

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 data analysis and data visualization
- Self-motivated, problem-solving and collaborative scientist with excellent communication skills and analytical skills
- Looking to contribute to use computational methods to gather and analyze genomic data and advance genomic medicine

TECHNICAL SKILLS

- **Programming Languages:** R programming, Shell script, sed/awk, Python (beginner)
- **Genomics:** GWAS, linear modelling, polygenic risk score implementation, DNA sequence simulations, ancestry inference, gene ontology analyses, functional annotation
- **Data analysis and Data visualization:** Biobank data analyses, frequentist statistics, biostatistics, ggplot2, beginner Shiny apps
- **Software:** Plink, Ldpred, MSMS, SLiM, Microsoft Word, Overleaf, RStudio, VSCode, bcftools, Hail (beginner), R Shiny (beginner), Apache Spark (beginner)
- **Reproducible Research:** GitHub, R Shiny, R Notebooks

RESEARCH EXPERIENCE

Department of Genetics, Perelman School of Medicine, Upenn

Postdoctoral Researcher

March 2018 to present

- Leveraging individual genetic ancestry into polygenic risk predictions and developing tools to correct for biases. Our work showed the determinants of loss of prediction power across different ancestries
- Used big data from UK Biobank, Penn Biobank and gnomAD, ancestry inference and polygenic risk prediction, GWAS
- Resulted in one publication (in press)

Max Planck Institute for Evolutionary Anthropology

Post doctoral Researcher

Oct 2016 to Dec 2017

- Led project to investigate signatures of balancing selection in human genomes
- Used computational methods to develop statistical test for balancing selection, leading to two publications

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

TEACHING AND MENTORING EXPERIENCE

- 2012 - Guest lecturer for Evolutionary Genomics course, Graduate level, University of São Paulo
- 2008 - Tutored English for students preparing to get into graduate school in Brazil

AWARDS

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

CONFERENCE PRESENTATIONS

- NY Area Population Genomics, "Low transferability of height polygenic risk scores in admixed ancestry populations" (01/2020)
- American Society of Human Genetics (ASHG), "Investigating the lack of transferability of polygenic risk scores in cohorts with admixed ancestry" (10/2019)
- American Society of Human Genetics (ASHG) "Polygenic risk scores perform poorly across populations." (10/2018)

PUBLICATIONS

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

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

Bitarello, B 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, B** et al. Mapping bias overestimates reference allele frequencies at the HLA genes in the 1000 genomes project phase I data. G3, 2015.

OTHER SKILLS

Languages English: native-like. Portuguese: native. French and Spanish: conversational.

Communication Scientific writing, scientific talks to scientists and non-scientists.

Task and time management: Quire, Slack