

ARJUN BIDDANDA

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RESEARCH INTERESTS

Population Genomics, Statistical Genetics, 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 Title: *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

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

2024 D. Yoo, A. Rhie, ..., **A. Biddanda**, A. M. ... Phillippy, and E. E. Eichler. Complete sequencing of ape genomes. *bioRxiv*.

PEER-REVIEWED PUBLICATIONS

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*.

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*.

- 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

- 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.

HONORS / AWARDS

2024 Lalor Foundation Fellowship
Lalor Foundation

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

FUNDING

2024 Lalor Foundation 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.

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
*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

MENTORSHIP

- 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*)
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 at UChicago
- Summer 2023 Emma M. Smith (*NSF REU Trainee at Johns Hopkins*)
Project: Genomic basis of dosage imbalance in human embryonic aneuploidy
Current: Post-baccalaureate researcher at NIH
- 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

- 2018 - American Society of Human Genetics (ASHG)
2021 - Genetics Society of America (GSA)
2021 - Society for Molecular Biology and Evolution (SMBE)