# Mitchell Robert Vollger

*Curriculum Vitae*

## Contact Information


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## Education

### Degree Programs

2016–Present **Ph.D Candidate in Genome Sciences**, *University of Washington*, Seattle, Washington, GPA – 3.86.

2011–2015 **B.S.E. in Computer Science Engineering**, *Princeton University*, Princeton, New Jersey, *GPA – 3.13*. Student of the Integrated Science Curriculum.

2011–2015 **Certificate in Quantitative and Computational Biology**, *Princeton University*, Princeton, New Jersey, *GPA – 3.48*.

2008–2011 **Associate of Arts Degree in Mathematics**, *College of the Redwoods*, Eureka, California, *GPA – 4.00*.

2008–2011 **Associate of Arts Degree in Science**, *College of the Redwoods*, Eureka, California, *GPA – 4.00*.

## Research Experience and Independent Work

Spring 2018 - Present **Doctoral Candidate**, *Resolving Collapsed Duplications in Genome Assembly*, University of Washington.
Advisor Evan Eichler, Genome Sciences. Developing and applying methods that use paralog specific variants (PSVs) to resolve collapsed duplications to 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. Relevant languages: Python, C, Java, R, and Matlab.

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*. Relevant languages: Python, C, Java, R, and Matlab.

2014 **iOS Software Developer**, *GeoTasker*, Princeton University.
Created GeoTasker, a location-based reminder app released on iOS 8 in the fall of 2014, developed under the instruction of Brian Kernighan. Relevant languages: Objective-C, and C

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. Relevant languages: R

## Fellowships and Awards

Fall 2017 - Present BDGN, Big Data in Genomics and Neuroscience. Funding for two years.

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

2011 National Hispanic Recognition Program Scholar

2011 National Merit Scholarship Semifinalist

2011 Valedictorian, Academy of the Redwoods

2011 Graduated with Highest Honors, College of the Redwoods

## Publications

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

Miga KH, Koren S, Rhie A, **Vollger MR**, Gershman A, Bzikadze A, Brooks S, Howe E, Porubsky D, Logsdon GA, Schneider VA, Potapova T, Wood J, Chow W, Armstrong J, Fredrickson J, Pak E, Tigyi K, Kremitzki M, Markovic C, Maduro V, Dutra A, Bouffard GG, Chang AM, Hansen NF, Thibaud-Nissen F, Schmitt AD, Belton J-M, Selvaraj S, Dennis MY, Soto DC, Sahasrabudhe R, Kaya G, Quick J, Loman NJ, Holmes N, Loose M, Surti U, Risques RA, Graves Lindsay TA, Fulton R, Hall I, Paten B, Howe K, Timp W, Young A, Mullikin JC, Pevzner PA, Gerton JL, Sullivan BA, Eichler EE, Phillippy AM. 2019. Telomere-to-telomere assembly of a complete human X chromosome. bioRxiv. doi:10.1101/735928

Shafin K, Pesout T, Lorig-Roach R, Haukness M, Olsen HE, Bosworth C, Armstrong J, Tigyi K, Maurer N, Koren S, Sedlazeck FJ, Marschall T, Mayes S, Costa V, Zook JM, Liu KJ, Kilburn D, Sorensen M, Munson KM, **Vollger MR**, Eichler EE, Salama S, Haussler D, Green RE, Akeson M, Phillippy A, Miga KH, Carnevali P, Jain M, Paten B. 2019. Efficient de novo assembly of eleven human genomes using PromethION sequencing and a novel nanopore toolkit. bioRxiv. doi:10.1101/715722

**Vollger MR**, Logsdon GA, Audano PA, Sulovari A, Porubsky D, Peluso P, Wenger AM, Concepcion GT, Kronenberg ZN, Munson KM, Baker C, Sanders AD, Spierings DCJ, Lansdorp PM, Surti U, Hunkapiller MW, Eichler EE. 2019. Improved assembly and variant detection of a haploid human genome using single-molecule, high-fidelity long reads. bioRxiv. doi:10.1101/635037

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

**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

## Posters

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.

## Presentations

Sep 2019 **Plenary talk**, *Pacific Biosciences User Group Meeting*, University of Delaware.
Improved Assembly of Segmental Duplications Using HiFi

Feb 2015 **Speaker**, *The Princeton High Throughput Sequencing Group*, Princeton University.
Invited to give a talk on the research that I did with Alison Gammie. The research is described in the Independent Work and Research section above.

## Computer Skills

Basic x86 Assembly, Objective C
Intermediate LaTeX, Java, C, C++
Advanced Python, R

## References

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S. Kannan ksreeram@uw.edu
M. Chaisson mchaisso@usc.edu