

Mitchell R. Vollger

Curriculum Vitae

Personal Information

Legal name Mitchell Robert Vollger
Birth 3 November 1992, Carson City (Nevada)

Email

Primary mvollger[at]uw.edu
Secondary mrvollger[at]gmail.com

Phone

Mobile (707) 407-8732

Address

Primary 11316 8th Ave. NE Unit A, Seattle Washington, 98125

Education

Sep 2016 – March 2021 **Ph.D in Genome Sciences**, *University of Washington*, Seattle, Washington, GPA – 3.86
Sep. 2011 – June 2015 **B.S.E. in Computer Science Engineering**, *Princeton University*, Princeton, New Jersey, GPA – 3.13. Student of the [Integrated Science Curriculum](#)
Sep. 2011 – June 2015 **Certificate in Quantitative and Computational Biology**, *Princeton University*, Princeton, New Jersey, GPA – 3.48
Sep. 2008 – June 2011 **Associate of Arts Degree in Mathematics**, *College of the Redwoods*, Eureka, California, GPA – 4.00
Sep. 2008– June 2011 **Associate of Arts Degree in Science**, *College of the Redwoods*, Eureka, California, GPA – 4.00

Postdoctoral Experience

April 2022 – Present **Postdoctoral Scholar in Medical Genetics**, *University of Washington*, Seattle, Washington, Lab of Andrew B. Stergachis
March 2021 – April 2022 **Postdoctoral Scholar at Genome Sciences**, *University of Washington*, Seattle, Washington, Lab of Evan E. Eichler

Honors and Awards

2011 Graduated with Highest Honors, College of the Redwoods
2011 National Merit Scholarship Semifinalist

2011 Valedictorian, Academy of the Redwoods

Professional Organizations

- 2020-Present Member of the Telomere to Telomere consortium (T2T)
2020-Present Member of the Human Pangenome Reference Consortium (HPRC)
2021 Member of American Society of Human Genetics (ASHG)

Research Funding

- Fall 2022 - NIH/NHGRI T32 Genome Training Grant through the Division of Medical Genetics
Fall 2023 at University of Washington.
Fall 2017 - BDGN, Big Data in Genomics and Neuroscience. Awarded for two years.
Fall 2019
Fall 2016 - NIH/NHGRI T32, through the Genome Training Grant. Awarded for two years.
Fall 2017

Bibliography

First author

- **Mitchell R. Vollger**, Philip C. Dishuck, William T. Harvey, William S. DeWitt, Xavi Guitart, Michael E. Goldberg, et al. Increased mutation and gene conversion within human segmental duplications. *Nature*. 2023. [10.1038/s41586-023-05895-y](https://doi.org/10.1038/s41586-023-05895-y)
- **Mitchell R. Vollger**, Xavi Guitart, Philip C. Dishuck, Ludovica Mercuri, William T. Harvey, Ariel Gershman, et al. Segmental duplications and their variation in a complete human genome. *Science*. 2022. [10.1126/science.abj6965](https://doi.org/10.1126/science.abj6965)
- **Mitchell R. Vollger**, Peter Kerpedjiev, Adam M Phillippy, Evan E Eichler. Stained-Glass: Interactive visualization of massive tandem repeat structures with identity heatmaps. *Bioinformatics*. 2022. [10.1093/bioinformatics/btac018](https://doi.org/10.1093/bioinformatics/btac018)
- **Mitchell R. Vollger**, Glennis A. Logsdon, Peter A. Audano, Arvis Sulovari, David Porubsky, Paul Peluso, et al. Improved assembly and variant detection of a haploid human genome using single-molecule, high-fidelity long reads. *Annals of Human Genetics*. 2019. [10.1111/ahg.12364](https://doi.org/10.1111/ahg.12364)
- **Mitchell R. Vollger**, Philip C. Dishuck, Melanie Sorensen, AnneMarie E. Welch, Vy Dang, Max L. Dougherty, et al. Long-read sequence and assembly of segmental duplications. *Nature Methods*. 2018. [10.1038/s41592-018-0236-3](https://doi.org/10.1038/s41592-018-0236-3)

Corresponding author

- Anupama Jha, Stephanie C. Bohaczuk, Yizi Mao, Jane Ranchalis, Benjamin J. Mallory, Alan T. Min, ... **Mitchell R. Vollger**. Fibertools: fast and accurate DNA-m6A calling using single-molecule long-read sequencing. *bioRxiv*. 2023. [10.1101/2023.04.20.537673](https://doi.org/10.1101/2023.04.20.537673)

Collaborative author

- Wen-Wei Liao, Mobin Asri, Jana Ebler, Daniel Doerr, Marina Haukness, Glenn Hickey, ... **Mitchell R. Vollger**..., et al. A draft human pangenome reference. *Nature*. 2023. [10.1038/s41586-023-05896-x](https://doi.org/10.1038/s41586-023-05896-x)
- David Porubsky, **Mitchell R. Vollger**, William T. Harvey, Allison N. Rozanski, Peter Ebert, Glenn Hickey, et al. Gaps and complex structurally variant loci in phased genome assemblies. *Genome Research*. 2023. [10.1101/gr.277334.122](https://doi.org/10.1101/gr.277334.122)
- William S. DeWitt, Luke Zhu, **Mitchell R. Vollger**, Michael E. Goldberg, Andrea Talenti, Annabel C. Beichman, et al. mutyper: assigning and summarizing mutation types for analyzing germline mutation spectra. *Journal of Open Source Software*. 2023. [10.21105/joss.05227](https://doi.org/10.21105/joss.05227)
- Xiangyu Yang, Xuankai Wang, Yawen Zou, Shilong Zhang, Manying Xia, **Mitchell R. Vollger**, et al. A refined characterization of large-scale genomic differences in the first complete human genome. *bioRxiv*. 2022. [10.1101/2022.12.17.520860](https://doi.org/10.1101/2022.12.17.520860)
- Sergey Aganezov, Stephanie M. Yan, Daniela C. Soto, Melanie Kirsche, Samantha Zarate, Pavel Avdeyev, ... **Mitchell R. Vollger**..., et al. A complete reference genome improves analysis of human genetic variation. *Science*. 2022. [10.1126/science.abl3533](https://doi.org/10.1126/science.abl3533)
- Nicolas Altemose, Glennis A. Logsdon, Andrey V. Bzikadze, Pragma Sidhwani, Sasha A. Langley, Gina V. Caldas, ... **Mitchell R. Vollger**..., et al. Complete genomic and epigenetic maps of human centromeres. *Science*. 2022. [10.1126/science.abl4178](https://doi.org/10.1126/science.abl4178)
- Ariel Gershman, Michael E. G. Sauria, Xavi Guitart, **Mitchell R. Vollger**, Paul W. Hook, Savannah J. Hoyt, et al. Epigenetic patterns in a complete human genome. *Science*. 2022. [10.1126/science.abj5089](https://doi.org/10.1126/science.abj5089)
- Savannah J. Hoyt, Jessica M. Storer, Gabrielle A. Hartley, Patrick G. S. Grady, Ariel Gershman, Leonardo G. de Lima, ... **Mitchell R. Vollger**..., et al. From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. *Science*. 2022. [10.1126/science.abk3112](https://doi.org/10.1126/science.abk3112)
- Sergey Nurk, Sergey Koren, Arang Rhie, Mikko Rautiainen, Andrey V. Bzikadze, Alla Mikheenko, **Mitchell R. Vollger**, et al. The complete sequence of a human genome. *Science*. 2022. [10.1126/science.abj6987](https://doi.org/10.1126/science.abj6987)
- PingHsun Hsieh, Vy Dang, **Mitchell R. Vollger**, Yafei Mao, Tzu-Hsueh Huang, Philip C. Dishuck, et al. Evidence for opposing selective forces operating on human-specific duplicated TCAF genes in Neanderthals and humans. *Nature Communications*. 2021. [10.1038/s41467-021-25435-4](https://doi.org/10.1038/s41467-021-25435-4)
- Glennis A. Logsdon, **Mitchell R. Vollger**, PingHsun Hsieh, Yafei Mao, Mikhail A. Liskovych, Sergey Koren, et al. The structure, function and evolution of a complete human chromosome 8. *Nature*. 2021. [10.1038/s41586-021-03420-7](https://doi.org/10.1038/s41586-021-03420-7)
- David Porubsky, Peter Ebert, Peter A. Audano, **Mitchell R. Vollger**, William T. Harvey, Pierre Marijon, et al. Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. *Nature Biotechnology*. 2020. [10.1038/s41587-020-0719-5](https://doi.org/10.1038/s41587-020-0719-5)

- Wesley C. Warren, R. Alan Harris, Marina Haukness, Ian T. Fiddes, Shwetha C. Murali, Jason Fernandes, ... **Mitchell R. Vollger**..., et al. Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. *Science*. 2020. [10.1126/science.abc6617](https://doi.org/10.1126/science.abc6617)
- Glennis A. Logsdon, **Mitchell R. Vollger**, Evan E. Eichler. Long-read human genome sequencing and its applications. *Nature Reviews Genetics*. 2020. [10.1038/s41576-020-0236-x](https://doi.org/10.1038/s41576-020-0236-x)
- Sergey Nurk, Brian P. Walenz, Arang Rhie, **Mitchell R. Vollger**, Glennis A. Logsdon, Robert Grothe, et al. HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. *Genome Research*. 2020. [10.1101/gr.263566.120](https://doi.org/10.1101/gr.263566.120)
- Karen H. Miga, Sergey Koren, Arang Rhie, **Mitchell R. Vollger**, Ariel Gershman, Andrey Bzikadze, et al. Telomere-to-telomere assembly of a complete human X chromosome. *Nature*. 2020. [10.1038/s41586-020-2547-7](https://doi.org/10.1038/s41586-020-2547-7)
- Kishwar Shafin, Trevor Pesout, Ryan Lorig-Roach, Marina Haukness, Hugh E. Olsen, Colleen Bosworth, ... **Mitchell R. Vollger**..., et al. Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. *Nature Biotechnology*. 2020. [10.1038/s41587-020-0503-6](https://doi.org/10.1038/s41587-020-0503-6)
- Arvis Sulovari, Ruiyang Li, Peter A. Audano, David Porubsky, **Mitchell R. Vollger**, Glennis A. Logsdon, et al. Human-specific tandem repeat expansion and differential gene expression during primate evolution. *Proceedings of the National Academy of Sciences*. 2019. [10.1073/pnas.1912175116](https://doi.org/10.1073/pnas.1912175116)
- PingHsun Hsieh, **Mitchell R. Vollger**, Vy Dang, David Porubsky, Carl Baker, Stuart Cantsilieris, et al. Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes. *Science*. 2019. [10.1126/science.aax2083](https://doi.org/10.1126/science.aax2083)
- Flavia A. M. Maggolini, Stuart Cantsilieris, Pietro D'Addabbo, Michele Manganelli, Bradley P. Coe, Beth L. Dumont, ... **Mitchell R. Vollger**..., et al. Genomic inversions and GOLGA core duplicons underlie disease instability at the 15q25 locus. *PLOS Genetics*. 2019. [10.1371/journal.pgen.1008075](https://doi.org/10.1371/journal.pgen.1008075)

Invited Talks

- April 2023 **Speaker**, *Division of Medical Genetics Seminar Series*, University of Washington
Comprehensive diploid genetic and epigenetic profiles with single-molecule precision
- Feb 2023 **Speaker**, *AGBT 2023*, Hollywood Florida, National
Comprehensive diploid genetic and epigenetic profiles with single-molecule precision
- Dec 2022 **Lighting talk**, *Genome Sciences 20th anniversary symposium*, University of Washington
A complete view of segmental duplications and their variation
- Oct 2022 **Invited talk**, *Long-Read, Long-Range scientific interest group*, NIH
Using a complete human reference to explore variation in segmental duplications
- Aug 2022 **Plenary talk**, *T2T-F2F conference, National*, University of California Santa Cruz
Increased mutation rate and interlocus gene conversion within human segmental duplications

- March 2022 **Speaker**, *UCSC BME departmental seminar series, Local*
Segmental duplications and their variation in a complete human genome
- Oct 2021 **Speaker**, *NHGRI computational biology seminar series, Local*
Segmental duplications and their variation in a complete human genome
- Sep 2021 **Section talk**, *American Society of Human Genetics, National*
A complete view of segmental duplications and their variation
- Sep 2020 **Plenary talk**, *T2T and HPRC conference, National*, University of Washington
A complete view of segmental duplications and their variation
- Sep 2019 **Plenary talk**, *Pacific Biosciences User Group Meeting, National*, University of Delaware
Improved Assembly of Segmental Duplications Using HiFi
- Feb 2015 **Speaker**, *The Princeton High Throughput Sequencing Group, Local*, Princeton University
Computational methods to quantify DNA damage done to *Saccharomyces cerevisiae* by UV and Cisplatin

Posters

- September 2022 **Fibertools: computational methods for chromatin accessibility with long-reads**, *Genome Sciences Annual Retreat*, Washington University
- May 2021 **A complete view of segmental duplications and their variation**, *Biology of genomes*, Cold Spring Harbor Laboratory
- December 2019 **Improved Assembly of Human Genomes Using HiFi**, *Annual Scientific Meeting*, Howard Hughes Medical Institute
Presented a poster on my research on assembly of human genomes using accurate long reads.
- October 2018 **Resolving segmental duplications using long reads and correlation clustering**, *Collaborative Seminar Series*, Allen Institute, Fred Hutch, and UW Medicine
Presented a poster on my thesis research on developing and applying methods that use paralog specific variants (PSVs) to resolve collapsed duplications to improve genome assembly.
- September 2017/2018 **Resolving Segmental Duplications with PSV based Community Detection**, *Genome Sciences Annual Retreat*, Washington University
Presented a poster on my thesis research on developing and applying methods that use paralog specific variants (PSVs) to resolve collapsed duplications to improve genome assembly.
- April 2017 **Identifying Multiple Charge States of Peptides in Mass Spectrometry**, *2017 NHGRI Annual Meeting*, Washington University in St. Louis
Presented a poster on the research I did with William Noble. A description of the research can be found in the Independent Work and Research section.

Research Experience

- April 2022 - Present **Postdoctoral Scholar**, *Exploring regulatory elements and chromatin architecture with Fiber-Seq*, University of Washington
Advisor Andrew B. Stergachis.

- Spring 2021 - **Postdoctoral Scholar**, *Resolving Duplications in Genome Assembly*, University of Washington
 April 2022
 Advisor Evan Eichler, Genome Sciences.
- Spring 2018 - **Doctoral Candidate**, *Resolving Duplications in Genome Assembly*, University of Washington
 2021
 Advisor Evan Eichler, Genome Sciences.
- Spring 2017 - **Predoctoral Candidate**, *See previous item*, University of Washington
 Spring 2018
- Winter 2017 **Predoctoral Candidate**, *Identifying Insertion/Deletion Events in Mendelian Diseases*, University of Washington
 Advisor Debbie Nickerson, Genome Sciences.
- Fall 2016 **Predoctoral Candidate**, *Tandem Identification of Multiple Charge States in MS*, University of Washington
 Advisor William Noble, Genome Sciences.
- Fall 2014 - **Undergraduate Researcher**, *Developing a Reference Genome for W303*, Princeton University
 Summer 2015
 Advisor Alison Gammie, Molecular Biology Department. Developed methods to create a reference genome for W303 *Saccharomyces cerevisiae* using existing high-throughput sequencing data.
- Fall 2014 - **Undergraduate Researcher**, *Quantifying Mutations Due to Cisplatin and UV*, Princeton University
 Summer 2015
 Advisor Alison Gammie, Molecular Biology Department.
- Fall 2013 **Undergraduate Researcher**, *Analysis of an Artificial Transcription Factor*, Princeton University
 Advisors Megan McClean, Alison Gammie, Marcus Noyes.

Teaching Experience

- October 2022 **Invited Lecture**, *Genomics and Proteomics (Genome 372)*, Gene discovery and comparative genomics
 University of Washington, Department of Genome Sciences
- Spring 2022 **Primary Lecturer**, *Introduction to Statistical Genomics (Genome 560)*
 University of Washington, Department of Genome Sciences
- Winter 2020 **Teaching Assistant**, *Introduction to Computational Molecular Biology*, Lead weekly discussion sections, organized and graded assignments, and held weekly office hours
 University of Washington, Department of Genome Sciences
- Summer 2019 **Teaching Assistant**, *Fundamentals of Genetics and Genomics*, Lead weekly discussion sections, graded assignments, and held weekly office hours
 University of Washington, Department of Genome Sciences

Programming Languages

- Daily Python, Snakemake, R
 Weekly Rust
 As needed C, C++, Java, \LaTeX

References

[A. Stergachis](#) absterga@uw.edu
[E. Eichler](#) eee@gs.washington.edu
[A. Phillippy](#) adam.phillippy@nih.gov
[M. Chaisson](#) mchaisso@usc.edu
[W. Timp](#) wtimp@jhu.edu