-A.
- **Rust, R, Scilab & Matlab**, understand and have written small programs.
- **Versionning**, experimented user with git on collaborative projects.
- **Adobe Photoshop, Illustrator & InDesign**, experimented user.
- **Office, LATEX.**
- **Ubuntu , MacOS and Windows .**