

Gustavo V. Barroso

POSTDOCTORAL RESEARCHER

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Computational Evolutionary Biology, Statistical Population Genetics

Summary

I am an evolutionary biologist focused on computational population genomics. I want to understand how molecular-level processes interact with population-level processes to shape patterns of variation at different scales. To this end, I develop novel theoretical methods, assemble them into inference tools and apply them to both simulated and real data. My long-term goal is to build more realistic models of nature.

Skills

Most of my research follows a comprehensive work-flow where I **(1)** develop and implement a statistical model; **(2)** bench-mark it using simulations; and **(3)** apply it to real datasets to draw biological conclusions. My approach touches on all of the core aspects of modern evolutionary biology, from describing a scientific problem as a solvable algorithm to interpretation of the results and investigation of follow-up questions in hypothesis-driven fashion.

I highlight the following as part of my tool-box:

PROGRAMMING:

- Development and maintenance of C++ source code implementing statistical models
- R scripting for data analyses and visualization
- UNIX Shell scripting for large-scale manipulation of big datasets

DATA AQUISITION & HANDLING

- Experience with computing cluster environments (SLURM, TORQUE)
- Experience with simulation engines (SLiM and ms-like coalescent simulators)
- Experience with wet-lab protocols for DNA extraction, amplification and sequencing
- Field work in the Atlantic Rainforest

Education

Max Planck Institute for Evolutionary Biology

Ph. D. in Evolutionary Genetics

Adviser: Dr. Julien Dutheil

Plön, Germany

2016 - 2019

Universidade de São Paulo

M. Sc. in Evolutionary Genetics

Adviser: Dr. Maria Cristina Arias

São Paulo, Brazil

2009 - 2011

Universidade Regional de Blumenau

B. Sc. in Biology

Adviser: Dr. Geraldo Moretto

Blumenau, Brazil

2005 - 2008

Academic Work Experience

University of Wisconsin

Post-doctoral research

Supervisor: Dr. Aaron Ragsdale

Madison, USA

2022 -

University of California, Los Angeles

Post-doctoral research

Supervisor: Dr. Kirk Lohmueller

Los Angeles, USA

2019 - 2022

Academic Service & Supervision

Co-supervision of internship student Armaan Singh

University of California, Los Angeles, 2021

We developed a data structure to compute summary statistics over tens of thousands of family trios.

Co-supervision of Hiwi student Nataša Puzovic

MPI for Evolutionary Biology, 2018

We used simulations to benchmark the inference of the recombination landscape under complex demography.

Co-supervision of internship student Pallavi Misra

MPI for Evolutionary Biology, 2017

We used simulations to benchmark the inference of demographic events.

Co-supervision of internship student Nataša Puzovic

MPI for Evolutionary Biology, 2016

We analysed single-cell transcriptomics data in the context of selection on gene expression noise.

Selected Talks

- Disentangling dominance, selection and epistasis using approximate Bayesian computation **(Invited)** 2021
Centre for Genomic Regulation (Barcelona). Hosts: David Castellano & Donat Wenghorn
- Mutation rate variation shapes the genome-wide distribution of diversity in *Drosophila melanogaster* 2021
2021 SBE Meeting (Virtual)
- Trio-based inference of dominance and selection 2021
Probabilistic Models in Genomics (Virtual)
- The Neanderthal recombination map **(Invited)** 2018
University of Bern. Hosts: Fanny Pouyet & Laurent Excoffier
- An integrative model for population genomics inference 2018
II Joint Meeting of Evolutionary Biology (Montpellier)

List of Publications

- **Barroso, GV**; Lohmueller, KE (2021). Inferring the mode and strength of ongoing selection. *BioRxiv*. DOI: doi.org/10.1101/2021.10.08.463705
- **Barroso, GV**; Dutheil, JY (2021). Mutation rate variation shapes genome-wide diversity in *Drosophila melanogaster*. *BioRxiv*. DOI: doi.org/10.1101/2021.09.16.460667
- da Fonseca, R; Campos, P; Rey de la Iglesia, A; **Barroso, GV**; Bergeron, L; Nande, M; Tuya, F; Abidli, S; Perez, M; Riveiro, I; Carrera, O; Jurado-Ruzafa, A; Santamaria, MTG; Faria, R; Machado, A; Fonseca, M; Froufe, E; Castro, LFC (2021). Low coverage whole genome sequencing reveals the underlying structure of European sardine populations. *Authorea*. DOI: [10.22541/au.161628445.52373083/v1](https://doi.org/10.22541/au.161628445.52373083/v1)
- Schweizer, G; Haider, MB; **Barroso, GV**; Roessel, N; Muench, K; Kahmann, R; Dutheil, JY (2021). Population genomics of the maize pathogen *Ustilago maydis*: demographic history and role of virulence clusters in adaptation. *Genome Biology and Evolution*. DOI: doi.org/10.1093/gbe/evab073
- **Barroso, GV**; Moutinho, AF; Dutheil, JY (2020). A Population Genomics Lexicon. In: Dutheil J. (eds) Statistical Population Genomics. Methods in Molecular Biology, vol 2090. Humana, New York, NY. DOI: [10.1007/978-1-0716-0199-0_1](https://doi.org/10.1007/978-1-0716-0199-0_1)
- **Barroso, GV**; Puzovic, N; Dutheil, JY (2019). Inference of recombination maps from a single pair of genomes and its application to archaic samples. *PLoS Genetics*. DOI: [10.1371/journal.pgen.1008449](https://doi.org/10.1371/journal.pgen.1008449)
- **Barroso, GV**, Puzovic, N; Dutheil, JY (2018) Selection at the pathway level drives the evolution of gene-specific transcriptional noise. *Genetics*. DOI: [10.1534/genetics.117.300467](https://doi.org/10.1534/genetics.117.300467) **Highlighted by the Journal**
- **Barroso, GV**; Luz, DR (2015). On the limits of complexity in living forms. *Journal of Theoretical Biology*. DOI: [10.1016/j.jtbi.2015.04.032](https://doi.org/10.1016/j.jtbi.2015.04.032)
- Carneiro, FF; **Barroso, GV**; Strapazzon, R; Moretto, G (2014). Reproductive ability and level of infestation of the *Varroa destructor* mite in *Apis mellifera* apiaries in Blumenau, state of Santa Catarina, Brazil. *Acta Scientiarum Biological Sciences*. DOI: [10.4025/actascibiolsci.v36i1.20366](https://doi.org/10.4025/actascibiolsci.v36i1.20366)

- Luz, DR; **Barroso, GV**; Althoff, SL (2010). Insecta, Hymenoptera, Apidae, Serra do Itajai National Park, state of Santa Catarina, Brazil. Check List. DOI : 10 . 15560/6 . 4 . 519