Gustavo V. Barroso

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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 editing of big genomic data sets (including vcf/bcftools)

DATA AQUISITION & MANIPULATION

- Experience with computing cluster environments (SLURM, TORQUE)
- Experience with simulation engines (SLiM, SCRM and other ms-like coalescent simulators)
- Familiarity with wet-lab pipelines (DNA extraction, electrophoresis)
- Field work in the Atlantic Rainforest

I also have strong 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   *Ploen, Germany*
Ph.D. in Evolutionary Genetics   *2019*

Universidade de Sao Paulo   *Sao Paulo, Brazil*
M. Sc. in Evolutionary Genetics   *2011*

Universidade Regional de Blumenau   *Blumenau, Brazil*
B. Sc. in Biology   *2008*

Academic Experience

University of California, Los Angeles   *Los Angeles, USA*
Post-doctoral training with Dr. Kirk Lohmueller at UCLA   *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 model of epistasis
- To investigate the signature of epistasis on sequence data

Funding and Awards

Best Talk prize in the Annual Aquavit Symposium *Max Plack Insitute 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*)

- 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 Genetcs*, `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 Scientarium 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
  Host: 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