ARJUN A. BIDDANDA

Address 3400 N. Charles St
250 Levi Hall
Baltimore, MD 20210
Email aabiddanda@gmail.com
Website aabiddanda.github.io
Updated December 20, 2023

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

PREPRINTS

* - *indicates equal contribution*

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*, 2023.

D. J. Taylor, S. B. Chhetri, **A. Biddanda**, M. G. Tassia, A. Battle, and R. C. McCoy. Sources of gene expression variation in a globally diverse human cohort. *bioRxiv*, 2023.

A. Biddanda* , E. Bandyopadhyay*, C. de la Fuente Castro*, D. Witonsky, ..., C. D. Kodira, A. P. Naren, M. Sikdar, N. Rai, and M. Raghavan. Integrating genetic and oral histories of Southwest Indian populations. *bioRxiv*, 2023.

PEER-REVIEWED PUBLICATIONS

E. Joshi, **A. Biddanda**, J. Popoola, A. Yakubu, O. Osakewe, D. Attipoe, g. Team, N.-G. 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*, 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*, 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*, 2022.

A. Biddanda, M. Steinrücken, and J. Novembre. Properties of two-locus genealogies and linkage disequilibrium in temporally structured samples. *Genetics*, 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*, 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. *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 PopGen (*Talk*), 2019.

POSTER PRESENTATIONS

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

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

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

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

Honors / Awards

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*

Teaching Experience

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 -	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*

Mentorship

2022 -	Axel Zagal-Norman (*UNAM Undergraduate Internship*) *Project: Visualization of Linkage Disequilibrium across multiple populations*

Summer 2023	Emma M. Smith (*NSF REU Trainee*) *Project: Genomic basis of dosage imbalance in human embryonic aneuploidy*
2020 - 2021	Achyutha Menon (*U. Chicago Undergraduate*) *Project: Storage and visualization of multi-population Linkage Disequilibrium* Sponsored by a College Summer Research Fellowship

Computational Skills

Python, Bash, R, C++, Java, OCaml

Git, LaTeX, 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)