

ARJUN BIDDANDA, PH.D.

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

FUNDING

- 2024 - 2026 Lalor Foundation Fellowship (PI: Arjun Biddanda)
Clarifying the origins and fitness effects of human segmental aneuploidies (\$110,000)
- 2015 - 2018 NIH Genetics and Regulation Training Grant
University of Chicago

HONORS & AWARDS

- 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

PREPRINTS

* - indicates equal contribution

- 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 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. [Nature \(in press\)](#).
- 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. <i>Science</i> , 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. <i>PLoS One</i> , 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. <i>Human Genetics</i> , (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. <i>Journal of Heredity</i> , 106(5):666-671.

ORAL PRESENTATIONS

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

POSTER PRESENTATIONS

2025	A. Biddanda , S. A. Carioscia, and R. C. McCoy. <i>Evaluating evidence of transmission distortion across 139,850 blastocyst-stage human embryos</i> . American Society of Human Genetics.
2024	A. Biddanda , S. A. Carioscia, E. R. Hoffman, and R. C. McCoy. <i>Genetic architecture and fitness costs of meiotic recombination across 99,132 in vitro fertilized embryos</i> . Biology of Genomes.
2024	A. Biddanda . <i>Two-Locus Genealogies under Isolation-by-Distance and Time</i> . The Allied Genetics Conference.
2022	A. Biddanda , Y. Zhang, P. Moorjani, and C. O'Dushlaine. <i>Recovering signatures of ghost admixture using genealogies</i> . 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 Peer-Review Training Program
 Genetics Society of America
- 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

Winter 2025

Carsten Hoeke (*CMDB Rotation Student at Johns Hopkins*)
Project: Evaluating genetic effects on crossover interference strength

Fall 2025

Brooke Weingard (*CMDB Rotation Student at Johns Hopkins*)
Project: Estimating relatedness across multiple reproductive testing datasets

Spring 2025

Olivia Choi (*CMDB Rotation Student at Johns Hopkins*)
Project: Genetic influences on euploid and aneuploid pregnancy losses

2024

Ameena K. Beg (*Johns Hopkins Undergraduate*)
Project: Evolutionary history of a human mitotic aneuploidy risk locus using ancient DNA

Spring 2024

Maya Mastronado (*CMDB Rotation Student at Johns Hopkins*)
Project: Quantifying centromere-haplotype effects on aneuploidy risk

2022 - 2024

Axel Zagal-Norman (*UNAM Undergraduate Internship*)
Project: Visualization of Linkage Disequilibrium across multiple populations
Current: PhD Student in Genetics at U. Chicago

Summer 2023

Emma M. Smith (*NSF REU Trainee at Johns Hopkins*)
Project: Genomic basis of dosage imbalance in human embryonic aneuploidy
Current: MSc Student in Genomic Medicine at Oxford

2020 - 2021

Achyutha Menon (*U. Chicago Undergraduate*)
Project: Storage and visualization of multi-population Linkage Disequilibrium
Sponsored by a College Summer Research Fellowship
Current: MS Student in Computer Science at UCSD

COMPUTATIONAL SKILLS

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

SOCIETY MEMBERSHIPS

2025 -

Origins of Aneuploidy Research Consortium (OARC)

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)