

**JUSTIN MILLER**



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**CURRICULUM VITAE**



# EDUCATION

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| Ph.D. Candidate: Brigham Young University, UT  **Bioinformatics**  **Dissertation: Uncovering the Phylogenetic History of Codon Usage Bias**  **3.95 G.P.A.**    Undergraduate: Brigham Young University, UT  Bachelor’s Degree: **Bioinformatics**  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** | 2015—Present  2010 – 2015 |
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| Three Minute Thesis BYU Life Science College 1st Place ($600)  Three Minute Thesis BYU Biology Department 1st Place ($100)  BYU Research Presentation Award ($400)  Willi Hennig Society Founder’s Award ($2,800)  Three Minute Thesis BYU Life Science College 1st Place ($600)  Three Minute Thesis BYU Biology Department 2nd Place ($50)  BYU Research Presentation Award ($400)  CREEDS travel grant (airfare + 2 weeks lodging in New York City + conference registration)  Phi Kappa Phi Membership.  Golden Key Honour Society Membership.  Phi Eta Sigma Membership.  BYU Academic Full Tuition Scholarship.  Boy Scouts of America, Eagle Scout  **WORK EXPERIENCE**  **Ph.D. student and teaching assistant in Biology Department**  Analyze the evolution of codon usage bias across the Tree of Life.  Assistant lecturer with dedicated lab office hours  Brigham Young University, Provo, UT  **Data Analyst**  **Created reports that helped generate about $5 million in revenue**  Imagine Learning, Provo, UT  **Research Assistant**  Used a variety of bioinformatics tools to analyze DNA sequences  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  Brigham Young University, Provo, UT  The Church of Jesus Christ of Latter-day Saints, Ribeirão Preto, SP, Brazil **Missionary**  Helped people with their physical and spiritual needs | February, 2018  February, 2018  October, 2017  May, 2017  February, 2017  February, 2017  September, 2016  June, 2016  Since December 2014  Since January 2013  Since February 2011  August 2010-April 2015  Since August 2006        2015 – Present  2015 – 2016  2014 – 2015  2014 – 2015  2011  2011– 2013 |

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# PUBLICATIONS

* Perry G. Ridge, Mark E. Wadsworth, **Justin B. Miller**, Andrew J. Saykin, Robert C. Green, the Alzheimer’s Disease Neuroimagining 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.

# MANUSCRIPTS UNDER REVIEW

* **Justin B. Miller**, Brandon D. Pickett, Perry G. Ridge, JustOrthologs: A Fast, Accurate, and User-Friendly Ortholog Identification Algorithm. Bioinformatics, 2018.
* **Justin B. Miller**, Lauren M. McKinnon, Michael F. Whiting, Perry G. Ridge, CAM: An alignment-free method to recover phylogenies using codon aversion motifs. PNAS, 2018.

# DRAFT MANUSCRIPTS NEARING SUBMISSION

* **Justin B. Miller**, Michael F. Whiting, Perry G. Ridge, Codon Usage Bias in Phylogenetic Systematics: A Review. 2018.
* **Justin B. Miller\***, Lauren M. McKinnon\*, Michael F. Whiting, Perry G. Ridge, Codon Pairs are phylogenetically conserved: Codon pairing as a novel phylogenetic character state for maximum parsimony and alignment-free methods. 2018.
* **Justin B. Miller\***, Logan R. Brase\*, Perry G. Ridge, ExtRamp: A novel algorithm for extracting the ramp sequence based on the tRNA adaptation index and the effective number of codons. 2018.
* **Justin B. Miller**, Michael F. Whiting, Perry G. Ridge, Congruence with the Open Tree of Life: Mapping codon usages to the Open Tree of Life shows strong phylogenetics signal in several taxonomic groups. 2018.

# 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

* Stewart Morley, **Justin Miller**, Perry Ridge, Brent Nelson (2018). Twinkle twinkle is a star; at the center of plant organelle DNA replication. Tri-Branch ASM Meeting 2018, Durango, CO.
* **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)