BÁRBARA BITARELLO, COMPUTATIONAL BIOLOGIST

1527 S 12th St 19147 Philadelphia | bbitarello.github.io | barbarabitarello@gmail.com | linkedin.com/in/barbarabitarello/

SUMMARY

- Computational biologist with experience in genomics, population genetics, statistical genetics, immunogenetics
- Management of research projects and teamwork, including 4 first-author papers
- Deep understanding of NGS and genotype data analysis and data visualization
- Self-motivated, problem-solving, with excellent oral communication skills, including 3 talks to international scientific audiences
- Scientific writing, including 10 scientific papers and four successful grant proposals
- Driven to use computational methods to gather and analyze human genetic data and advance genomic medicine

TECHNICAL SKILLS

- **Programming** R programming, Python, Bash/shell scripting, sed/awk
- **Genomics** GWAS, linear modelling, polygenic risk score implementation, DNA sequence simulations, ancestry inference, gene ontology analyses, functional annotation
- **Genomic Data analysis** Biobank data analyses, frequentist statistics, biostatistics
- **Software** Plink, ldpred, MSMS, SLiM, Microsoft Word, Overleaf, RStudio, VSCode, bcftools, Hail, Apache Spark (beginner)
- **Reproducible Research** GitHub, R Shiny, R Notebooks
- **Communication** Excellent communication skills for scientist and non-scientists, use of ggplot2 and R Shiny for data visualization
- **Languages** English and Portuguese: native. French and Spanish: conversational.
- **Task and time management** Quire, Slack

RESEARCH EXPERIENCE

University of Pennsylvania, Perelman School of Medicine

Postdoctoral Researcher, Department of Genetics   *March 2018-present*

- Lead project to understand the drivers of polygenic risk prediction accuracy in admixed populations, resulting in one first author publication[2]
- Use big data from UK Biobank, 1000 Genomes, Women's Health Initiave, Health and Retirement Study and gnomAD
- ancestry inference, leverage individual genetic ancestry into polygenic risk predictions
- GWAS and linear modelling
- Develop tools to correct for biases, showing the determinants of loss of prediction power across different ancestries
- Three conference talks, one local talk and one interactive poster
- Collaborated on other projects, resulting in one co-authorship[1]

Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany

Postdoctoral Researcher, Department of Evolutionary Genetics   *Oct 2016-Dec 2017*

- Led and collaborated on projects to investigate signatures of balancing selection in human genomes, resulting in two co-authorship publications[3,5]
- Used 1000 Genomes data, ancient genomes, R data analysis, population genetics methods

University of São Paulo, São Paulo, Brazil

Doctoral Researcher, Genetics and Evolutionary Biology Department   *Aug 2011-Aug 2016*

- Quantify the pervasiveness of balancing selection throughout human evolutionary history and its effects in neighboring regions in the genome, resulting in one first author paper[4], two international conference posters, two local talks
- MSMS for balancing selection simulations, R programming and bash/linux for data analysis and visualization, ENSEMBL for genomic annotations, bcftools to analyze 1000 Genomes dataset, parallel computing in R
- Collaborated with 6 geneticists across two institutions
- Mentored one undergraduate student and was guest lecturer for one graduate course in genomics
- Collaborated on other projects, resulting in co-authorship in 3 publications[7-9]

University of São Paulo, São Paulo, Brazil

MSc Researcher, Genetics and Evolutionary Biology Department   *March 2009 to Aug 2011*

- Investigate the timescale of natural selection in human HLA genes, resulting in one first author paper[6] and two international conference poster presentations
- Technical Skills: phylogenetic analyses of HLA genes using PAML software, DNA sequence simulations, R programming and bash/linux to analyze and visualize the data
- Mentored one masters student
- Engaged in scientific outreach resulting in two peer-reviewed publications in Portuguese

State University of Campinas, Campinas, Brazil

Undergraduate Researcher, Department of Genetics   *Aug 2005 to Dec 2007*

- Develop genetic markers for the human botfly in order to understand its diversity in Brazil, resulting in one first author publication[10] and two conference posters
- DNA extraction, primer design, sanger sequencing, poliacrylamide gels, used statistical approaches to assess and compare genetic diversity in two populations

EDUCATION

- PhD, Biology (Genetics), University of São Paulo, Brazil, 2016
- MSc, Biology (Genetics), University of São Paulo, Brazil, 2011
- BS, Biological Sciences, State University of Campinas, Brazil, 2007

AWARDS

Support

- 2011-2016: PhD Research Grant from São Paulo Research Foundation (FAPESP, Grant # 11/12500-2)
- 2013: PhD Research Grant for visiting period at the Max Planck Institute, Leipzig (FAPESP, Grant # 12/19563-2)
- Master's Research Grant (FAPESP, Grant # 08/56502-6)
- Undergraduate Research Grant (FAPESP, Grant # 06/50793-3)

Prizes

- Best graduate student paper award for Genome Biology and Evolution (SMBE, 2019)
- Spotlight Trainee Paper, by the American Society of Human Genetics (ASHG, 2019)
- 1st place in for the graduate program, University of São Paulo, Department of Genetics and Evolutionary Biology (2009)

CONFERENCE PRESENTATIONS 4 OUT OF 15

- "Low transferability of height polygenic risk scores in admixed ancestry populations" (Contributed talk, NY Area Population Genomics, New York, NY, 2020)
- "Investigating the lack of transferability of polygenic risk scores in cohorts with admixed ancestry" (Contributed talk, SMBE, Houston, TX, 2019)
- "Polygenic risk scores perform poorly across populations." (Contributed talk, ASHG, 2018, San Diego, CA)
- "Balancing selection in humans: insights from a novel SFS-based method" (Poster, SMBE, Vienna, Austria, 2015)

PUBLICATIONS

[1] Mathieson, I, Day, F, Barban, N, Tropf, F, Brazel, D, Vaez, A, Zuydam, N, Bitarello, BD et al. Genome-wide analysis identifies genetic effects on reproductive success and ongoing natural selection at the FADS locus.BiorXiv, 2020

[2] Bitarello, BD Mathieson, I. Polygenic scores for height in admixed populations. BiorXiv,2020

[3] Giner-Delgado,Villatoro,CS, Lerga-Jaso,J, Gayà-Vidal, M, Oliva, M, Castellano, D, Pantano, L, Bitarello, BD et al. Evolutionary and functional impact of common polymorphic inversions in the human genome. Nature Communications, 2019.

[4] Bitarello, BD et. al. Signatures of long-term balancing selection in human genomes. GBE, 2018.

[5] Meyer, D, Aguiar, V, Bitarello, BD et al. A genomic perspective on HLA evolution. Immunogenetics, 2017.

[6] Bitarello, BD et al. Heterogeneity of dN/dS ratios at the classical HLA class I genes over divergence time and across the allelic phylogeny. JME, 2016

[7] Le Duc, D, Renaud, G, Krishnan, A, Almén, MS, Huynen, L, Prohaska, SJ, Ongyerth, M Bitarello, BD et al. Kiwi genome provides insights into evolution of a nocturnal lifestyle. Genome Biology, 2015.

[8] Brandt, D, Aguiar, V, Bitarello, BD et al. Mapping bias overestimates reference allele frequencies at the HLA genes in the 1000 genomes project phase I data. G3, 2015.

[9] Francisco, RDS, Buhler, S, Nunes, JM, Bitarello, BD et al. HLA supertype variation across populations: new insights into the role of natural selection in the evolution of HLA-A and HLA-B polymorphisms. Immungogenetics, 2015.

[10] Bitarello, BD, Torres, TT, Lyra, ML, Azeredo-Espin, AML. Development of polymorphic microsatellite markers for the human botfly, Dermatobia hominis (Diptera: Oestridae). Molecular Ecology Resources, 2009.

VOLUNTEER EXPERIENCE

2020 Teaching Assistant for Intro to R and Intro to Machine Learning with Tidymodels (R Med Virtual Conference)
2020 Abstract and grant reviewer for The National Diversity in STEM Conference (Society for the Advancement of Chicanos/Hispanics and Native Americans in Science)
2020 Member of Diversity Committee of Biomedical Postdoctoral Council, University of Pennsylvania
2016-Present Reviewer of scientific manuscripts for peer-reviewed journals
2015 Consultant on ancient DNA for identification of forensic skeletal remains