

Gustavo V. Barroso

POSTDOCTORAL RESEARCHER

Department of Ecology and Evolutionary Biology @ UCLA

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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.

Education

Max Planck Institute for Evolutionary Biology

Ph.D. in Evolutionary Genetics

Ploen, Germany

2019

Universidade de Sao Paulo

M. Sc. in Evolutionary Genetics

Sao Paulo, Brazil

2011

Universidade Regional de Blumenau

B. Sc. in Biology

Blumenau, Brazil

2008

Experience

University of California, Los Angeles

Post-doctoral training with Dr. Kirk Lohmueller at UCLA, focusing on the development of models for inferring natural selection.

Los Angeles, USA

2019 -

Instituto Educacional Jangada

High school teacher (Biology and Math)

Jaragua do Sul, Brazil

2014 - 2015

Self-employed

Professional Poker Player (Online)

Jaragua do Sul, Brazil

2012 - 2013

Funding and Awards

Best Talk prize in the Annual Aquavit Symposium

Max Planck Institute for Evolutionary Biology, Ploen, 2018

Scholarship for the Summer Institute in Statistical Genetics (SISG)

University of Washington, Seattle, 2016

Academic Service & Supervision

Workshop Organization

International Max Planck Research School Retreat, 2018

Co-supervision of internship student Natasa Puzovic (M.sc)

Max Planck Institute for Evolutionary Biology, 2018

Co-supervision of internship student Pallavi Misra

Max Planck Institute for Evolutionary Biology, 2017

Co-supervision of internship student Natasa Puzovic

Max Planck Institute for Evolutionary Biology, 2016

Organization of Aquavit Symposium

Max Planck Institute for Evolutionary Biology, 2016

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)*

- **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/actascibiolsoci.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

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