

ARJUN BIDDANDA

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RESEARCH INTERESTS

Population Genomics, Statistical Genetics, 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 Title: *Investigating the spatio-temporal structure of human genetic diversity*
 Advisor: John Novembre

2011 - 2015 BS.Eng · Computer Science (*Cum Laude*) · Cornell University
 Advisor: Alon Keinan

HONORS / AWARDS

2024 Lalor Foundation Fellowship
 Lalor Foundation

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

FUNDING

2024 Lalor Foundation Fellowship (PI: Arjun Biddanda)
 Fully wrote proposal on segmental aneuploidy detection in IVF embryos.

PREPRINTS

* - indicates equal contribution

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. *bioRxiv*, 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. *bioRxiv*, 2024.

PEER-REVIEWED PUBLICATIONS

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*, page 100305, 2024.

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*, 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, 2023.

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), 2022.

A. Biddanda, D. P. Rice, and J. Novembre. Geographic patterns of human allele frequency variation: a variant-centric perspective. *eLife*, 2020.

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), 2018.

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*, pages 1–17, 2016.

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, 2015.

ORAL PRESENTATIONS

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), 2024.

A. Biddanda. *A variant-centric view of human population structure.* Population Genetics Simulation and Visualization - 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, 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), 2021.

A. Biddanda, M. Steinrücken, and J. Novembre. *Linkage Disequilibrium in Ancient DNA: Theory and Applications.* Midwest Population Genetics Meeting, 2019.

POSTER PRESENTATIONS

A. Biddanda. *Two-Locus Genealogies under Isolation-by-Distance and Time.* The Allied Genetics Conference, 2024.

A. Biddanda, Y. Zhang, P. Moorjani, and C. O'Dushlaine. *Recovering signatures of ghost admixture using ancestral recombination graphs.* American Society of Human Genetics, 2022.

A. Biddanda, M. Steinrücken, and J. Novembre. *Properties of two-locus genealogies and linkage disequilibrium in temporally stratified samples.* Probabilistic Models in Genomics, 2021.

A. Biddanda, M. Steinrücken, and J. Novembre. *Linkage Disequilibrium in Ancient DNA: Theory and Applications.* American Society of Human Genetics, 2019.

A. Biddanda and J. Novembre. *Inference and visualization of the geographic distribution for variant sets.* American Society of Human Genetics, 2018.

TEACHING EXPERIENCE

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

2023	Teaching Certificate <i>Johns Hopkins University Teaching Institute</i>
2022	ASHG Session Chair / Organizer

2021 - 2024	<i>Demographic history, natural selection, and disease risk in diverse global biobanks</i> Genetics Peer-Review Training Program
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 -	<i>Ad Hoc Peer Review</i> <i>Genetics, eLife, Molecular Biology and Evolution, Genes, Scientific Reports</i> <i>Frontiers in Genetics, BMC Genomics, PLoS One</i>

OUTREACH / SCIENCE COMMUNICATION

2024	Skype a Scientist
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MENTORSHIP

2024 -	Ameena K. Beg (<i>Johns Hopkins Undergraduate</i>) <i>Project: Evolutionary history of a human mitotic aneuploidy risk locus using ancient DNA</i>
Spring 2024	Maya Mastronardo (<i>CMDB Rotation Student at Johns Hopkins</i>) <i>Project: Quantifying centromere-haplotype effects on aneuploidy risk</i>
2022 - 2024	Axel Zagal-Norman (<i>UNAM Undergraduate Internship</i>) <i>Project: Visualization of Linkage Disequilibrium across multiple populations</i> <i>Current: PhD Student at UChicago</i>
Summer 2023	Emma M. Smith (<i>NSF REU Trainee at Johns Hopkins</i>) <i>Project: Genomic basis of dosage imbalance in human embryonic aneuploidy</i> <i>Current: Post-baccalaureate researcher at NIH</i>
2020 - 2021	Achyutha Menon (<i>U. Chicago Undergraduate</i>) <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)