# Bárbara D. Bitarello, Ph.D

# Assistant Professor | Bryn Mawr College

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#### **EDUCATION**

# Ph.D. in Biology (Evolutionary Genetics) Department of Genetics and Evolutionary Biology, University of São Paulo, São Paulo, Brazil

## M.Sc. in Biology (Evolutionary Genetics)

08/2011

08/2016

Department of Genetics and Evolutionary Biology, University of São Paulo, São Paulo, Brazil

## **B.Sc.** in Biological Sciences

12/2007

University of Campinas, Campinas, Brazil Licentiate Degree in Biological Sciences: teaching training for elementary school

#### RESEARCH APPOINTMENTS

Assistant Professor 07/2021–Present

Department of Biology, Bryn Mawr College

Postdoctoral Researcher 03/2018–06/2021

Department of Genetics, Perelman School of Medicine, University of Pennsylvania

Postdoctoral Researcher 10/2016–12/2017

Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology

# Ongoing Projects

Developing computational tools to assess life history traits for phylogenetic inference

Collaborator: Maja Šešelj (Anthropology Department, Bryn Mawr College)

Mendelian randomization as a tool to understand causal and mediated effects of alcohol and smoking on blood traits in diverse populations

Collaborator: Christopher Thom (Children's Hospital of Philadelphia)

**Polygenic scores in admixed populations** Collaborators: Michel Naslavsky & Helena Brentani (University of São Paulo); Tatiana Almeida (Einstein Hospital, São Paulo, Brazil)

Evolution of bitter taste receptor genes in primates

**Developing an R package to carry out balancing selection tests in genomic data.** Collaborator: Débora Y. C. Brandt (University College London)

## MANUSCRIPTS IN PREP

- 1. Raskin, L. (HV '24), Šešelj, M. Bitarello, B.D. The effect of redundancy in a hominin character matrix on parsimony-inferred tree topologies. [late stage]
- 2. Hansell, D. (BMC '24), Brandt, D.Y.C., Bitarello, B.D. (2023) balselr: an R package to carry out balancing selection tests in genomic data. [early stage]
- 3. Raskin, L. (HV '24), Bitarello, B.D., Šešelj, M. Phylogenetic Signal in Small Clades: testing the phylogenetic information content of great ape perikymata" [early stage]

#### Preprints currently in review

- 1. Shivakumar, S. (BMC '25), Wilken, M. B., Tsao, V., Bitarello, B. D., & Thom, C. S. (2023). Genetically influenced tobacco and alcohol use behaviors impact erythroid trait variation. MedRxiv. https://doi.org/10.1101/2023.05.01.23289329
- 2. Barreiro, R. A. S., Almeida, T. F., Gomes, C. S., Monfardini, F., Farias, A. A., Tunes, G. C., Souza, G. M., Duim, E., Correia, J. S., Coelho, A. V. C., Caraciolo, M. P., Duarte, Y. A. O., Zatz, M., Amaro, E., Oliveira, J. B., Bitarello, B. D., Brentani, H., & Naslavsky, M. S. (2022). Assessing the risk stratification of breast cancer polygenic risk scores in two Brazilian samples. MedRxiv. https://doi.org/10.1101/2022.09.09.22279721

#### RESEARCH ARTICLES

- 1. Mathieson, I., Day, F. R., Barban, N., Tropf, F. C., Brazel, D. M., van Heemst, D., Vaez, A., van Zuydam, N., Bitarello, B. D., Gardner, E. J., Akimova, E. T., Azad, A., Bergmann, S., Bielak, L. F., Boomsma, D. I., Bosak, K., Brumat, M., Buring, J. E., Cesarini, D., et al. (2023). Genome-wide analysis identifies genetic effects on reproductive success and ongoing natural selection at the FADS locus. Nature Human Behaviour, 7(5). https://doi.org/10.1038/s41562-023-01528-6
- 2. Cox, S. L., Moots, H. M., Stock, J. T., Shbat, A., Bitarello, B. D., Nicklisch, N., Alt, K. W., Haak, W., Rosenstock, E., Ruff, C. B., & Mathieson, I. (2022). Predicting skeletal stature using ancient DNA. American Journal of Biological Anthropology, 177(1). https://doi.org/10.1002/ajpa.24426
- 3. Bitarello, B. D., & Mathieson, I. (2020). Polygenic scores for height in admixed populations. G3: Genes, Genomes, Genetics, 10(11). https://doi.org/10.1534/g3.120.401658
- 4. Giner-Delgado, C., Villatoro, S., Lerga-Jaso, J., Gayà-Vidal, M., Oliva, M., Castellano, D., Pantano, L., Bitarello, B. D., Izquierdo, D., Noguera, I., Olalde, I., Delprat, A., Blancher, A., Lalueza-Fox, C., Esko, T., O'Reilly, P. F., Andrés, A. M., Ferretti, L., Puig, M., & Cáceres, M. (2019). Evolutionary and functional impact of common polymorphic inversions in the human genome. Nature Communications, 10(1). https://doi.org/10.1038/s41467-019-12173-x
- 5. Bitarello, B. D., de Filippo, C., Teixeira, J. C., Schmidt, J. M., Kleinert, P., Meyer, D., & Andres, A. M. (2018). Signatures of long-term balancing selection in human genomes. Genome Biology and Evolution, 10(3). https://doi.org/10.1093/gbe/evy054

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- 6. **Bitarello, B. D.**, Francisco, R. S., & Meyer, D. (2016). Heterogeneity of dN/dS Ratios at the Classical HLA Class I Genes over Divergence Time and Across the Allelic Phylogeny. Journal of Molecular Evolution, 82(1). https://doi.org/10.1007/s00239-015-9713-9
- 7. Le Duc, D., Renaud, G., Krishnan, A., Almén, M. S., Huynen, L., Prohaska, S. J., Ongyerth, M., **Bitarello, B. D.**, Schiöth, H. B., Hofreiter, M., Stadler, P. F., Prüfer, K., Lambert, D., Kelso, J., & Schöneberg, T. (2015). Kiwi genome provides insights into evolution of a nocturnal lifestyle. Genome Biology, 16(1). https://doi.org/10.1186/s13059-015-0711-4
- 8. Brandt, D. Y. C., Aguiar, V. R. C., **Bitarello, B. D.**, Nunes, K., Goudet, J., & Meyer, D. (2015). Mapping bias overestimates reference allele frequencies at the HLA genes in the 1000 genomes project phase I data. G3: Genes, Genomes, Genetics, 5(5). https://doi.org/10.1534/g3.114.015784
- 9. **Bitarello, B. D.**, Torres, T. T., Lyra, M. L., & de Azeredo-Espin, A. M. L. (2009). Development of polymorphic microsatellite markers for the human botfly, Dermatobia hominis (Diptera: Oestridae). Molecular Ecology Resources, 9(1). https://doi.org/10.1111/j.1755-0998.2008.02454.x

### REVIEW ARTICLES

- 1. **Bitarello, B. D.**, Brandt, D. Y. C., Meyer, D., & Andrés, A. M. (2023). Inferring Balancing Selection From Genome-Scale Data. Genome Biology and Evolution, 15(3). https://doi.org/10.1093/gbe/evad032
- 2. Meyer, D., C. Aguiar, V. R., **Bitarello, B. D.**, C. Brandt, D. Y., & Nunes, K. (2018). A genomic perspective on HLA evolution. Immunogenetics, 70(1). https://doi.org/10.1007/s00251-017-1017-3

#### COMMENTARY ARTICLES IN PORTUGUESE

- 1. **Bitarello, B.D.** Intercruzmento de humanos modernos e neandertais: novas perspectivas a luz da genética. [*Interbreeding of modern humans with Neanderthals: new perspectives in the light of genetics.*] (2011). Revista da Biologia, 6(1): 6-9. https://www.revistas.usp.br/revbiologia/article/view/108622
- 2. **Bitarello, B.D.** & Meyer, D. Projeto Genográfico e as implicações da popularização dos estudos de genealogia gênica. [The Genographic Project and the implications of the popularization of Gene Genealogy Studies.] (2009). Revista da Biologia, 3(1): 21-23. https://www.revistas.usp.br/revbiologia/article/view/108597

#### OTHER PRODUCTS

#### Software

Hansell, D. (BMC '24) & **Bitarello, B.D.** (2023) balselr: an R package to carry out balancing selection tests in genomic data.https://github.com/bitarellolab/balselr

**Bitarello, B.D.** Browser-only tool for intro to command-line programming and FASTQ files in genomics: An update to St. Jacques et al. 2021. https://mybinder.org/v2/gh/bitarellolab/B216\_S23/HEAD

#### Research

**10/2022.** *Polygenic risk scores in the Brazilian population,* II Einstein Symposium on Precision Medicine. Albert Einstein Hospital, São Paulo, Brazil.

**06/2021.** *Investigating the lack of transferability of polygenic risk scores in cohorts with admixed ancestry,* Department of Genetics and Evolutionary Biology, University of São Paulo, Brazil.

**12/2020.** *Investigating the lack of transferability of PRS in cohorts with mixed ancestry,* Annual Meeting of the Association of Genomic Diagnostics, Bonn, Germany

**09/2020.** What drives the reduced prediction accuracy of polygenic risk scores in non-European individuals?, Center for Theoretical and Evolutionary Genomics Seminar Series, Berkeley, USA.

# **Pedagogy**

**Upcoming (01/2024)** Browser-only tools for genomics education: teaching an introduction to command-line programming and about FASTQ files, International Plant & Animal Genome Conference. San Diego, USA. Session: Resources and Programs for Undergraduate Education in Genomics

**06/2022.** *GEP implementation (lighning talk)*, Genomics Education Partnership (GEP) Alumni Workshop. Online

## CONTRIBUTED TALKS & POSTERS

## **Submitted Abstracts**

**11/2023.** Raskin, L. (BMC/HV '24), Šešelj, M. & **Bitarello, B.D.** *The effect of trait redundancy on parsimony-inferred tree topologies from a hominin character matrix.* The 2024 Paleoanthropology Society Meeting, Los Angeles California.

**11/2023.** Koh, G. (BMC'24)\*, Chen, C. (BMC'24), Kovačić, K. (BMC'22) & **Bitarello, B.D.** *Adaptive evolution in* TAS2R14 *and* TAS2R38 *bitter taste receptor genes in primates.* The 2024 Allied Genetics Conference, Washington, D.C.

#### **Talks**

**04/2022.** Ancestry Matters: lack of representation of human genetic diversity in genomic databases, Emerging Scholars program Addressing Race and Racism in Anthropological Genetics and Genomics, Boston University.

**01/2020. Bitarello, B.D.** & Mathieson, I. *Low transferability of height polygenic risk scores in admixed ancestry populations,* New York Area Population Genomics, New York, USA.

**10/2019. Bitarello, B.D.** & Mathieson, I. *Investigating the lack of transferability of polygenic risk scores in cohorts with admixed ancestry,* Annual American Society of Human Genetics Meeting, Houston, USA.

**10/2018. Bitarello, B.D.** & Mathieson, I. *Polygenic risk scores perform poorly across populations,* Annual American Society of Human Genetics Meeting, San Diego, USA.

#### **Posters**

**07/2021.** *Increased local genetic load as a result of selective sweeps in human populations,* Society for Molecular Biology and Evolution (Virtual).

**07/2020.** Loss of predictive power of polygenic risk scores in admixed populations, The Allied Genetics Conference (Virtual).

**07/2015.** *Balancing selection in humans: insights from a novel SFS-based method,* Annual Meeting of the Society for Molecular Biology and Evolution, Vienna, Austria.

**06/2014.** *NCV:* A site frequency spectrum based method to detect balancing selection in humans, Annual Meeting of the Society for Molecular Biology and Evolution, San Juan, Puerto Rico.

**07/2013.** *Variation of dN/dS ratios at HLA genes over time and functional classes,* Annual Meeting of the Society for Molecular Biology and Evolution, Chicago, USA.

**07/2010.** *Time dependence of dN/dS measures at HLA loci under balancing selection,* Annual Meeting of the Society for Molecular Biology and Evolution, Lyon, France

#### **GRANTS PENDING**

National Science Foundation (\$536,345 total award to Bryn Mawr College). "RUI: Morphology, life history, and phylogeny: a new look at an old problem" (co-PIs: Maja Šešelj & Bárbara Domingues Bitarello). Submitted on 07/31. Proposed start date: 04/01/2024 (duration: 36 months).

#### Scholarships & Awards

**07/2023.** Digital Bryn Mawr Project Grant Award, \$5,000. "R package for bio data analysis with R (BIOL B215)"

**07/2019.** Best Graduate Student Paper (Bitarello et al. 2018), Genome Biology and Evolution, Society for Molecular Biology and Evolution, \$2,000.

**05/2019.** Spotlight Trainee Paper (Bitarello et al. 2018), American Society of Human Genetics.

10/2011–04/2016 Ph.D. scholarship grant, São Paulo Research Foundation, Grant # 11/12500-2.

**02/2013-01/2014.** Visiting graduate student scholarship grant,São Paulo Research Foundation, Grant # 12/19563-2.

**07/2012.** Scholarship to attend the Summer Institute for Statistical Genetics in Seattle, USA.

03/2009-02/2011. Master's Student Scholarship, São Paulo Research Foundation, Grant # 08/56502-6.

**12/2009.** 1<sup>st</sup> place in the entrance examination for the graduate program, Department of Genetics and Evolutionary Biology, University of São Paulo.

**09/2006-12/2007.** Undergraduate research scholarship from São Paulo Research Foundation, Grant # 06/50793-3

#### **TEACHING**

# Courses taught at Bryn Mawr College

BIOL B398 Senior Thesis: Human Evolution (S23)

BIOL B216 Genomics with Computer Lab (S22, S23)

BIOL B215 Biostatistics with R (F22, F23)

BIOL B403 Supervised Laboratory Research in Biology (S22, F22, S23, F23)

BIOL B400 Senior Thesis (S22)

BIOL B110 Biological Explorations I (F21)

# Other teaching experiences

**04/2015** Guest lecturer. I taught neutral coalescent simulations for a Graduate course in Evolutionary Genomics. Length: 4 hours.

**04/2008–10/2008** English Tutoring (self-employed). I prepared material and tutored English to undergraduate students. Length: one semester.

**2007** Supervised classroom experience, Elementary School in Campinas, Brazil. I prepared and delivered Science classes to fifth-graders under supervision. Length: 56 hours.

## BMC Research Thesis Students, Mentees, and Advisees

# **Undergraduate researchers mentored (BMC)**

Kyra Kovačić (BMC '22): F21-S22. Currently Research Assistant at UPenn Next-Generation Sequencing Core

Gillyoung Koh (BMC '24): Summer 22-Present.

Clementine Chen (BMC '24): Summer 22 - Present.

Levi Raskin (BMC/HC '24): Fall 22 -Present.

Shriya Shivakumar (BMC '25): Fall 22 –Present.

Daphne Hansell (BMC '24): Summer 23-Present.

Kuankuan Ku (BMC '25): Fall 23-Present.

Cammi Bielawa (BMC '24): F22 -F22.

# **Biology Major Advisees**

Annabelle Bale (BMC '24): 2023 - Present.

Shriya Shivakumar (BMC '25): 2023 –Present.

Levi Raskin (BMC/HV '24): 2023 - Present.

Kylie Ede (BMC '24): 2022 2022 - Present.

Syalomee Pradham (BMC '24): 2022 - Present.

Molly Clark (BMC '24): 2022 – Present.

Daphne Hansell (BMC '24): 2022–2022 (switched to an independent studies major).

#### Second reader for the senior thesis

Vanessa Gitau (BMC '22): "Debris-Eating Phagocytes to Target Frontotemporal Dementia (FTD)"

Katrina Sparks (BMC '23): "Reconstitution of phagocytosis using engineered tissue microenvironments and physiological synthetic particles"

Meera Pattanayak (BMC '24): upcoming. Will present on 12/18 and thesis defense will occur later that week.

#### **Summer Science Research Mentor**

**Summer 2023** Five students: Daphne Hansell, Clementine Chen, Gillyoung Koh, Levi Raskin (co-mentored with Maja Šešelj), Shriya Shivakumar

Summer 2022 Two students: Clementine Chen, Gillyoung Koh

## **STEMLA Mentoring**

One student since Fall 2022.

One student since Fall 2023.

## SELECTED ADDITIONAL SERVICE SINCE STARTING AT BRYN MAWR

Fall 2023 Attended student poster session (Summer Science Research Program).

Fall 2023 Attended Biochemistry and Molecular Biology Major Info Session.

Fall 2023 Attended Biology Major Info Session.

Fall 2023 Participated in the Biology department "lab crawl".

Fall 2023 Search committee for tenure-track position in Neuroscience.

**2022-2024** Recruited keynote speaker Dr. Katrina Claw for Bryn Mawr College's Rothenberg Lecture (for the spring of 2024).

Spring 2023 Organized senior seminar event for biology majors presenting their thesis.

04/2023 Recruited speaker Dr. Samantha Cox for departmental seminar.

Fall 2022-Spring 2023 Search committee for successful tenure-track hire in Physiology.

Fall 2022 Attended student poster session (Summer Science Research Program).

Fall 2022 Attended Biology Major Info Session.

Fall 2022 Participated in the Biology department "lab crawl".

**July 2022–Present** Data Science Steering Committee.

**Spring 2022** Search committee for successful visiting professor hire in Ecology.

#### Professional Development

Fall 2023 STEMLA (STEM in the Liberal arts) Training.

Summer 2022 Faculty Success Program (from the National Center for Faculty Development and Diversity.

#### Professional Service

**2013–Present** Manuscript reviewer: *Bioinformatics, Gen. Biol. Evol., Mol. Biol. Evol., Human Immun., Sci Rep., Mol. Ecol. Res., Peer Community in Evol. Biol.* 

**01/2022–Present** Consultant on polygenic risk scores for diverse human populations with the Albert Einstein Hospital in São Paulo, Brazil.

**09/2020–Present** LatinGenomes: Latin American Alliance for Genomic Diversity. Roles: Founding member and member of the Imputation Resources and Community Engagement workgroups.

**08/2020** Brazilian Effort on Multifactorial Inheritance (BEMi). Goal: address under-representation of non-Europeans in genomic studies. Roles: Founding and Steering Committee member.

**08/2020** Abstract reviewer: Society for Advancement of Chicanos/Hispanics & Native Americans in Science (SACNAS).

07/2020-07/21 Biomedical Postdoctoral Council Diversity Committee. Co-lead mentoring circles.

**01/2019** Abstract reviewer: Biomedical Postdoctoral Council Research Symposium, University of Pennsylvania.

03/2015 Consultant on ancient DNA for identification of forensic skeletal remains from victims of the military dictatorship in Brazil.

#### SCIENCE OUTREACH

**08/2023** Podcast interview (in Portuguese). Genética pode prever altura? Genética populacional com Bárbara Bitarello] *Can genetics predict height? Population genetics with Bárbara Bitarello*] https://www.youtube.com/watch?v=ZIep-ggeR3A&ab\_channel=UniversoGeneralista

**04/2022** Expert interviewee for the series entitled *THE CODE*, produced by Day's Edge. I spoke about polygenic risk scores and the lack of representation of diverse ancestries in genomics in general. The series and the expert interviews should be released in the winter (2023-2024).

**02/2021** Podcast interview for *Bioinformatics Chat*): "Polygenic risk scores in admixed populations with Bárbara Bitarello (56)". https://bioinformatics.chat/polygenic-risk-scores

03/2022 Podcast interview for American Society of Human Genetics (ASHG) Trainee Paper Spotlight (Bitarello & Mathieson 2020) https://share.transistor.fm/s/682fb248

## Professional Affiliations and Affinity Groups

#### Professional affiliations

Genomics Education Partnership, PA Node. (member)

American Society of Human Genetics (ASHG)(member)

Society for Molecular Biology and Evolution (SMBE)(member)

Genetics Society of America (GSA)(member)

Society for Advancement of Chicanos/Hispanics & Native Americans in Science (SACNAS)(member)

# **Affinity groups**

2020-Present 500 Queers in Science (member).

2020-Present R Ladies (member).