Jordan M. Eizenga

Genomics Institute
University of California Santa Cruz
1156 High St.
Santa Cruz, CA 95064
jeizenga@ucsc.edu

EDUCATION

2021 PhD Bioinformatics
University of California Santa Cruz

2011 BS Mathematics and Political Science, Highest Distinction
University of Michigan Ann Arbor

PROFESSIONAL AND RESEARCH EXPERIENCE

2021-present Postdoctoral Researcher
Benedict Paten Lab
University of California Santa Cruz
Santa Cruz, CA

2016-2021 Graduate Student Researcher
Benedict Paten Lab
University of California Santa Cruz
Santa Cruz, CA

2019-2020 Bioinformatics Consultant
Amanita Informatics
Santa Cruz, CA

2014-2015 Software Development Contractor
Behavioral Medical Interventions (now R3 Continuum)
Edina, MN

2011-2012 Program Evaluator/Research Assistant
AmeriCorps State and National
The Guidance Center
Southgate, MI

2010-2011 Research Assistant
Global Proliferation of Truth Commissions Project
Department of Sociology
University of Michigan
Ann Arbor, MI

2009-2010 Research Assistant
World Bank WUASP Evaluation Project
School of Public Policy
University of Michigan
Ann Arbor, MI

PUBLICATIONS

* Contributed equally to publication

1. Human Pangenome Reference Consortium (incl. **Eizenga, JM**). (2023) A draft human pangenome reference. *Nature*, *617*, 312-324.

2. Hickey, G, Monglong, J, Ebler, J, Novak, AM, **Eizenga, JM**, Gao, Y, Marschall, T, Li, H, and Paten, B. Pangenome graph construction from genome alignments with Minigraph-Cactus. *Nature Biotechnology*, *1270*, 1-11.

3. Lorig-Roach, R, Meredith, M, Monlong, J, Jain, M, Olsen, H, McNulty, B, Porubsky, D, Montague, T, Lucas, J, Condon, C, **Eizenga, J**, Juul, Sissel, McKenzie, S, Simmonds, SE, Park, J, Asri, M, Koren, S, Eichler, E, Axel, R, Martin, B, Carnevali, P, Miga, K, and Paten, B. (2023) Phased nanopore assembly with Shasta and modular graph phasing with GFAse. *bioRxiv.*

4. Marco-Sola, S, **Eizenga, JM**, Guarracino, A, Paten, B, Garrison, E, and Moreto, Miquel. (2023) Optimal gap-affine alignment in *O*(*s*) space. *Bioinformatics*, 39(2).

5. Sibbesen, JA*, **Eizenga, JM***, Novak, AM, Sirén, J, Chang, X, Garrison, E, and Paten, B. (2023) Haplotype-aware pantranscriptome analyses using spliced pangenome graphs. *Nature Methods*, 20, 239-247.

6. Walker, N, Rashid, M, Yu, S, Bignell, H, Lumby, C, Livi C, Howell, K, Morley, D, Morganella, S, Barrell, D, Caim, S, Gosal, W, Fullgrabe, J, Charlesworth, T, Vasquez, L, Ahdesmaki, M, **Eizenga, J**, Prabhat, P, Proutski, Vitali, Murat-Onana, M, Greenwood, C, Kirkwood, L, Maisuria-Armer, M, Li, M, Coats, E, Winfield, V, Macbean, L, Stock, T, Tome-Fernandez, A, Chan, Y, Sheikh, N, Golder, P, Ost, T, Steward, M, Stewart, D, Vilella, A, Noursalehi, M, Paten, B, Lucarelli, D, Mason, J, Ridge, G, Mellad, J, Shirodkar, S, Balasubramanian, S, and Holbrook, J. (2022) Hydroxymethylation profile of cell-free DNA is a biomarker for early colorectal cancer. *Scientific Reports*, 12.

7. Markello, C, Huang, C, Rodriguez, A, Carroll, A, Chang, P, **Eizenga, J**, Markello, T, Haussler, D, and Paten, B. (2022) A complete pedigree-based graph workflow for rare candidate variant analysis. *Genome Research*, 32(5), 893-903.

8. **Eizenga, JM** and Paten, B. (2022) Improving the time and space complexity of the WFA algorithm and generalizing its scoring. *bioRxiv*.

9. Sirén, J*, Monlong, J*, Chang, X*, Novak, AM*, **Eizenga, JM***, Markello, C, Sibbesen, J, Hickey, G, Chang, P, Carroll, A, Haussler, D, Garrison, E, and Paten, B. (2021) Genotyping common, large structural variations in 5,202 using pangenomes, the Giraffe mapper, and the vg toolkit. *Science*, 374(6574).

10. Shafin, K, Peasout, T, Chan, P, Nattestad, M, Kolesnikov, A, Goel, S, Baid, G, **Eizenga, JM**, Miga, KH, Carnevali, P, Jain, M, Carroll, A, and Paten, B. (2021) Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. *Nature Methods*, 18, 1322-1332.

11. **Eizenga, JM***, Lorig-Roach, R*, Meredith, MM, and Paten, B. (2021) Walk-preserving transformation of overlapped sequence graphs into blunt sequence graphs with GetBlunted. *Proceedings of Conference on Computability in Europe 2021*.

12. **Eizenga, JM***, Novak, AM*, Kobayashi, E, Villani, F, Cisar, C, Heumos, S, Hickey, G, Colonna, V, Paten, B, Garrison, E. (2020) Efficient dynamic variation graphs. *Bioinformatics*, 36(21), 5139-5144.

13. **Eizenga, JM**, Novak, AM, Sibbesen, JA, Heumos, S, Ghaffaari, A, Hickey, G, Chang, X, Seaman, JD, Rounthwaite, R, Ebler, J, Rautiainen, M, Garg, S, Paten, B, Marschall, T, Sirén, J, and Garrison, E. (2020) Pangenome graphs. *Annual Review of Genomics and Human Genetics*, 21, 139-162.

14. Vivian, J, **Eizenga, JM**, Beale, HC, Morozova-Vaske, O, and Paten, B. (2020) Bayesian framework for detecting gene expression outliers in individual samples. *JCO Clinical Informatics*, 4, 160-170.

15. Hickey, G, Heller, D, Monlong, J, Sibbesen, JA, Sirén, J, **Eizenga, JM**, Dawson, ET, Garrison, E, Novak, AM, and Paten, B. (2020) Genotyping structural variants in pangenome graphs using the vg toolkit. *Genome Research*, 21(35).

16. Schultz, DT, **Eizenga, JM**, Corbett-Detig, RB, Francis, WR, Christianson, LM, and Haddock, SHD. (2020) Novel ORFs in the mitochondrial genome of ctenophore Beroe forskalii. *PeerJ*.

17. Chang, X, **Eizenga, JM**, Novak, AM, Sirén, J, and Paten, B. (2019) Distance indexing and seed clustering in sequence graphs. *Bioinformatics*, 36(Supplement 1), i146-i153.

18. Pangenomics Hackathon Participants (incl. **Eizenga, JM**). (2019) A strategy for building and using a human reference pangenome. *F1000 Research*.

19. Mescioglu, E, Rahav, E, Belkin, N, Xian, P, **Eizenga, JM**, Vichik, A, Herut, B, Paytan, A. (2019) Aerosol microbiome over the Mediterranean Sea diversity and abundance. *Atmosphere*, 440-457.

20. Paten, B, **Eizenga, JM**, Rosen, YM, Novak, AM, Garrison, E, Hickey, G. (2018) Superbubbles, ultrabubbles, and cacti. *Journal of Computational Biology*, 25(7).

21. Garrison, E, Siren, J, Novak, AM, Hickey, G, **Eizenga, JM**, Dawson, ET, Jones, W, Garg, S, Markello, C, Lin, MF, Paten, B, and Durbin, R. (2018) Variation graph toolkit improves read mapping by representing genetic variation in the reference. *Nature Biotechnology*, 36(9), 875-879.

22. Haussler, D, Smugga-Otto, M, **Eizenga, JM**, Paten, B, Novak, AM, Nikitin, S, Zueva, M, Miagkov, D. (2018) A flow procedure for the linearization of genome sequence graphs. *Journal of Computational Biology*, 25(7).

23. Rosen, Y, **Eizenga, JM**, and Paten, B. (2017) Modeling haplotypes with respect to reference cohort variation graphs. *Bioinformatics*, 15, 118-123.

24. Vohr, SH, Gordon, R, **Eizenga, JM**, Erlich, HA, Calloway, CD, and Green, RE (2017). Phylogenetic deconvolution of whole mitochondrial haplotypes from complex mixtures. *FSI Genetics*, 30, 93-105.

25. Rand, AC*, Jain, M*, **Eizenga, JM***, Musselman-Brown, A, Olsen, HE, Akeson, M, and Paten, B (2017). Mapping DNA methylation with high throughput nanopore sequencing. *Nature Methods*, 14, 411-413.

26. Rosen, Y, **Eizenga, JM**, and Paten, B (2017). Describing the local structure of sequence graphs. *Algorithms for Computational Biology 2017*, 24-46.

27. Paten, B, Novak, AM, **Eizenga, JM**, Garrison, E (2017) Genome graphs and the evolution of genome inference. *Genome Research*, 27.

28. Novak, AM, Hickey, G, Garrison, E, Blum, S, Connelly, A, Dilthey, A, **Eizenga, JM**, Elmohomad, S, Guthrie, S, Kahles, A, Keenan, S, Kelleher, J, Kural, D, Li, H, Lin, MF, Miga, K, Ouyang, N, Rakocevic, G, Smuga-Otto, M, Zaranek, AW, Durbin, R, McVean, G, Haussler, D, and Paten, B (2017). Genome graphs. *bioRxiv*.

TEACHING EXPERIENCE

2023	Instructor University of Tennessee Health Science Center Course: Practical pangenomics (MemPanG23)
2020-21	Undergraduate research mentor University of California Santa Cruz Course: Independent study – Hardware-optimized sequence graph alignment
2020-21	Undergraduate research co-mentor University of California Santa Cruz Course: Independent study – Integrated genome inference using MCMC
2019	Teaching assistant University of California Santa Cruz Course: Scientific principles of life
2018	Teaching assistant University of California Santa Cruz Course: Bioinformatics algorithms
2018	Course assistant Instituto Gulbenkian de Ciência Course: Computational pangenomics (CPANG18)
2018	Undergraduate research mentor University of California Santa Cruz Course: Independent study – Methods for encoding sequence graphs
2018	Undergraduate research mentor University of California Santa Cruz Course: Independent study – Developing effective proposal distributions for genome inference on genome graphs
2017	Undergraduate research mentor University of California Santa Cruz Course: Independent study – Path algorithms for snarls in genome graphs
2017	Co-organizer/Co-instructor University of California Santa Cruz Course: Incoming Graduate Student Bootcamp
2011	Grader University of Michigan Ann Arbor Course: Advanced Multivariable Calculus

PRESENTATIONS AND POSTERS

6/28/2021 Walk-preserving transformation of overlapped sequence graphs into blunt sequence graphs with GetBlunted. Presentation delivered virtually at Computability in Europe.

4/14/2021 Haplotype aware pantranscriptome analyses using spliced pangenome graphs. Poster presented virtually at Probabilistic Modeling in Genomics.

9/23/2020 Haplotype-specific transcript inference using spliced variation graphs. Poster presented virtually at T2T Consortium/Human Pangenome Reference Consortium Conference.

7/15/2020 Distance indexing and seed clustering in sequence graphs. Presentation delivered virtually at Intelligent Systems for Molecular Biology.

7/15/2020 Improving RNA-seq mapping and haplotype-specific transcript inference using variation graphs. Presentation delivered virtually at Intelligent Systems for Molecular Biology.

10/12/2019 Variant-aware analysis of RNA-seq data using variation graphs. Poster presented at Northern California Computational Biology Symposium in Davis, CA, USA.

5/7/2018 Mapping DNA sequencing reads to populations of genomes. Poster presented at ARCS NCC Symposium in San Mateo, CA, USA.

2/1/2018 Genome graphs for precision medicine. Presentation delivered at GSP-TOPMed Analysis Workshop in Nashville, TN, USA.

7/27/2017 Modeling haplotypes with respect to reference cohort variation graphs. Presentation delivered at European Conference on Computational Biology/Intelligent Systems for Molecular Biology in Prague, Czech Republic.

5/6/2017 A flow procedure for the linearization of genome graphs. Presentation delivered at RECOMB in Hong Kong, China.

5/6/2017 Superbubbles, ultrabubbles, and cacti. Presentation delivered at RECOMB in Hong Kong, China.

4/13/2017 Mapping DNA methylation with high throughput nanopore sequencing. Poster presented at National Human Genome Research Institute Annual Meetup in St. Louis, MO, USA.

GRANTS AND FELLOWSHIPS

2020	University of Washington Summer Institute in Statistical Genetics Scholarship
2018	Jack Baskin and Peggy Downes-Baskin Fellowship
2018	Phi Beta Kappa Graduate Student Scholarship
2018	Koret Undergraduate Research Mentor Fellowship
2017	ARCS Scholar
2016	T-32 Predoctoral Training Grant
2015	QB3 Training Fellowship
2010	Regents Merit Scholarship
2010	N. R. Keeler Scholarship
2010	Center for South Asian Studies Summer Fellowship
2009	John C. O'Leary Scholarship
2009	Diane C. Swonk Scholarship
2007	N. R. Cortright Memorial Scholarship

AWARDS

2011	Phi Beta Kappa
2011	Outstanding Achievement in Mathematics Award
2007-2011	University Honors
2007-2011	James B. Angell Scholar
2010	Underclassman Honors

VOLUNTEER AND SERVICE

2021-present	UCSC Unit Chair, UAW 5810
2020-2021	UCSC organizing committee member and chairperson of working conditions research, Student Researchers United
2019	ESL tutor, Santa Cruz Volunteer Center
2014	ESL teacher, Church of the Servant
2014	GED tutor, Hispanic Center of Western Michigan
2013	GED tutor, Heartside Ministries
2013	Volunteer, William C. Loving Elementary School
2011-2012	Service member, AmeriCorps
2011	ESL tutor, Washtenaw Literacy
2010-2011	Treasurer, Black Elk Housing Cooperative
2009-2010	Outreach manager, Human Rights Through Education
2008	Residence hall committee officer, University of Michigan College Democrats
2008	Volunteer, Habitat for Humanity of Kent County