

# ARJUN BIDDANDA, PH.D.

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*Updated* November 17, 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

## FUNDING

*2024 - 2026* Lalor Foundation Fellowship (PI: Arjun Biddanda)  
*Segmental aneuploidy interpretation in IVF embryos (\$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 \(provisionally accepted\)](#).
- 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. Carioscia, ..., 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. Carioscia, ..., 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. Carioscia, 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. Carioscia, 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 genealogies*. American Society of Human Genetics.

2021	<b>A. Biddanda</b> , M. Steinrücken, and J. Novembre. <i>Properties of two-locus genealogies and linkage disequilibrium in temporally stratified samples</i> . Probabilistic Models in Genomics.
2019	<b>A. Biddanda</b> , M. Steinrücken, and J. Novembre. <i>Linkage Disequilibrium in Ancient DNA: Theory and Applications</i> . American Society of Human Genetics.
2018	<b>A. Biddanda</b> and J. Novembre. <i>Inference and visualization of the geographic distribution for variant sets</i> . American Society of Human Genetics.

## TEACHING EXPERIENCE

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

## ACADEMIC SERVICE

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

## OUTREACH / SCIENCE COMMUNICATION

2024 -	Skype a Scientist
2023 -	Careerspring Advisor

## MENTORSHIP

Winter 2025	Carsten Hoeke (CMDB Rotation Student at Johns Hopkins) <i>Project: Evaluating genetic effects on crossover interference strength</i>
Fall 2025	Brooke Weingard (CMDB Rotation Student at Johns Hopkins) <i>Project: Estimating relatedness across multiple reproductive testing datasets</i>
Spring 2025	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 U. Chicago</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<sup>A</sup>T<sub>E</sub>X, 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)