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Jonathan Belyeu

Education

August 2016–May 2021 **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

May 2023–Present **Senior Scientist, Bioinformatics**, *Computational Biology*, Pacific Biosciences, Salt Lake City, UT (remote).
Computational genomics algorithm development

June 2021–May 2023 **Senior Bioinformatics Scientist**, *Department of Genome Informatics*, Illumina Inc., Salt Lake City, UT (remote).
Human genomic variant discovery methods development
- Developing algorithms for variant identification in repetitive genomic regions
- Evaluating methods by leveraging orthogonal technologies
- Guiding implementation of new algorithms in DRAGEN
- Presenting methods to internal and external audiences via talks, white papers, posters, and manuscripts
- Working with legal teams to file patents for IP protection
- Leading research collaborations with clients

August 2016–May 2021 **Graduate Research Assistant**, *Aaron Quinlan, Ph.D., University of Utah*, Salt Lake City, UT, Eccles Institute of Human Genetics.
Doctoral studies in computational genomics
- Analyzing patterns of *de novo* structural variation in a large WGS family cohort
- Developing/distributing command-line tools for solving problems in genomics
- Using supercomputing resources for analysis of genomic structural variants in large cohorts

September 2014–April 2016 **Research Assistant**, *Perry Ridge, Ph.D., Brigham Young University*, Provo, UT, Department of Biology.
Undergrad research in bioinformatics
- Built phylogenetic trees from species sets
- Performed evolution-based analyses of synonymous codon bias
- Graphically analyzed data with R

Scientific Communication

Selected Peer-Reviewed 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" *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" *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" *Bioinformatics*, 2021. 10.1093/bioinformatics/btab454

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." *PLOS Computational Biology*, 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." *Cladistics*, 2017. 10.1111/cla.12183

Other Publications

Jonathan Belyeu, Vitor Onuchic, Mitchell Bekritsky. "Using whole-genome sequencing to evaluate copy number variants of the LPA Kringle-IV type 2 domain with DRAGEN" *Illumina Research Hub Article*, 2023. https://www.illumina.com/science/genomics-research/articles/using-whole-genome-sequencing-to-evaluate-copy-number-variants-o.html

Sairam Behera, **Jonathan Belyeu**, Xiao Chen, Luis F. Paulin, Ngoc Quynh Nguyen, Emma Newman, Medhat Mahmoud, Vipin K. Menon, Qibin Qi, Parag Joshi, Santica Marcovina, Massimiliano Rossi, Eric Roller, James Han, Vitor Onuchic, Christy L. Avery, Christie M. Ballantyne, Carlos J. Rodriguez, Robert C. Kaplan, Donna M. Muzny, Ginger A. Metcalf, Richard Gibbs, Bing Yu, Eric Boerwinkle, Michael A. Eberle, Fritz J. Sedlazeck. "Identification of allele-specific KIV-2 repeats and impact on Lp(a) measurements for cardiovascular disease risk" *bioRxiv*, 2023. 10.1101/2023.04.24.538128

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 R. Belyeu, Sairam Behera, Xiao Chen, N. Quynh Nguyen, Luis Paulin, Vipin K. Menon, Christie Ballantyne, Carlos J. Rodriguez, Robert C. Kaplan, Ginger A. Metcalf, Bing Yu, Eric Boerwinkle, Michael A. Eberle, Fritz J. Sedlazeck. Illumina Total and Allele-Specific Copy Number Quantification of the LPA KIV-2 Tandem Repeat with DRAGEN. American Society of Human Genetics, October 2022.

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

Programming Languages

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

Bioinformatics Skills

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

Other

- Git
- LaTeX