Mitchell R. Vollger

Curriculum Vitae

Personal Information

Legal name Mitchell Robert Vollger

Website https://mrvollger.github.io

Email

Primary mvollger[at]uw.edu

Secondary mrvollger[at]gmail.com

Phone

Mobile (707) 407-8732

Address

Primary 1214 141st PL SW, Lynnwood Washington, 98087

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 in Genome Sciences**, *University of Washington*, Seattle, Washington, Lab of Evan E. Eichler

Professional Organizations

2023-Present Member of the Somatic Mosaicism Across Human Tissues consortium (SMaHT)

2020-Present Member of the Telomere to Telomere consortium (T2T)

2020-Present Member of the Human Pangenome Reference Consortium (HPRC)

2021-Present Member of American Society of Human Genetics (ASHG)

Research Funding

Summer 2024 - present: K99/R00 Pathway to Independence Award from the National Institute of General Medical Sciences.

Fall 2022 - Fall 2024: NIH/NHGRI T32 Genome Training Grant through the Division of Medical Genetics at University of Washington.

Fall 2017 - Fall 2019: BDGN, Big Data in Genomics and Neuroscience. Awarded for two years.

Fall 2016 - Fall 2017: NIH/NHGRI T32 Genome Training Grant through Genome Sciences at University of Washington. Awarded for two years.

Bibliography

First author

— **Mitchell R. Vollger**, Elliott G. Swanson, Shane J. Neph, Jane Ranchalis, Katherine M. Munson, Ching-Huang Ho, et al. A haplotype-resolved view of human gene regulation. *bioRxiv*. *Online*. 2024. 10.1101/2024.06.14.599122

— **Mitchell R. Vollger**, Jonas Korlach, Kiara C. Eldred, Elliott Swanson, Jason G. Underwood, Yong-Han H. Cheng, et al. Synchronized long-read genome, methylome, epigenome, and transcriptome for resolving a Mendelian condition. *Nature Genetics, accepted in principle*. *Online*. 2024. 10.1101/2023.09.26.559521

— **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*. *325–334,7960,617*. 2023. 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*. *6588,376*. 2022. 10.1126/science.abj6965

— **Mitchell R. Vollger**, Peter Kerpedjiev, Adam M Phillippy, Evan E Eichler. StainedGlass: Interactive visualization of massive tandem repeat structures with identity heatmaps. *Bioinformatics*. *Online*. 2022. 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*. *125–140,2,84*. 2019. 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*. *88–94,1,16*. 2018. 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**. DNA-m6A calling and integrated long-read epigenetic and genetic analysis with fibertools. *Genome Research*. *gr.279095.124*. 2024. 10.1101/gr.279095.124

Collaborative author

— Kerry L. Bubb, Morgan O. Hamm, Joseph K. Min, Bryan Ramirez-Corona, Nicholas A. Mueth, Jane Ranchalis, **Mitchell R. Vollger**, et al. The regulatory potential of transposable elements in maize. *bioRxiv*. *Online*. 2024. 10.1101/2024.07.10.602892

— Stephanie C. Bohaczuk, Zachary J. Amador, Chang Li, Benjamin J. Mallory, Elliott G Swanson, Jane Ranchalis, **Mitchell R. Vollger**, et al. Resolving the chromatin impact of mosaic variants with targeted Fiber-seq. *bioRxiv*. *Online*. 2024. 10.1101/2024.07.09.602608

— Wen-Wei Liao, Mobin Asri, Jana Ebler, Daniel Doerr, Marina Haukness, Glenn Hickey, ... **Mitchell R. Vollger**..., et al. A draft human pangenome reference. *Nature*. *312–324,7960,617*. 2023. 10.1038/s41586-023-05896-x

— 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*. *5227,85,8*. 2023. 10.21105/joss.05227

— 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*. *496–510,4,33*. 2023. 10.1101/gr.277334.122

— 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*. *Online*. 2022. 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*. *6588,376*. 2022. 10.1126/science.abl3533

— Nicolas Altemose, Glennis A. Logsdon, Andrey V. Bzikadze, Pragya Sidhwani, Sasha A. Langley, Gina V. Caldas, ... **Mitchell R. Vollger**..., et al. Complete genomic and epigenetic maps of human centromeres. *Science*. *6588,376*. 2022. 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*. *6588,376*. 2022. 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*. *6588,376*. 2022. 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*. *44–53,6588,376*. 2022. 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*. *1,12*. 2021. 10.1038/s41467-021-25435-4

— Glennis A. Logsdon, **Mitchell R. Vollger**, PingHsun Hsieh, Yafei Mao, Mikhail A. Liskovykh, Sergey Koren, et al. The structure, function and evolution of a complete human chromosome 8. *Nature*. *101–107,7857,593*. 2021. 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*. *Online*. 2020. 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*. *eabc6617,6523,370*. 2020. 10.1126/science.abc6617

— Glennis A. Logsdon, **Mitchell R. Vollger**, Evan E. Eichler. Long-read human genome sequencing and its applications. *Nature Reviews Genetics*. *597–614,10,21*. 2020. 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*. *1291–1305,9,30*. 2020. 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*. *79–84,7823,585*. 2020. 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*. *1044–1053,9,38*. 2020. 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*. *23243–23253,46,116*. 2019. 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*. *6463,366*. 2019. 10.1126/science.aax2083

— Flavia A. M. Maggiolini, 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*. *e1008075,3,15*. 2019. 10.1371/journal.pgen.1008075

Invited Talks

May 2025 **Speaker**, *European Society of Human Genetics (ESHG)*, Allianz MiCo in Milan
Fiber-seq and tools to understand the regulatory genome in a disease context

Summer 2024 **Speaker**, *Telomere to telomere face to face*, University of California Santa Cruz
Fiber-seq Inferred Regulatory Elements with diploid T2T genomes

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.

Teaching Responsibilities

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 Rust, Python, R

Weekly Snakemake

As needed C, C++, Java, LaTeX

References

A. Stergachis absterga@uw.edu

E. Eichler eee@gs.washington.edu

A. Phillippy adam.phillippy@nih.gov

W. Noble wnoble@uw.edu

W. Timp wtimp@jhu.edu