

Joëlle BARIDO-SOTTANI

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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).
- **Apr 2012 – June 2012:** Research internship supervised by Prof. Arcady Mushegian at the Stowers Medical Institute in Kansas City, US. Worked on the influence of the choice of similarity measure in clustering genetic interaction networks.

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* (*submitted*)

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 (*in review*)

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).

TEACHING EXPERIENCE

- **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

- Associate editor for PLOS Computational Biology, section Ecology and Evolution.
- Reviewer for Nature Ecology and Evolution, 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, using a format inspired by Taming the BEAST, in association with Transmitting Science.
- **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.
- **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.
- **July 2020 – July 2021:** Mentor for a first-year PhD student, offering guidance on research projects, classes and general organization through weekly meetings.
- **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.
- **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.

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)