Mitchell Robert Vollger

Curriculum Vitae

Personal Data

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

Email

Primary	mvollger@uw.com
Secondary	mrvollger@gmail.com

Phone

Mobile	(707) 407-8732

Address

Primary	1540 Eastlake Ave. East Apt 404, Seattle Washington, 98102

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*.

Postgraduate Training

March 2021 – Present **Postdoctoral Fellow at Genome Sciences**, *University of Washington*, Seattle, Washington.

Honors

2011 Graduated with Highest Honors, College of the Redwoods

2011 National Hispanic Recognition Program Scholar

2011 National Merit Scholarship Semifinalist

2011 Valedictorian, Academy of the Redwoods

Organizations

2021 Member of the Telomere to Telomere consortium (T2T)

2021 Member of the Human Pangenome Reference Consortium (HPRC)

2021 Member of American Society of Human Genetics (ASHG)

Research Funding

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

Fall 2016 - Fall 2017 NIH/NHGRI T32, through the Genome Training Grant. Awarded for two years.

Bibliography

Primary author

— **Vollger MR**, Logsdon GA, Audano PA, Sulovari A, Porubsky D, Peluso P, et al. Improved assembly and variant detection of a haploid human genome using single-molecule, high-fidelity long reads. Ann Hum Genet. 2020;84: 125âĂŞ140. doi:10.1111/ahg.12364

— **Vollger MR**, Dishuck PC, Sorensen M, Welch AE, Dang V, Dougherty ML, Graves-Lindsay TA, Wilson RK, Chaisson MJP, Eichler EE. 2019. Long-read sequence and assembly of segmental duplications. Nat Methods. doi:10.1038/s41592-018-0236-3

Collaborative author

— Logsdon GA, **Vollger MR**, Hsieh P, Mao Y, Liskovykh MA, Koren S, Nurk S, Mercuri L, Dishuck PC, Rhie A, et al. 2021. The structure, function and evolution of a complete human chromosome 8. Nature 593: 101âĂŞ107. https://www.nature.com/articles/s41586-021-03420-7 (Accessed May 11, 2021).

— Porubsky D, Ebert P, Audano PA, **Vollger MR**, Harvey WT, Marijon P, Ebler J, Munson KM, Sorensen M, Sulovari A, et al. 2021. Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. Nat Biotechnol 39: 302âĂŞ308. http://dx.doi.org/10.1038/s41587-020-0719-5.

— Miga KH, Koren S, Rhie A, **Vollger MR**, Gershman A, Bzikadze A, et al. Telomere-to-telomere assembly of a complete human X chromosome. Nature. 2020;585: 79âĂŞ84. doi:10.1038/s41586-020-2547-7

— Logsdon GA, **Vollger MR**, Eichler EE. Long-read human genome sequencing and its applications. Nat Rev Genet. 2020. doi:10.1038/s41576-020-0236-x

— Nurk S, Walenz BP, Rhie A, **Vollger MR**, Logsdon GA, Grothe R, et al. HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. Genome Res. 2020;30: 1291âĂŞ1305. doi:10.1101/gr.263566.120

— Warren WC, Harris RA, Haukness M, Fiddes IT, Murali SC, Fernandes J, Dishuck PC, Storer JM, Raveendran M, Hillier LW, et al. 2020. Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. Science 370. http://dx.doi.org/10.1126/science.abc6617 (Accessed February 24, 2021).

— Shafin K, Pesout T, Lorig-Roach R, Haukness M, Olsen HE, Bosworth C, et al. Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. Nat Biotechnol. 2020. doi:10.1038/s41587-020-0503-6

— Sulovari A, Li R, Audano PA, Porubsky D, **Vollger MR**, Logsdon GA, et al. Human-specific tandem repeat expansion and differential gene expression during primate evolution. Proc Natl Acad Sci U S A. 2019; 201912175. doi:10.1073/pnas.1912175116

— Hsieh P, **Vollger MR**, Dang V, Porubsky D, Baker C, Cantsilieris S, Hoekzema K, Lewis AP, Munson KM, Sorensen M, Kronenberg ZN, Murali S, Nelson BJ, Chiatante G, Maggiolini FAM, Blanche H, Underwood JG, Antonacci F, Deleuze J-F, Eichler EE. 2019. Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes. Science 366. doi:10.1126/science.aax2083

— Maggiolini FAM, Cantsilieris S, D Addabbo P, Manganelli M, Coe BP, Dumont BL, Sanders AD, Pang AWC, **Vollger MR**, Palumbo O, Palumbo P, Accadia M, Carella M, Eichler EE, Antonacci F. 2019. Genomic inversions and GOLGA core duplicons underlie disease instability at the 15q25 locus. PLoS Genet 15:e1008075. doi:10.1371/journal.pgen.1008075

Invited Talks

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

May 2021 **A complete view of segmental duplications and their variation**, *Biology of genomes*, Cold spring harbor.

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

Spring 2021 - present **Postdoctoral fellow**, *Resolving Duplications in Genome Assembly*, University of Washington.
Advisor Evan Eichler, Genome Sciences. Developing and applying methods to resolve duplications and improve genome assembly.

Spring 2018 - 2021 **Doctoral Candidate**, *Resolving Duplications in Genome Assembly*, University of Washington.
Advisor Evan Eichler, Genome Sciences. Developing and applying methods that use paralog specific variants (PSVs) to resolve duplications and improve genome assembly.

Spring 2017 - Spring 2018 **Predoctoral Candidate**, *See previous item*, University of Washington.

Winter 2017 **Predoctoral Candidate**, *Identifying Insertion/Deletion Events in Mendelian Diseases*, University of Washington.
Advisor Debbie Nickerson, Genome Sciences. Implemented a variety of variant callers on a large number of genomes across many Mendelian Diseases in order to more consistently identify insertion and deletion events

Fall 2016 **Predoctoral Candidate**, *Tandem Identification of Multiple Charge States in MS*, University of Washington.
Advisor William Noble, Genome Sciences. Implemented group LASSO to confirm the existence of a single peptide in multiple charge states in mass spectrometry data for use in data independent acquisition (DIA) deconvolution.

Fall 2014 - Summer 2015 **Undergraduate Researcher**, *Developing a Reference Genome for W303*, Princeton University.
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 - Summer 2015 **Undergraduate Researcher**, *Quantifying Mutations Due to Cisplatin and UV*, Princeton University.
Advisor Alison Gammie, Molecular Biology Department. Developed computational methods to quantify DNA damage done to *Saccharomyces cerevisiae* by UV and Cisplatin *in vivo*.

Fall 2013 **Undergraduate Researcher**, *Analysis of an Artificial Transcription Factor*, Princeton University.
Advisors Megan McClean, Alison Gammie, Marcus Noyes. Analyzed the transcriptomes of *Saccharomyces cerevisiae* induced by Msn2 and by an artificial transcription factor mimicking Msn2.

Programming Languages

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

References

E. Eichler	eee@gs.washington.edu
A. Phillippy	adam.phillippy@nih.gov
M. Chaisson	mchaisso@usc.edu
S. Kannan	ksreeram@uw.edu