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, 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

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" *bioRxiv preprint*, 2020. 10.1101/2020.09.23.310110

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

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.

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