

# Jonathan Belyeu | Computational Genetics

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## 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

**Salt Lake City, UT**

*Graduate Research Assistant, Eccles Institute of Human Genetics*

*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

**Provo, UT**

*Research Assistant, Department of Biology*

*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

**Provo, UT**

*Research Assistant, Department of Biology*

*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***Teaching Assistant*

Tutoring in command-line and Unix skills

- Tutored in Unix/computational biology tools
- Graded assignments

**Salt Lake City, UT***January–April 2018***Department of Computer Science, Brigham Young University***Teaching Assistant*

Instruction and tutoring in programming skills

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

**Provo, UT***January–April 2014***Department of Biology, Brigham Young University***Teaching Assistant*

Instruction and tutoring in principles of biology

- Presented group review sessions
- Tutored individuals
- Graded assignments

**Provo, UT***August–December 2014***Other.....****Center for Teaching and Learning, Brigham Young University***Web Developer*

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

**Provo, UT***April 2014–September 2015***App Raptors***Web Developer*

Full stack PHP and JavaScript Web development

Selected Projects:

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

**Provo, UT***April–July 2016***Volunteer.....****The Church of Jesus Christ of Latter-day Saints**

*Spanish language missionary*

**Barranquilla, Colombia***December 2010–December 2012***Scientific Communication**

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**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" 2020. <https://doi.org/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. <https://doi.org/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**, 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

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### 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<sup>A</sup>T<sub>E</sub>X