BÁRBARA BITARELLO, PHD

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SUMMARY

- Computational biologist with skills and experience in genomics, population genetics, statistical genetics, immunogenetics
- Led collaborative projects, resulting in 8 peer-reviewed publications, including 3 first-authored publications
- Deep understanding of NgS and genotype data analysis and data visualization
- Self-motivated, problem-solving and collaborative scientist with excellent communication skills, including 3 talks to international scientific audiences
- Driven to use computational methods to gather and analyze genomic 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 writing and oral 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
- Use big data from UK Biobank, 1000 Genomes, Women's Health Initiave, Health and Retirement Studyand gnomAD
- ancestry inference and GWAS analyses
- Leverage individual genetic ancestry into polygenic risk predictions
- Develop tools to correct for biases, showing the determinants of loss of prediction power across different ancestries
- Give three conference talks on this
- Collaborated with projects using the Upenn Biobank, the UK biobank and ancient DNA, resulting in one co-authorship

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
- 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
- Skills: 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

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
- 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
- Technical skills: DNA extraction, primer design,sanger sequencing, poliacrylamide gels
- Used statistical approaches to assess and compare genetic diversity in two populations of the botfly in Brazil

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

- Best graduate student paper award for Genome Biology and Evolution (2019)
- Spotlight Trainee Paper, by the American Society of Human Genetics (2019)

CONFERENCE TALKS

- NY Area Population Genomics (01/2020, New York, NY), "Low transferability of height polygenic risk scores in admixed ancestry populations" (Contributed talk)
- American Society of Human Genetics Conference (10/18/2019, Houston, TX), "Investigating the lack of transferability of polygenic risk scores in cohorts with admixed ancestry". (Contributed talk)
- American Society of Human Genetics Conference (10/2018, San Diego, CA) "Polygenic risk scores perform poorly across populations." (Contributed talk)

PUBLICATIONS - 6 OUT OF 10

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

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

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

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

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.

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 Reviewer of abstracts for SACNAS – 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