



Gustavo V. Barroso

POSTDOCTORAL RESEARCHER

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Computational Biology, Statistical Population Genomics, Bioinformatics

Summary

I study evolutionary biology using computational methods. My long-term goal is to understand how population-level processes (genetic drift, natural selection) interact with molecular-level processes (mutation, recombination) to shape patterns of genetic variation. To this end, I develop statistical models based on population genetics theory. I build these models into inference tools using a combination of the C++ and R programming languages and apply them to both simulated and empirical data sets from a variety of species.

Skills

Most of my research follows a comprehensive work-flow where I **(1)** develop a new model; **(2)** implement it in C++; **(3)** benchmark it using extensive simulations; and **(4)** employ it in real data sets to draw novel biological conclusions. Therefore, my approach touches on all the core aspects of modern evolutionary genomics, from statistical modelling to interpretation of 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 my own statistical models
- R scripting for high-level data analyses and visualization
- Shell scripting for large-scale manipulation of big genomic data sets

DATA ACQUISITION & HANDLING

- Experience with computing cluster environments (SLURM, TORQUE)
- Experience with simulation engines (SLiM, SCRM and other ms-like coalescent simulators)
- Field work in the Atlantic rainforest

I also have good presentation skills as well as a record of active participation in discussions at journal clubs and lab meetings.

Education

Max Planck Institute for Evolutionary Biology

Ph. D. in Evolutionary Genetics

Plön, Germany

2019

Universidade de São Paulo

M. Sc. in Evolutionary Genetics

São Paulo, Brazil

2011

Universidade Regional de Blumenau

B. Sc. in Biology

Blumenau, Brazil

2008

Academic Experience

University of California, Los Angeles

Post-doctoral training with Dr. Kirk Lohmueller at UCLA

Los Angeles, USA

2019 -

We focus on the effect of different modes of natural selection on genetic diversity, with three goals:

- To develop an ABC-based model for inferring dominance and the strength of selection in a single generation
- To develop a population genetics model of epistasis in diploid individuals
- To investigate the signature of epistasis on sequence data

Funding and Awards

Best Talk prize in the Annual Aquavit Symposium

MPI for Evolutionary Biology, 2018

Scholarship for the Summer Institute in Statistical Genetics (SISG)

University of Washington, 2016

Academic Service & Supervision

Event Organization

MPI for Evolutionary Biology, 2018

International Max Planck Research School Retreat

Event Organization

MPI for Evolutionary Biology, 2016

Annual Aquavit Symposium

Co-supervision of internship student Armaan Singh

University of California, Los Angeles, 2021

We are developing a data structure to efficiently compute population genetic summary statistics over tens of thousands of family trios.

Co-supervision of Hiwi student Nataša Puzovic

MPI for Evolutionary Biology, 2018

We used coalescent simulations to test the performance of iSMC to recover the recombination landscape according to demographic models.

Co-supervision of internship student Pallavi Misra

MPI for Evolutionary Biology, 2017

We used coalescent simulations to test the performance of iSMC to recover the demographic history (10-fold instantaneous bottleneck or growth).

Co-supervision of internship student Nataša Puzovic

MPI for Evolutionary Biology, 2016

We analysed single-cell transcriptomics data from mice in the context of environmental stimuli.

Reviewing (Journals)

- PeerCommunityIn Evolutionary Biology
- Journal of Evolutionary Biology

Publications

- **Barroso, GV**; Lohmueller, KE (2021). Inferring ongoing selection using family trios. (*in prep*)
- **Barroso, GV**; Dutheil, JY (2021). Mutation rate variation shapes genome-wide diversity in the fruit fly (*in prep*)
- Schweizer, G; Haider, MB; **Barroso, GV**; Roessel, N; Muench, K; Kahmann, R; Dutheil, JY (2020). Population genomics of the maize pathogen *Ustilago maydis*: demographic history and role of virulence clusters in adaptation. *BiorXiv*, DOI: <https://doi.org/10.1101/2020.12.21.423782>
- **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
- **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
- **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 **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
- 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
- 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

Selected Presentations

- The Neanderthal recombination map **(Invited Talk)** 2019
Max Planck Institute for Evolutionary Anthropology
Host: Benjamin Peter
- An integrative model for population genomics inference **(Invited Talk)** 2018
University of Bern
Hosts: Fanny Pouyet & Laurent Excoffier
- An integrative model for population genomics inference **(Talk)** 2018
II Joint Meeting of Evolutionary Biology
- The Markov-modulated Sequentially Markovian Coalescent **(Talk)** 2017
New Developments of the Ancestral Recombination Graph Workshop
- Towards more realistic models in population genomics **(Talk)** 2016
Joint Meeting of the DFG Priority Programs SPP-1590 and SPP-1819