Mitchell R. Vollger

Curriculum Vitae

Personal Information

Legal name	Mitchell Robert Vollger
Place of Birth	Carson City, Nevada, USA

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

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

Research Funding

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**, 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. *bioRxiv*. *Online*. 2023. 10.1101/2023.09.26.559521

— **Mitchell R. Vollger**, Philip C. Dishuck, William T. Harvey, William S. DeWitt, Xavi Guitart, Michael E. Goldberg, ... **Mitchell R. Vollger**..., 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. Stained-Glass: 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**. Fibertools: fast and accurate DNA-m6A calling using single-molecule long-read sequencing. *bioRxiv*. *Online*. 2023. 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*. *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

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 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

W. Timp wtimp@jhu.edu

B. Paten bpaten@ucsc.edu