

# Jonathan Belyeu

*Computational Genetics*

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## Education

August 2016–Present **PhD Human Genetics**, *University of Utah*, Salt Lake City, UT, GPA: 3.92.

August 2009–April 2016 **BS Bioinformatics, Minor: Computer Science**, *Brigham Young University*, Provo, UT, GPA: 3.77.

## 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

- Analyzing patterns of *de novo* structural variation in a large WGS family cohort
- Developing/distributing command-line tools for solving problems in genomics
- 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

## Scientific Communication

### Selected Publications

**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" *Genome Biology*, 2021. 10.1186/s13059-021-02380-5

**Jonathan R Belyeu**, Thomas A. Sasani, Brent S. Pedersen, Aaron R Quinlan. "Unfazed: parent-of-origin detection for large and small de novo variants" *bioRxiv*, 2021. 10.1101/2021.02.03.429658

**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" *The American Journal of Human Genetics*, 2021. 10.1016/j.ajhg.2021.02.012

Michael J. Cormier, **Jonathan Belyeu**, Brent S. Pedersen, Joseph Brown, Johannes Koster, Aaron R. Quinlan. "Go Get Data (GGD) is a framework that facilitates reproducible access to genomic data" *Nature Communications*, 2021. 10.1038/s41467-021-22381-z

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." *GigaScience*, 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.

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## Computational/programming skills

### Programming Languages

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

### Bioinformatics Skills

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

### Other

- Git
- $\text{\LaTeX}$