

Jonathan Belyeu | Computational Genetics

✉ jrbelyeu@gmail.com • @jon_belyeu

Education

University of Utah

PhD Human Genetics, GPA 3.913/4.00

Salt Lake City, UT

August 2016–Present

Brigham Young University

BS Bioinformatics, Minor: **Computer Science**

Provo, UT

August 2009–April 2016

GRE 165 Quantitative (95th percentile), 170 Verbal (99th percentile). GPA 3.77/4.00

Experience

Research/Academic.....

Aaron Quinlan, Ph.D., University of Utah

Graduate Research Assistant, Eccles Institute of Human Genetics

Salt Lake City, UT

May 2017–Present

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 call curation

Perry Ridge, Ph.D., Brigham Young University

Research Assistant, Department of Biology

Provo, UT

September 2014–April 2016

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 positive selection

Richard Gill, Ph.D., Brigham Young University

Research Assistant, Department of Biology

Provo, UT

April 2015–April 2016

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.....

Advanced Sequencing Technologies & Applications

Cold Spring Harbor Laboratory, NY

Instructor

November 2018, November 2019

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

Eccles Institute of Human Genetics

Salt Lake City, UT

Teaching Assistant

January–April 2018

Tutoring in command-line and Unix skills

- Tutored in Unix/computational biology tools
- Graded assignments

Department of Computer Science, Brigham Young University

Provo, UT

Teaching Assistant

January–April 2014

Instruction and tutoring in programming skills

- Tutored in C++
- Gave group presentations on project specifications
- Graded assignments

Department of Biology, Brigham Young University

Provo, UT

Teaching Assistant

August–December 2014

Instruction and tutoring in principles of biology

- Presented group review sessions
- Tutored individuals
- Graded assignments

Other

Center for Teaching and Learning, Brigham Young University

Provo, UT

Web Developer

April 2014–September 2015

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

App Raptors

Provo, UT

Web Developer

April–July 2016

Full stack PHP and JavaScript Web development

Selected Projects:

- missionarymemories.com
- alderandtweed.com
- naturalbiologics.com

Volunteer

The Church of Jesus Christ of Latter-day Saints

Barranquilla, Colombia

Spanish language missionary

December 2010–December 2012

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.

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
- L^AT_EX