

Joëlle BARIDO-SOTTANI

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Nationality: French

RESEARCH EXPERIENCE

- **Nov 2021 – present:** Marie-Curie fellow with Prof. Hélène Morlon at the Institute of Biology, ENS Ulm (France).
- **Feb 2019 – Jul 2021:** Post-doctoral researcher with Prof. Tracy Heath at the Department of Evolution, Ecology and Organismal Biology, Iowa State University (USA).
 - Developed and maintained modules for the Bayesian inference software RevBayes.
 - Led a team-wide effort to improve the quality and reliability of 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.
- **Oct 2014 – Dec 2018:** PhD thesis supervised by Prof. Tanja Stadler at the Department of Biosystems Science and Engineering, ETH Zürich (Switzerland).
 - Thesis title: Complex birth-death models for Bayesian phylodynamic inferences.
 - Developed the MSBD package for inference of lineage-specific birth and death rates in the Bayesian inference software BEAST2.
 - Developed FossilSim, an R package for simulating birth-death-fossilization processes, in collaboration with Dr. Rachel Warnock.
- **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

J. Barido-Sottani, D. Żyła, T. Heath. “Estimating the age of fossil deposits using a total-evidence approach” *Systematic Biology* (in revision)

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 (in revision)

J. Scire, **J. Barido-Sottani**, D. Kühnert, T. G. Vaughan, T. Stadler. “Improved multi-type birth-death phylodynamic inference in BEAST 2” (in revision)

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, Tracy A. Heath. “Lessons learned from organizing and teaching virtual phylogenetics workshops” (in preparation)

J. Andréoletti*, A. Zwaans*, R. Warnock, G. Aguirre-Fernández, **J. Barido-Sottani**, A. Gupta, T. Stadler, M. Manceau. “A skyline birth-death process for inferring the population size from a reconstructed tree with occurrences” (in preparation)

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*, S. D. Chapman*, E. Kosman, A. R. Mushegian. “Measuring similarity between gene interaction profiles” BMC Bioinformatics, 2019. DOI: 0.1186/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 POSTERS

- **June 2019:** “A Multi-State Birth-Death model for Bayesian inference of lineage-specific birth and death rates”. Invited talk at the Evolution meeting, Providence, 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, Montpellier, France.
- **June 2017:** “Detection of HIV transmission clusters from phylogenetic trees through a multi-states birth-death model”. Poster at the Mathematical and Computational Evolutionary Biology conference, Porquerolles, 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, Austin, US.
- **August 2015:** “Fitting lineage dependent speciation and extinction rates on a phylogeny: a multi-states birth-death model”. Poster at the European Society for Evolutionary Biology Congress, Lausanne, Switzerland.

TEACHING EXPERIENCE

- **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:** Lecturer for the online Summer Institute in Statistics and Modeling in Infectious Diseases (SISMID), as part of module 14: 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 and phylodynamic 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

- Reviewer for Nature Ecology and Evolution, Systematic Biology, Evolution, Palaeontology, Methods in Ecology and Evolution and BMC Evolutionary Biology.
- Reviewer of R packages for rOpenSci (<https://ropensci.org/>).
- **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:** Mentoring a first-year PhD student, offering guidance on research projects, classes and general organization through weekly meetings.
- **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)