Jonathan Belyeu

Computational Genetics

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Education

August 2016–Present	**PhD Human Genetics** , *University of Utah*, Salt Lake City, UT.
August 2009–April 2016	**BS Bioinformatics, Minor: Computer Science**, *Brigham Young University*, Provo, UT.

Experience

Research/Academic

May 2017–Present	**Graduate Research Assistant**, *Aaron Quinlan, Ph.D., University of Utah*, Salt Lake City, UT, Eccles Institute of Human Genetics.

Computational research in genetics/genomics
- Performing statistical analysis of de novo structural variation in a large WGS family cohort
- Developing/distributing command-line tools for solving genomic problems
- Generating ideas for new research directions
- Performing data visualization in Python/R
- Using supercomputing resources for analysis of genomic structural variants
- Developed web and command-line tool (SV-plaudit) for structural variant curation

September 2014–April 2016	**Research Assistant**, *Perry Ridge, Ph.D., Brigham Young University*, Provo, UT, Department of Biology.

Computational research in genetics/genomics
- Built phylogenetic trees from species sets
- Performed evolution-based analyses of synonymous codon bias
- Graphically analyzed data with R
- Used supercomputer resources for large-scale analyses
- Developed command-line tool (SelecT) for statistical identification of selection

April 2015–April 2016	**Research Assistant, Department of Biology**, *Richard Gill, Ph.D., Brigham Young University*, Provo, UT.

Ecological data pipeline development
- Built data pipeline for automated or manual storage of ecological time-series data
- Managed Ubuntu server and MySQL database of time-series data
- Performed time-series data analyses and quality control

Teaching

November 2018, November 2019	**Instructor**, *Advanced Sequencing Technologies & Applications*, Cold Spring Harbor Laboratory, NY.

Classroom instruction in computational skills
- Prepared and taught lectures on Bash scripting, Unix skills
- Taught on genomic structural variant identification & prioritization
- Provided one-on-one mentoring and support for hands-on student projects

January–April 2018	**Teaching Assistant**, *Eccles Institute of Human Genetics*, Salt Lake City, UT.
	Tutoring in command-line and Unix skills
	○ Tutored in Unix/computational biology tools
	○ Graded assignments
January–April 2014	**Teaching Assistant**, *Department of Computer Science, Brigham Young University*, Provo, UT.
	Instruction and tutoring in programming skills
	○ Tutored in C++
	○ Gave group presentations on project specifications
	○ Graded assignments
August–December 2014	**Teaching Assistant**, *Department of Biology, Brigham Young University*, Provo, UT.
	Instruction and tutoring in principles of biology
	○ Presented group review sessions
	○ Tutored individuals
	○ Graded assignments

Other

April 2014–September 2015	**Web Developer**, *Center for Teaching and Learning, Brigham Young University*, Provo, UT.
	Developer for the BYU course management website
	○ Back-end web development
	○ Some front-end web development
	○ Used MySQL database
	○ Led individual projects and team projects
April–July 2016	**Web Developer**, *App Raptors*, Provo, UT.
	Full stack PHP and JavaScript Web development
	Selected Projects:
	○ missionarymemories.com
	○ alderandtweed.com
	○ naturalbiologics.com

Scientific Communication

Publications

Jonathan R Belyeu, Harrison Brand, Harold Wang, Xuefang, Zhao, Brent S. Pedersen, Julie Feusier, Meenal Gupta, Thomas J Nicholas, Lisa Baird, Bernie Devlin, Stephan J Sanders, Lynne B Jorde, Michael E Talkowski, Aaron R Quinlan. "*De novo* structural mutation rates and gamete-of-origin biases revealed through genome sequencing of 2,396 families" 2020. 10.1101/2020.10.06.329011

Jonathan R Belyeu, Murad Chowdhury, Joseph Brown, Brent S. Pedersen, Michael J. Cormier, Aaron R. Quinlan. "Samplot: A Platform for Structural Variant Visual Validation and Automated Filtering" 2020. 10.1101/2020.09.23.310110

Michael J. Cormier, **Jonathan Belyeu**, Brent S. Pedersen, Joseph Brown, Johannes Koster, Aaron R. Quinlan. "Go Get Data (GGD): simple, reproducible access to scientific data" 2020. 10.1101/2020.09.10.291377

Jordan A Berg, **Jonathan Belyeu**, Jeffrey T Morgan, Yeyun Ouyang, Alex J Bott, Aaron R Quinlan, Jason Gertz, Jared Rutter. "XPRESSyourself: Enhancing, Standardizing, and Automating Ribosome Profiling Computational Analyses Yields Improved Insight into Data." 2020. 10.1371/journal.pcbi.1007625

Jonathan Belyeu, Thomas J Nicholas, Brent S Pedersen, Thomas A Sasani, James M Havrilla, Stephanie N Kravitz, Megan E Conway, Brian K Lohman, Aaron R Quinlan, Ryan M Layer. "SV-plaudit: A cloud-based framework for manually curating thousands of structural variants." 2018. 10.1101/265058

Justin B. Miller, Ariel A. Hippen, **Jonathan R. Belyeu**, Michael F. Whiting, and Perry G. Ridge. "Missing something? Codon aversion as a new character system in phylogenetics." 2017. 10.1111/cla.12183

Talks

Jonathan Belyeu. Analysis of spontaneous human genomic structural variation in 2300 WGS families. Invited seminar, Brigham Young University Department of Biology, February 2020.

Jonathan Belyeu, Aaron Quinlan. Analysis of de novo structural variation rates in a large cohort. University of Utah Department of Human Genetics Retreat, November 2019.

Jonathan Belyeu, Ryan Layer, Julie Feusier, Lynn Jorde, Aaron Quinlan. Direct measurement of de novo structural variation through whole-genome sequencing of three-generation human pedigrees. Genome Informatics, September 2018.

Jonathan Belyeu, Ryan Layer. SV-plaudit: Rapid Visual Review of Structural Variants. Virtual invited seminar, Genome in a Bottle Consortium, July 2018.

Darian Ramage, Artem Golotin, **Jonathan Belyeu**. Streaming Correlation-based Seismic Event Detector. Lawrence Livermore National Laboratory, April 2016.

Posters

Jonathan Belyeu, Harrison Brand, Harold Wang, Brent S Pedersen, Aaron R Quinlan. Analysis of parent-of-origin and parental age effects on the rate of *de novo* structural variation in 2363 ASD cases and 2372 unaffected controls. American Society of Human Genetics, October 2020.

Jonathan Belyeu, Thomas A Sasani, Brent S Pedersen, Aaron R Quinlan. Unfazed: extended read-based phasing for *de novo* mutations and heterozygous genomic variants of all sizes. Genome Informatics, September 2020.

Jonathan Belyeu, Brent S Pedersen, Aaron R Quinlan. Identification of elusive copy number variation by targeted coverage depth analysis. American Society of Human Genetics, October 2019.

Jonathan Belyeu, Ryan M. Layer, Julie Feusier, Lynn Jorde, Aaron Quinlan. Measuring the rate of spontaneous structural variation through whole-genome sequencing of three-generation human pedigrees. American Society of Human Genetics, October 2018.

Artem Golotin, **Jonathan Belyeu**, Darian Ramage, Steven Magana-Zook, Douglas A. Dodge, Quinn Snell. Streaming Correlation-based Seismic Event Detector. Brigham Young University, April 2016.

Jonathan Belyeu, Artem Golotin, Ashlee Gerlach, Mark Ebbert, John Kauwe, Perry Ridge. Computationally locating selection signals in diploid genomes with next-generation sequencing data. BIOT Symposium for Biotechnology and Bioinformatics, December 2015.

Computational/programming skills

Bioinformatics Skills

- Unix tools
- Algorithm development
- Computational tool development
- Parallel processing
- Supercomputing
- AWS
- Conda
- Nextflow
- Matplotlib
- ggplot2

Programming Languages

- Python
- Bash/Shell
- R
- C++ (some)
- Java (some)

Other

- Git
- LaTeX