

ARJUN BIDDANDA, PH.D.

Address 3400 N. Charles St
250 Levi Hall
Baltimore, MD 20210
Email abiddan1@jhu.edu
Website aabiddanda.github.io
Updated September 6, 2025

RESEARCH INTERESTS

Statistical Genetics, Population Genomics, Reproductive Genetics, Ancient DNA

PROFESSIONAL EXPERIENCE

Feb. 2023 - Postdoctoral Fellow · Department of Biology · Johns Hopkins University
Advisor: Rajiv C. McCoy
Nov. 2021 - Feb. 2023 Computational Scientist · Genomics & Data Science · 54gene
Jan. 2021 - Nov. 2021 Postdoctoral Research Associate · Department of Statistics · University of Oxford
Advisor: Pier Francesco Palamara

EDUCATION

2015 - 2020 PhD · Human Genetics · University of Chicago
Dissertation: *Investigating the spatio-temporal structure of human genetic diversity*
Advisor: John Novembre
2015 - 2020 M.Sc · Human Genetics · University of Chicago
2011 - 2015 B.S · Computer Science (*Cum Laude*) · Cornell University
Advisor: Alon Keinan

HONORS & AWARDS

2024 - 2026 Lalor Foundation Fellowship (PI: Arjun Biddanda)
Segmental aneuploidy interpretation in IVF embryos (\$110,000)
2024 Best Poster Award
MD-GEM Training Grant Meeting, Johns Hopkins University
2021 Postdoctoral Associate
Corpus Christi College, University of Oxford
2020 Presidential Membership
Genetics Society of America
2019 Reviewer's Choice Abstract
American Society of Human Genetics
2017 Honorable Mention
NSF Graduate Research Fellowship
2015-2018 NIH Genetics and Regulation Training Grant
University of Chicago

PREPRINTS

* - indicates equal contribution

- 2025 S. A. Carioscia*, **A. Biddanda***, M. R. Starostik, X. Tang, E. R. Hoffman, Z. P. Demko, and R. C. McCoy. Common variation in meiosis genes shapes human recombination phenotypes and aneuploidy risk. [medRxiv](#).
- 2025 A. Das, **A. Biddanda**, R. C. McCoy, and M. C. Schatz. Assembling unmapped reads reveals hidden variation in South Asian genomes. [bioRxiv](#).

PEER-REVIEWED PUBLICATIONS

- 2025 J. A. Urban, ..., **A. Biddanda**, ..., N. Rai, and M. Raghavan. Population histories of the Indigenous Adivasi and Sinhalese from Sri Lanka using whole genomes. [Current Biology](#).
- 2025 M. C. Steiner, D. P. Rice, **A. Biddanda**, M. K. Ianni-Ravn, C. Porras, and J. Novembre. Study design and the sampling of deleterious rare variants in biobank-scale datasets. [PNAS](#).
- 2025 D. Yoo, A. Rhie, ..., **A. Biddanda**, A. M. ... Phillippy, and E. E. Eichler. Complete sequencing of ape genomes. [Nature](#).
- 2024 K. D. Makova, B. D. Pickett, ..., **A. Biddanda**, ..., E. E. Eichler, and A. M. Phillippy. The complete sequence and comparative analysis of ape sex chromosomes. [Nature](#), 630:401–411.
- 2024 **A. Biddanda***, E. Bandyopadhyay*, C. de la Fuente Castro*, D. Witonsky, ..., C. D. Kodira, A. P. Naren, M. Sikdar, N. Rai, and M. Raghavan. Distinct positions of genetic and oral histories: Perspectives from India. [Human Genetics and Genomics Advances](#).
- 2024 D. J. Taylor, S. B. Chhetri, M. G. Tassia, **A. Biddanda**, S. M. Yan, G. L. Wojcik, A. Battle, and R. C. McCoy. Sources of gene expression variation in a globally diverse human cohort. [Nature](#), 632:122–130.
- 2023 E. Joshi, **A. Biddanda**, J. Popoola, A. Yakubu, O. Osakewe, D. Attipoe, 54gene Team, NCD-GHS Consortium, E. Dogbo, B. Salako, O. Nash, O. Salako, O. Oyedele, G. Eze-Echesi, S. Fatumo, A. Ene-Obong, and C. O'Dushlaine. Whole-genome sequencing across 449 samples spanning 47 ethnolinguistic groups provides insights into genetic diversity in Nigeria. [Cell Genomics](#), 3(9).
- 2023 B. C. Zhang, **A. Biddanda**, A. F. Gunnarson, F. Cooper, and P. F. Palamara. Biobank-scale inference of ancestral recombination graphs enables genealogy-based mixed model association of complex traits. [Nature Genetics](#), 55(5):768–776.
- 2023 M. E. Lauterbur, M. I. A. Cavassim, A. L. Gladstein, ..., **A. Biddanda**, ..., P. L. Ralph, D. R. Schrider, and I. Gronau. Expanding the stdpopsim species catalog, and lessons learned for realistic genome simulations. [eLife](#), 12.
- 2022 C. Washington III, M. Dapas, **A. Biddanda**, K. M. Magnaye, ..., C. G. McKennan, and C. Ober. African-specific alleles modify risk for asthma at the 17q12-q21 locus in African Americans. [Genome Medicine](#), 14(1):112.
- 2022 **A. Biddanda**, M. Steinrücken, and J. Novembre. Properties of two-locus genealogies and linkage disequilibrium in temporally structured samples. [Genetics](#), 221(1).
- 2020 **A. Biddanda**, D. P. Rice, and J. Novembre. Geographic patterns of human allele frequency variation: a variant-centric perspective. [eLife](#).
- 2018 C. W. K. Chiang, J. H. Marcus, C. Sidore, **A. Biddanda**, H. Al-Asadi, M. Zoledziewska, M. Pitzalis, F. Busonero, A. Maschio, G. Pistis, M. Steri, A. Angius, K. E. Lohmueller, G. R. Abecasis, D. Schlessinger, F. Cucca, and J. Novembre. Genomic history of the Sardinian population. [Nature Genetics](#).

- 2018 P. de Barros Damgaard, R. Martiniano, J. Kamm, J. V. Moreno-Mayar, ..., **A. Biddanda**, ..., M. Sikora, A. K. Outram, R. Durbin, and E. Willerslev. The first horse herders and the impact of early Bronze Age steppe expansions into Asia. *Science*, 360(6396).
- 2016 Y. Y. Waldman*, **A. Biddanda***, N. R. Davidson, P. Billing-Ross, M. Dubrovsky, C. L. Campbell, C. Oddoux, E. Friedman, G. Atzmon, E. Halperin, H. Ostrer, and A. Keinan. The genetics of Bene Israel from India reveals both substantial Jewish and Indian ancestry. *PLoS One*, 11(3):e0152056.
- 2016 Y. Y. Waldman, **A. Biddanda**, M. Dubrovsky, C. L. Campbell, C. Oddoux, E. Friedman, G. Atzmon, E. Halperin, H. Ostrer, and A. Keinan. The genetic history of Cochin Jews from India. *Human Genetics*, (135):1–17.
- 2015 F. Gao*, D. Chang*, **A. Biddanda***, L. Ma, Y. Guo, Z. Zhou, and A. Keinan. XWAS: a software toolset for genetic data analysis and association studies of the X chromosome. *Journal of Heredity*, 106(5):666–671.

ORAL PRESENTATIONS

- 2026 **A. Biddanda**. *Human Fertility: Genome Stability Across Human Conceptions*. University of Copenhagen CAG-SURF PhD Course.
- 2025 **A. Biddanda**, S. A. Cariosia, ..., E. R. Hoffman, and R. C. McCoy. *Common variation in meiosis genes shapes human recombination phenotypes and aneuploidy risk*. UC Berkeley Center for Theoretical and Evolutionary Genomics (Invited Talk).
- 2025 **A. Biddanda**, S. A. Cariosia, ..., E. R. Hoffman, and R. C. McCoy. *Common variation in meiosis genes shapes human recombination phenotypes and aneuploidy risk*. Origins of Aneuploidy Research Consortium Meeting.
- 2024 R. C. McCoy, **A. Biddanda**, S. A. Cariosia, and E. R. Hoffmann. *Genetic architecture of meiotic recombination across 99,495 in vitro fertilized embryos*. American Society of Human Genetics (Plenary Talk - RCM presented due to parental leave).
- 2024 **A. Biddanda**. *Genetic architecture and fitness costs of meiotic recombination across 138,495 in vitro fertilized embryos*. Statistical Genetics Working Group - Johns Hopkins University (Invited Talk).
- 2023 **A. Biddanda**, S. A. Cariosia, I. Vogel, E. R. Hoffmann, and R. C. McCoy. *Genetic architecture and fitness costs of meiotic recombination across 69,223 in vitro fertilized embryos*. American Society of Human Genetics (Platform Talk).
- 2023 **A. Biddanda**. *The spatio-temporal structure of human genetic diversity*. Johns Hopkins University - Department of Biology (Invited Talk).
- 2021 **A. Biddanda**. *Theoretical models for haplotype diversity with time-stratified sampling*. University of Oxford - Department of Statistics (Invited Talk).
- 2019 **A. Biddanda**, M. Steinrücken, and J. Novembre. *Linkage Disequilibrium in Ancient DNA: Theory and Applications*. Midwest Population Genetics Meeting.

POSTER PRESENTATIONS

- 2025 **A. Biddanda**, S. A. Carioscia, and R. C. McCoy. *Evaluating evidence of transmission distortion across 139,850 blastocyst-stage human embryos*. American Society of Human Genetics.
- 2024 **A. Biddanda**, S. A. Carioscia, E. R. Hoffman, and R. C. McCoy. *Genetic architecture and fitness costs of meiotic recombination across 99,132 in vitro fertilized embryos*. Biology of Genomes.
- 2024 **A. Biddanda**. *Two-Locus Genealogies under Isolation-by-Distance and Time*. The Allied Genetics Conference.
- 2022

- A. Biddanda**, Y. Zhang, P. Moorjani, and C. O'Dushlaine. *Recovering signatures of ghost admixture using ancestral recombination graphs*. American Society of Human Genetics.
- 2021 **A. Biddanda**, M. Steinrücken, and J. Novembre. *Properties of two-locus genealogies and linkage disequilibrium in temporally stratified samples*. Probabilistic Models in Genomics.
- 2019 **A. Biddanda**, M. Steinrücken, and J. Novembre. *Linkage Disequilibrium in Ancient DNA: Theory and Applications*. American Society of Human Genetics.
- 2018 **A. Biddanda** and J. Novembre. *Inference and visualization of the geographic distribution for variant sets*. American Society of Human Genetics.

TEACHING EXPERIENCE

- Winter 2023 Guest Speaker, *Johns Hopkins University*
Population Genetics Simulation and Visualization
- Winter 2019 Guest Lecturer, *University of Chicago*
Computing Skills for Biologists
- Winter 2018 Teaching Assistant, *University of Chicago*
HG 486: Fundamentals of Computational Biology
- Summer 2017 Course Assistant, *University of Chicago*
Marine Biological Laboratory - Quantitative Approaches to Biology Bootcamp
- Spring 2017 Teaching Assistant, *University of Chicago*
HG 469: Human Variation and Disease
- 2016 - 2018 Tutor, *University of Chicago*
Introduction to Statistics for Geneticists
- 2016 - present Instructor, *Software Carpentry*
- 2013 - 2015 Teaching Assistant, *Cornell University*
CS 3110 : Functional Programming and Data Structures

ACADEMIC SERVICE

- 2025 Communications Liason
JHU Biology Postdoc Association
- 2023 Teaching Certificate
Johns Hopkins University Teaching Institute
- 2022 ASHG Session Chair / Organizer
Demographic history, natural selection, and disease risk in diverse global biobanks
- 2021 - 2024 Genetics Peer-Review Training Program
- Summer 2020 Co-Organizer
Genetics and Society Reading Group (Departmental Group)
- 2019-2020 Novembre - He - Stephens (NHS) Meeting Coordinator
University of Chicago
- 2019 - Ad Hoc Peer Review
Nature, Genetics, eLife, Molecular Biology and Evolution, Genome Biology and Evolution Genes, Scientific Reports, Frontiers in Genetics, BMC Genomics Molecular Ecology Resources, PLoS One

OUTREACH / SCIENCE COMMUNICATION

- 2024 - Skype a Scientist
- 2023 - Careerspring Advisor

MENTORSHIP

Spring 2024	Olivia Choi (CMDB Rotation Student at Johns Hopkins) <i>Project: Genetic influences on euploid and aneuploid pregnancy losses</i>
2024	Ameena K. Beg (Johns Hopkins Undergraduate) <i>Project: Evolutionary history of a human mitotic aneuploidy risk locus using ancient DNA</i>
Spring 2024	Maya Mastronardo (CMDB Rotation Student at Johns Hopkins) <i>Project: Quantifying centromere-haplotype effects on aneuploidy risk</i>
2022 - 2024	Axel Zagal-Norman (UNAM Undergraduate Internship) <i>Project: Visualization of Linkage Disequilibrium across multiple populations</i> <i>Current: PhD Student in Genetics at UChicago</i>
Summer 2023	Emma M. Smith (NSF REU Trainee at Johns Hopkins) <i>Project: Genomic basis of dosage imbalance in human embryonic aneuploidy</i> <i>Current: MSc Student in Genomic Medicine at Oxford</i>
2020 - 2021	Achyutha Menon (U. Chicago Undergraduate) <i>Project: Storage and visualization of multi-population Linkage Disequilibrium</i> <i>Sponsored by a College Summer Research Fellowship</i> <i>Current: MS Student in Computer Science at UCSD</i>

COMPUTATIONAL SKILLS

Python, Bash, R, C++ , Java, OCaml
Git, L^AT_EX, Microsoft Office
*nix, AWS, plink, bcftools, snakemake

SOCIETY MEMBERSHIPS

2018 -	American Society of Human Genetics (ASHG)
2021 -	Genetics Society of America (GSA)
2021 -	Society for Molecular Biology and Evolution (SMBE)
2024 -	Society for Modeling and Theory in Population Biology (SMTPB)
2024 -	Origins of Aneuploidy Research Consortium (OARC)