

# JUSTIN MILLER

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## CURRICULUM VITAE

### EDUCATION

Brigham Young University, UT  
Ph.D. Candidate **2015—present**  
Areas of Concentration: Evolution of codon bias, predictability of human DNA, Phylogenetic Analysis, Algorithm Design

Brigham Young University, UT  
Undergraduate **2010 – 2015**  
Areas of Concentration: Bioinformatics, Computer Science, Portuguese **Graduated Cum Laude with 3.91 G.P.A.**

### COMPUTER SKILLS

- Programming languages: Python, VBA, Java, C#, R, bash, C++, SQL, MATLAB, Julia
- Operating systems: MS Windows, Linux, Unix
- Applications: MS Office Suite, MS Visual Studio, Adobe Suite
- Concepts: Big Data Analysis, Machine Learning, Parallel Processing, Big O

### AWARDS AND HONORS

- Phi Kappa Phi Membership **December 2014**
- Golden Key Honour Society Membership **January 2013**
- Phi Eta Sigma Membership **February 2011**
- BYU Academic Full Tuition Scholarship **Since August 2010**
- Boy Scouts of America Eagle Scout **August 2006**

### WORK EXPERIENCE

Brigham Young University, Provo, UT **2015 – Present**  
**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

Imagine Learning, Provo, UT **2015 – 2016**  
**Data Analyst**  
Created reports that helped generate about \$5 million in revenue

Brigham Young University, Provo, UT **2014 – 2015**  
**Research Assistant**  
Used a variety of bioinformatics tools to analyze DNA sequences

Brigham Young University, Provo, UT **2014 – 2015**  
**Teaching Assistant – to Dr. Perry Ridge in “Intro to Bioinformatics”**  
Taught students needing help during office hours, passed off programming projects

The Church of Jesus Christ of Latter-day Saints, Ribeirão Preto, SP, Brazil **2011 – 2013**  
**Missionary**  
Helped people with their physical and spiritual needs

**PUBLICATIONS**

- *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 Bioinformatics, 2014.*

**ORAL PRESENTATIONS**

- **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**, 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 2015, 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 2014, 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 2014, 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 2014, San Diego, CA.*

**REFeree/REVIEWER:**

- BMC Bioinformatics (December 2015)

**TRAINING/CONFERENCES:**

- *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)

**LANGUAGES**

- English – native language
- Portuguese – 2 years living in Brazil. **ACTFL certified; Advanced Proficiency**