

ARJUN BIDDANDA, PH.D.

Address 3400 N. Charles St
250 Levi Hall
Baltimore, MD 20210
Email aabiddanda@gmail.com
Website aabiddanda.github.io
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RESEARCH INTERESTS

Statistical Genetics, Population Genomics, Genomic Medicine, 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

LEAD-AUTHOR PUBLICATIONS

* - 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](#).

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](#).

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](#).

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.

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.

PREPRINTS

- 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 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 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 D. Yoo, A. Rhie, ..., **A. Biddanda**, A. M. ... Phillippy, and E. E. Eichler. Complete sequencing of ape genomes. [Nature](#).
- 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.
- 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.
- 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.
- 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**, 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.

ORAL PRESENTATIONS

- 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).
- 2024 **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).
- 2021 **A. Biddanda**, D. P. Rice, and J. Novembre. *Geographic patterns of human allele frequency variation: a variant-centric perspective*. UC Berkeley Population Genomics Reading Group (Invited Talk).
- 2019 **A. Biddanda**, M. Steinrücken, and J. Novembre. *Linkage Disequilibrium in Ancient DNA: Theory and Applications*. Midwest Population Genetics Meeting.

POSTER PRESENTATIONS

- 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.

FUNDING

- 2024 - 2026 Lalor Foundation Postdoctoral Fellowship (PI: Arjun Biddanda)
Fully wrote proposal on segmental aneuploidy interpretation in IVF embryos.
- 2020 - 2021 NIH R01 HG010773 (PI: John Novembre & Xin He)
Contributed methods and preliminary data for Aim 2 on negative selection.

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

2015-2018 *NSF Graduate Research Fellowship*
NIH Genetics and Regulation Training Grant
University of Chicago

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

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, 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*)
Project: Genetic influences on euploid and aneuploid pregnancy losses

2024 Aameena K. Beg (*Johns Hopkins Undergraduate*)
Project: Evolutionary history of a human mitotic aneuploidy risk locus using ancient DNA

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 Genetics 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)