

Joëlle BARIDO-SOTTANI

46 rue d'Ulm
75005 Paris (France)
Cellphone (+33) 6 99 91 79 67
joelle.barido-sottani@m4x.org
Nationality: French

RESEARCH EXPERIENCE

- **Feb 2024 – present:** Chargée de recherche CNRS (permanent researcher) at the Institute of Biology, ENS Ulm (France).
- **Nov 2021 – Jan 2024:** Marie-Curie fellow with Prof. Hélène Morlon at the Institute of Biology, ENS Ulm (France). Project title: Accurate phylogenetic tree reconstruction using rate-heterogeneous birth-death models.
- **Feb 2019 – Jul 2021:** Post-doctoral researcher with Prof. Tracy Heath at the Department of Evolution, Ecology and Organismal Biology, Iowa State University (USA).
- **Oct 2014 – Dec 2018:** “Complex birth-death models for Bayesian phylodynamic inferences”. PhD thesis supervised by Prof. Tanja Stadler at the Department of Biosystems Science and Engineering, ETH Zürich (Switzerland).
- **Mar 2014 – Aug 2014:** “A 3D Cell-based Single-layer Model Applied to Branching Morphogenesis” Master thesis supervised by Prof. Dagmar Iber at the Department of Biosystems Science and Engineering, ETH Zürich (Switzerland).

EDUCATION

- **15/10/2018:** PhD in Computational Biology from the Swiss Federal Institute of Technology Zürich (ETHZ). Thesis title: Complex birth-death models for Bayesian phylodynamic inferences.
- **11/09/2014:** Joint Master of Science in Computational Biology and Bioinformatics at the Swiss Federal Institute of Technology Zürich (ETHZ) and the University of Zürich (UZH).
- **06/06/2014:** Master in Bioinformatics at the Ecole Polytechnique (France).

PUBLICATIONS

T. Chambe, R.C.M. Warnock, **J. Barido-Sottani**. “The FossilSimShiny app for simulating under the fossilized birth-death process and plotting the results” *Paleobiology* (*accepted*)

J. Barido-Sottani, O. Schwery, R.C.M. Warnock, C. Zhang, A.M. Wright. “Practical guidelines for Bayesian phylogenetic inference using Markov Chain Monte Carlo (MCMC)” *Open Research Europe* (*accepted*)

H. Morlon, J. Andréoletti, **J. Barido-Sottani**, S. Lambert, B. Perez-Lamarque, I. Quintero, V. Senderov, P. Veron. “Phylogenetic Insights Into Diversification” *Annual Review of Ecology, Evolution, and Systematics* (*in press*)

J.M. Wolfe, L. Ballou, J. Luque, V.M. Watson-Zink, S.T. Ahyong, **J. Barido-Sottani**, T. Chan, K.H. Chu, K.A. Crandall, S.R. Daniels, D.L. Felder, H. Mancke, J.W. Martin, P.K.L. Ng, J. Ortega-Hernández, E. Palacios Theil, N.D. Pentcheff, R. Robles, B.P. Thoma, L.M. Tsang, R. Wetzler, A.M. Windsor, H.D. Bracken-Grissom. “Convergent Adaptation of True Crabs (Decapoda: Brachyura) to a Gradient of Terrestrial Environments” *Systematic Biology*, 2023. DOI: 10.1093/sysbio/syad066

J. Barido-Sottani, K. de Baets, D. Murdock, A. Pohle, J. Sciré, R.C.M. Warnock. "Putting the F in FBD analysis: tree constraints or morphological data?" *Palaeontology*, 2023. DOI: 10.1111/pala.12679

J. Barido-Sottani, H. Morlon. "Full phylogenetic inference using the ClaDS model in BEAST2" *Systematic Biology*, 2023. DOI: 10.1093/sysbio/syad027

T.R. Simões, N. Greifer, **J. Barido-Sottani**, S.E. Pierce. "EvoPhylo: an R package for pre- and postprocessing of morphological data from relaxed clock Bayesian phylogenetics" *Methods in Ecology and Evolution*, 2023. DOI: 10.1111/2041-210X.14128

J. Barido-Sottani, D. Żyła, T.A. Heath. "Estimating the age of fossil deposits using a total-evidence approach" *Systematic Biology*, 2023. DOI: 10.1093/sysbio/syac073

J. Sciré, **J. Barido-Sottani**, D. Kühnert, T.G. Vaughan, T. Stadler. "Robust phylodynamic analysis of genetic sequencing data from structured populations" *Viruses*, 2022. DOI: 10.3390/v14081648

A.M. Wright, D.W. Bapst, **J. Barido-Sottani**, R.C.M. Warnock. "Integrating Fossil Observations Into Phylogenetics Using the Fossilized Birth-Death Model" *Annual Review of Ecology, Evolution, and Systematics*, 2022. DOI: 10.1146/annurev-ecolsys-102220-030855

J. Barido-Sottani, J.A. Justison, R. Borges, J.M. Brown, W. Dismukes, B. do Rosario Petrucci, L. Guimarães Fabreti, S. Höhna, M.J. Landis, P.O. Lewis, M.R. May, F.K. Mendes, W. Pett, B.D. Redelings, C.M. Tribble, A.M. Wright, R. Zenil-Ferguson, T.A. Heath. "Lessons learned from organizing and teaching virtual phylogenetics workshops" *Bulletin of the Society of Systematic Biologists*, 2022. DOI: 10.18061/bssb.v1i2.8425

J. Andréoletti*, A. Zwaans*, R. Warnock, G. Aguirre-Fernández, **J. Barido-Sottani**, A. Gupta, T. Stadler, M. Manceau. "The Occurrence Birth-Death Process for combined-evidence analysis in macroevolution and epidemiology" *Systematic Biology*, 2022. DOI: 10.1093/sysbio/syac037

C. M. Tribble, W.A. Freyman, M.J. Landis, L.J. Ying, **J. Barido-Sottani**, B.T. Kopperud, S. Höhna, M.R. May. "RevGadgets: an R Package for visualizing Bayesian phylogenetic analyses from RevBayes" *Methods in Ecology and Evolution*, 2021. DOI: 10.1111/2041-210X.13750

J. Barido-Sottani, T.G. Vaughan, T. Stadler. "A multitype birth-death model for Bayesian inference of lineage-specific birth and death rates" *Systematic Biology*, 2020. DOI: 10.1093/sysbio/syaa016

J. Barido-Sottani, E. Saupe, T.M. Smiley, L.C. Soul, A. Wright, R.C.M. Warnock. "Seven rules for simulations in paleobiology" *Paleobiology*, 2020. DOI: 10.1017/pab.2020.30

J. Barido-Sottani*, N. van Tiel*, M.J. Hopkins, D.F. Wright, T. Stadler, R.C.M. Warnock. "Ignoring fossil age uncertainty leads to inaccurate topology and divergence time estimates in time calibrated tree inference" *Frontiers in Ecology and Evolution*, 2020. DOI: 10.3389/fevo.2020.00183

J. Barido-Sottani, J.A. Justison, A.M. Wright, R.C.M. Warnock, W. Pett, T. A. Heath. "Estimating a time-calibrated phylogeny of fossil and extant taxa using RevBayes" 2020. In Scornavacca, Delsuc & Galtier, *Phylogenetics in the Genomic Era*. Authors open access book.

J. Barido-Sottani*, S.D. Chapman*, E. Kosman, A.R. Mushegian. "Measuring similarity between gene interaction profiles" *BMC Bioinformatics*, 2019. DOI: 10.1186/s12859-019-3024-x

J. Barido-Sottani, G. Aguirre-Fernández, M.J. Hopkins, T. Stadler, R. Warnock. "Ignoring stratigraphic age uncertainty leads to erroneous estimates of species divergence times under the fossilized birth-death process" *Proceedings of the Royal Society B*, 2019. DOI: 10.1098/rspb.2019.0685

R. Bouckaert, T.G. Vaughan, **J. Barido-Sottani**, S. Duchêne, M. Fourment, A. Gavryushkina, J. Heled, G. Jones, D. Kühnert, N. De Maio, M. Matschiner, F.K. Mendes, N.F. Müller, H.A. Ogilvie, L. du Plessis, A. Poppinga, A. Rambaut, D. Rasmussen, I. Siveroni, M.A. Suchard, C. Wu, D. Xie, C. Zhang, T. Stadler, A.J. Drummond. "BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis" *PLOS Computational Biology*, 2019. DOI: 10.1371/journal.pcbi.1006650

J. Barido-Sottani, W. Pett, J.E. O'Reilly, R.C.M. Warnock. "FossilSim: an R package for simulating fossil occurrence data under mechanistic models of preservation and sampling" *Methods in Ecology and Evolution*, 2019. DOI: 10.1111/2041-210X.13170

J. Barido-Sottani, T.G. Vaughan, T. Stadler. "Accurate detection of HIV transmission clusters from phylogenetic trees through a multi-states birth-death model" *Journal of the Royal Society Interface*, 2018. DOI: 10.1098/rsif.2018.0512

J. Barido-Sottani*, V. Bošková*, L. Du Plessis*, D. Kühnert*, C. Magnus*, V. Mitov*, N.F. Müller*, J. Pečerska*, D.A. Rasmussen*, C. Zhang*, A.J. Drummond, T.A. Heath, O.G. Pybus, T.G. Vaughan, T. Stadler. "Taming the BEAST—A Community Teaching Material Resource for BEAST 2" Systematic Biology, 2018. DOI: 10.1093/sysbio/syx060

* shared first authors

PRESENTATIONS AND TALKS

- **June 2023:** "A combined model for heterogeneous fossilized birth-death inferences". Presentation at the Mathematical and Computational Evolutionary Biology conference (France).
- **August 2022:** "Integrating phylogenetic estimation with complex evolutionary models in phylogenetic inference". Presentation at the ESEB congress (Czech Republic).
- **June 2022:** "Integrating ecological niche models with phylogenetic inference using the FBD process". Presentation at the Evolution meeting (USA).
- **April 2022:** "Integrating fossil evidence in phylogenetic inference using the Fossilized Birth-Death process". Invited virtual talk at the Palaeobiology Discussion Group (University of Bristol, UK).
- **December 2021:** "The fossilized birth-death process in practice: applications and challenges". Invited talk at Phyloseminar (phyloseminar.org).
- **July 2021:** "A Multi-Type Birth-Death model for Bayesian inference of lineage-specific birth and death rates". Invited virtual talk at the Pierce Lab (Harvard University, USA).
- **June 2021:** "Sustainable scientific software development for large and distributed teams". Invited speaker at a round table for the iEvoBio workshop.
- **June 2021:** "Estimating the age of poorly dated fossil specimens and deposits using a total-evidence approach". Presentation at the virtual Evolution meeting.
- **June 2019:** "A Multi-State Birth-Death model for Bayesian inference of lineage-specific birth and death rates". Invited talk at the Evolution meeting (USA).
- **August 2018:** "Comparison and evaluation of different approaches to dealing with fossil age uncertainty in divergence time estimation". Presentation at the Joint Conference on Evolutionary Biology (France).
- **June 2016:** "Estimating lineage dependent speciation and extinction rates from a phylogeny using a multi-states birth-death model". Presentation at the Evolution meeting (USA).

SUPERVISION EXPERIENCE

- **Dec 2023 – present:** Supervising Minghao Du, a visiting PhD student for a 2-years project on integrating mass extinctions in phylogenies funded by the Chinese Scholarship Council.
- **Nov 2023 – Mar 2024:** Supervised a 5-months master-level ERASMUS internship on molecular-morphological discordance in phylogenetic inference, by Tim Chandler.
- **Oct 2022 – Mar 2023:** Supervised a 5-months master project on integrating fossil data into the ClaDS birth-death model by Nils Chabrol.
- **April – May 2022:** Supervised a 6-weeks undergraduate research project "Building a Shiny web app for simulating phylogenies with fossils" by Titouan Chambe.
- **July 2020 – July 2021:** Mentor for a first-year PhD student, offering guidance on research projects, classes and general organization through weekly meetings.
- **March – August 2016:** Co-supervised a master project "Improvement of numerical likelihood calculations in the Birth-Death-Migration Model package for software BEAST2" by Jérémie Scire.

TEACHING EXPERIENCE

- **July 2023, Mar 2024:** Lecturer for an online BEAST2 workshop, teaching Bayesian phylogenetic inference using BEAST2 (20 students).
- **July 2023:** Lecturer at the Taming the BEAST workshop in Squamish, Canada, teaching divergence times estimation and multi-type birth-death processes (30 students).
- **June 2022:** Guest lecturer for master-level students at the FAU Erlangen (Germany), teaching multi-type birth-death processes (5 students).
- **August 2020, April 2021:** Lecturer for the RevBayes Stay-at-Home online workshop, teaching Bayesian phylogenetic inference using RevBayes (25 students).
- **August 2020, July 2021, July 2022:** Lecturer for the online Summer Institute in Statistics and Modeling in Infectious Diseases (SISMID), as part of the module Evolutionary Dynamics and Molecular Epidemiology of Viruses (40 students).
- **Spring 2020:** Teaching assistant for the graduate-level class “Macroevolution” at the Iowa State University, responsible for preparing and teaching two phylogenetics tutorials (20 students).
- **October 2019:** Substitute lecturer for the graduate-level class “Introduction to Python” at the Iowa State University, covering two lectures (30 students).
- **August 2019:** Lecturer at the Taming the BEAST workshop in Squamish, Canada, teaching divergence times estimation and the Fossilized Birth-Death process (30 students).
- **May 2018, 2019:** Lecturer at the Computational molecular evolution (CoME) course, teaching divergence times estimation and the Fossilized Birth-Death process (35 students).
- **Fall 2016, 2017:** Teaching assistant for the master-level Computational Biology class at ETH Zürich (60 students). Responsible for tutorial exercises and graded programming exercises.
- **September 2017:** Lecturer at the Computational Biology for Infectious Diseases (CBID) summer school in Quy Nhon, Vietnam, teaching Bayesian phylogenetic inference (30 students).
- **July 2017:** Lecturer at the Taming the BEAST workshop in London, UK, teaching divergence times estimation and the Fossilized Birth-Death process (20 students).

GRANTS

- **2021:** Marie-Curie individual fellowship for the 24-months project PHYLOBD, focused on multi-type birth-death processes, 185 000 EUR
- **2016:** Continuation funding for follow-up Taming the BEAST workshops under the Swiss Universities Conference (SUK) doctoral programme 2017-2020, 50 000 CHF
- **2015:** Funding for the first Taming the BEAST workshop under the Swiss Universities Conference (SUK) doctoral programme 2013-2016, 25 000 CHF

OTHER CONTRIBUTIONS

- Academic editor for PLOS Computational Biology, section Ecology and Evolution.
- Reviewer for Nature Ecology and Evolution, Science Advances, PNAS, Systematic Biology, Evolution, Palaeontology, Paleobiology, Methods in Ecology and Evolution, Molecular Phylogenetics and Evolution and BMC Evolutionary Biology.
- Reviewer of R packages for rOpenSci (<https://ropensci.org/>).
- **Feb 2024:** Co-organizer of the 2024 Statistical Methods for Post Genomic Data (SMPGD) conference in Paris, France (150 attendees).
- **July 2023, Mar 2024:** Organizer of the first online BEAST2 workshops in association with Transmitting Science. Created new materials and an adapted schedule for the online format.

- **June 2021, June 2022:** Participated in the bilingual mentoring program at the Evolution meeting, helping a French-speaking student with presentation materials, language issues and general advice on international conferences.
- **August 2020, April 2021:** Co-organizer of the first online RevBayes workshops. Recorded video walkthroughs of tutorials, and planned and coordinated interactive sessions before and during the workshop.
- **Apr 2019 – July 2022:** Led a team-wide effort to improve the quality and reliability of the Bayesian inference software RevBayes. Established code and documentation guidelines and implemented a new workflow for proposing and validating changes, including an automated build and test system and code reviews.
- **June 2016:** Co-organizer of the first Taming the BEAST workshop, in Engelberg, Switzerland. Managed a 6-person team and supervised the selection of participants, creation of teaching materials and practical organization before and during the workshop.

OTHER SKILLS

Programming languages: advanced skills in Java, C++ and R; basic skills in Python and Matlab
 Basic knowledge of OpenMPI parallel programming
 Experience with Bash scripting, Unix command-line tools, HPC clusters and schedulers
 Familiar with software management tools Git and Travis

Languages spoken: English (fluent), French (native), German (basic)