

JUSTIN MILLER

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CURRICULUM VITAE

EDUCATION

Ph.D. Candidate: Brigham Young University, UT

Bioinformatics

2015—Present

Dissertation: Uncovering the Phylogenetic History of Codon Usage Bias
3.95 G.P.A.

Undergraduate: Brigham Young University, UT

Bachelor's Degree: **Bioinformatics**

2010 – 2015

Minor: **Computer Science**

Language Certificate in **Portuguese: ACTFL certified, Advanced Proficiency**

Areas of Concentration: Bioinformatics, Computer Science, **Portuguese**

Graduated Cum Laude with 3.91 G.P.A.

COMPUTER SKILLS

Programming languages: Python, VBA, bash, Java, C#, R, C++, SQL, MATLAB, Julia

Operating systems: Windows, Linux

Applications: MS Office Suite, MS Visual Studio, Adobe Suite

Concepts: Big Data Analysis, Machine Learning, Parallel Processing, Big O

Amateur Radio Operator. Call sign: KE7GTS

GRANTS, AWARDS, AND HONORS

BYU Research Presentation Award (\$400)

October, 2017

Willi Hennig Society Founder's Award (\$2,800)

May, 2017

Three Minute Thesis BYU Life Science College 1st Place (\$600)

February, 2017

Three Minute Thesis BYU Biology Department 2nd Place (\$50)

February, 2017

BYU Research Presentation Award (\$400)

September, 2016

CREEDS travel grant (airfare + 2 weeks lodging in New York City + conference registration)

June, 2016

Phi Kappa Phi Membership.

Since December 2014

Golden Key Honour Society Membership.

Since January 2013

Phi Eta Sigma Membership.

Since February 2011

BYU Academic Full Tuition Scholarship.

August 2010-April 2015

Boy Scouts of America, Eagle Scout

Since August 2006

WORK EXPERIENCE

Ph.D. student and teaching assistant in Biology Department

Analyze the evolution of codon usage bias across the Tree of Life.

2015 – Present

Assistant lecturer with dedicated lab office hours

Brigham Young University, Provo, UT

Data Analyst

Created reports that helped generate about \$5 million in revenue

2015 – 2016

Imagine Learning, Provo, UT

Research Assistant

Used a variety of bioinformatics tools to analyze DNA sequences

2014 – 2015

Brigham Young University, Provo, UT

Teaching Assistant – “Intro to Bioinformatics” (Dr. Perry Ridge)

Taught basic bioinformatics skills. Held regular office hours. Passed off programming projects

2014 – 2015

Brigham Young University, Provo, UT

The Church of Jesus Christ of Latter-day Saints, Ribeirão Preto, SP, Brazil **Missionary**

2011– 2013

Helped people with their physical and spiritual needs

PUBLICATIONS

- Perry G. Ridge, Mark E. Wadsworth, **Justin B. Miller**, Andrew J. Saykin, Robert C. Green, the Alzheimer's Disease Neuroimaging Initiative, John S. K. Kauwe. Assembly of 809 whole mitochondrial genomes with clinical, imaging, and fluid biomarker phenotyping. *Alzheimers & Dementia*, doi: <http://dx.doi.org/10.1016/j.jalz.2017.11.013>.
- **Miller, J. B.**, Hippen, A. A., Wright, S. M., Morris, C. & Ridge, P. G. Human viruses have codon usage biases that match highly expressed proteins in the tissues they infect. *Biomedical Genetics and Genomics* 2, doi:10.15761/bgg.1000134 (2017).
- Pickett, B.D., **J.B. Miller**, and P.G. Ridge, Kmer-SSR: A Fast and Exhaustive SSR Search Algorithm. *Bioinformatics*, 2017.
- **Miller, J. B.**, Hippen, A. A., Belyeu, J. R., Whiting, M. F. & Ridge, P. G. Missing something? Codon aversion as a new character system in phylogenetics. *Cladistics*, doi:10.1111/cla.12183 (2017).
- Mark T.W. Ebbert, Mark E. Wadsworth, Lyndsay A. Staley, Kaitlyn L. Hoyt, Brandon D. Pickett, **Justin B. Miller**, John D. Duce, John S.K. Kauwe, Perry G. Ridge: Evaluating the necessity of PCR duplicate removal from next-generation sequencing data and a comparison of approaches. *BMC Bioinformatics*, July 2016
- Stewart G. Gardner, **Justin B. Miller**, Tanner Dean, Tanner Robinson, McCall Erickson, Perry Ridge, William R. McCleary: Genetic analysis, structural modeling and direct coupling analysis suggest a mechanism for phosphate signaling in *E. coli*. *BMC Genetics*, April 2014.

ORAL PRESENTATIONS

- **Justin B. Miller**, Lauren M. McKinnon, Michael F. Whiting, Perry G. Ridge (2017). Codon Aversion Motifs: An alignment-free method to recover phylogenies. *ISCB Rocky Mountain Bioinformatics Conference, Aspen/Snowmass, CO*.
- **Justin B. Miller**, Ariel A. Hippen, Sage M. Wright, Caroline Morris, Perry G. Ridge (2016). Human-infecting viruses have codon usage biases which are highly correlated with proteins that are expressed in infected tissues, *Brigham Young University, Provo, UT*.
- **Justin B. Miller**, Ariel A. Hippen, Jonathon R. Belyeu, Michael F. Whiting, Perry G. Ridge (2015). Missing something?: Codon nonusage as a character in phylogenetic inference in Tetrapods. *Biotechnology and Bioinformatics Symposium 2015, Brigham Young University, Provo, UT*.

POSTER PRESENTATIONS

- **Justin B. Miller**, Lauren M. McKinnon, Michael F. Whiting, Perry G. Ridge (2017). Codon Aversion Motifs: An alignment-free method to recover phylogenies. *ISCB Rocky Mountain Bioinformatics Conference, Aspen/Snowmass, CO*.
- **Justin B. Miller**, Brandon D. Pickett, Perry G. Ridge (2017). JustOrthologs: A Fast, Accurate, and User-Friendly Ortholog-Identification Algorithm. *ISMB/ECCB Intelligent Systems for Molecular Biology and Computational Biology Conference, Prague, Czech Republic*.
- Stewart Morley, **Justin Miller**, Perry Ridge, Brent Nielson (2017). Assembling the Arabidopsis Mitochondrial DNA Replisome. *28th International Conference on Arabidopsis Research, St. Louis, MO*.
- Mark Wadsworth, **Justin Miller**, Michael Cormier, Sage Wright, Perry G. Ridge (2016). Determining the Effects Variants have on Gene Splicing. *Biotechnology and Bioinformatics Symposium, Brigham Young University, Provo, UT*.
- **Justin B. Miller**, Brandon D. Pickett, Perry G. Ridge (2016). JustOrthologs: A Fast, Accurate, and User-Friendly Ortholog-Identification Algorithm. *American Society of Human Genetics, Vancouver, B.C., Canada*.
- Brandon D. Pickett, **Justin B. Miller**, Perry G. Ridge (2016). Efficient, Accurate, and Complete Identification of Simple Sequence Repeats in Genomic Sequences. *American Society of Human Genetics, Vancouver, B.C., Canada*.
- **Justin B. Miller**, Brandon D. Pickett, Perry G. Ridge (2016). JustOrthologs: A Fast, Accurate, and User-Friendly Ortholog-Identification Algorithm. *LDS Life Science Symposium, Thanksgiving Point, UT*.
- Brandon D. Pickett, **Justin B. Miller**, Perry G. Ridge (2016). Efficient, Accurate, and Complete Identification of Simple Sequence Repeats in Genomic Sequences. *LDS Life Science Symposium, Thanksgiving Point, UT*.
- **Justin B. Miller**, Ariel A. Hippen, Jonathon R. Belyeu, Michael F. Whiting, Perry G. Ridge (2016). Missing Something?: Codon Aversion as a New Character System in Phylogenetics. *Community Research Education and Engagement for Data Science at Icahn School of Medicine, New York City, NY*.
- **Justin Miller**, Ariel Hippen, Andy Himebaugh, Ryan Miller, Caroline Morris, Perry Ridge (2015). Viral Codon Bias Mimics Human Host Proteins. *Biotechnology and Bioinformatics Symposium, Brigham Young University, Provo, UT*.
- **Justin B. Miller**, John D. Duce, Perry G. Ridge (2014). The Alignable Portion. *Biotechnology and Bioinformatics Symposium 2014, Brigham Young University, Provo, UT*.
- **Justin B. Miller**, Kaitlyn L. Hoyt, Jordon B. Richie, Artem V. Golotin (2014). Assembling a Chromosome from Overlap Regions. *Biotechnology and Bioinformatics Symposium, Brigham Young University, Provo, UT*.
- Mark E. Wadsworth, Brandon D. Pickett, **Justin B. Miller**, John D. Duce, Ronald G. Munger, Christopher D. Corcoran, JoAnn T. Tschanz, Maria C. Norton, John S.K. Kauwe, Karl V. Voelkerding, Perry G. Ridge (2014). The Variant Characterization of 211 Whole Genome Sequences: The Cache County Study on Memory Health and Aging. *Biotechnology and Bioinformatics Symposium, Brigham Young University, Provo, UT*.

- Mark E. Wadsworth, Brandon D. Pickett, **Justin B. Miller**, John D. Duce, Ronald G. Munger, Christopher D. Corcoran, JoAnn T. Tschanz, Maria C. Norton, John S.K. Kauwe, Karl V. Voelkerding, Perry G. Ridge (2014). *The Variant Characterization of 211 Whole Genome Sequences: The Cache County Study on Memory Health and Aging*. The American Society of Human Genetics, San Diego, CA.

REFEREE/REVIEWER

- BMC Bioinformatics (December 2016)
- BMC Bioinformatics (December 2015)

TRAINING/CONFERENCES

- ISCB Rocky Mountain Bioinformatics Conference in Apen/Snowmass, Colorado (December, 2017)
- ISMB/ECCB *Intelligent Systems for Molecular Biology and Computational Biology* in Prague, Czech Republic (July, 2017)
- *Biotechnology and Bioinformatics Symposium* at Brigham Young University in Provo, Utah (December, 2016)
- *LDS Life Science Symposium* at Thanksgiving Point, Utah (July 2016)
- I was accepted to and participated in an extensive two week bioinformatics training program for the *Community Research Education and Engagement for Data Science* at Icahn School of Medicine at Mount Sinai in New York City, New York (June 2016).
- *Biotechnology and Bioinformatics Symposium* at Brigham Young University in Provo, Utah (December, 2015)
- *Biotechnology and Bioinformatics Symposium* at Brigham Young University in Provo, Utah (December, 2014)

COMMUNITY OUTREACH

- Science fair judge at Wasatch Elementary School (November, 2017)
- Science fair judge at Westridge Elementary School (November, 2017)
- Boy Scout leader (2016-present)