# Chase Joyner

O-110 Martin Hall, Box 340975
Clemson, SC 29634

chasej@g.clemson.edu
(704) 830-4730

---

**Education**

- Ph.D. in Mathematical Sciences (Statistics) (4.0/4.0) — May 2016 – Present
  Clemson University, Clemson, SC
- M.S. in Mathematical Sciences (Statistics) (4.0/4.0) — Aug 2014 – May 2016
  Clemson University, Clemson, SC
- B.S. in Mathematical Sciences (Statistics) (3.89/4.0) — Aug 2010 – 2014
  Clemson University, Clemson, SC

**Research Experience: Clemson University**

- Research Assistant sponsored by National Institute of Health — Jan 2017 – Present
  - Developed a Bayesian mixed effects model with variable selection to analyze data from any group testing algorithm while accounting for imperfect testing.
  - Analyzed a chlamydia data set out of Iowa's state hygienic laboratory.
  - Techniques used: Generalized linear models, spike and slab priors.
- Research Assistant sponsored by Biorealm, Principal Investigator — Jan 2016 – Dec 2016
  - Analyzed rice data provided from fields in Indonesia to develop a mixed effects model accounting for complex genetic similarity.
  - Modeled rice production and resistance to climate change in Indonesia.
  - Simulated data in R using Clemson's cluster to validate the model.
  - Techniques used: Expectation-Maximization algorithm, generalized linear models, and mixed effects models.
- Master's Thesis — Aug 2014 – May 2016
  - Developed univariate and multivariate Bayesian models to estimate the optimal biomarker density threshold in pooled testing of individuals for various diseases.
  - Implemented algorithms in R to estimate the parameters of these Bayesian models.
  - Techniques used: Gibbs sampling, Metropolis-Hastings, and Bayesian iteratively reweighted least squares.
- Undergraduate Thesis — Aug 2013 – Aug 2014
  - Analyzed Bayesian techniques and Markov chain Monte Carlo methods for inference.
  - Documented the implementation of these methods and ran simulations.

**Research Presentations**

- A mixed effects model for group testing data with variable selection.
  *ENAR Spring Meeting, Atlanta, GA* (Mar 2018).
- Assessing the relationship between SNPs and yield in various rice varieties.
  *Jakarta, Indonesia* (Nov 2016).
- Bayesian approach of biomarker density estimation using pooled data.
  *Clemson University* (Feb 2016).

**Publications**

- Joyner, C., McMahan, C., Tebbs, J., and Bilder, C. (2018+). From mixed effects modeling to spike and slab variable selection: A Bayesian regression model for group testing data. In preparation.

- McMahan, C., Baurley, J., Bridges, W., Joyner, C., Fitra Kacamarga, M., Lund, R., Pardamean, C., and Pardamean, B. (2017). A Bayesian hierarchical model for identifying significant polygenic effects while controlling for confounding and repeated measures. *Statistical Applications in Genetics and Molecular Biology.* 16, 407-419.

**Teaching Experience**

- BINUS University, Department of Mathematical Statistics, Jakarta, Indonesia May 2018
  - Introduction to statistics and R

- Clemson University, Departmental of Mathematical Sciences, Clemson, SC
  - MATH 1070: Differential and Integral Calculus Spring 2017
  - MATH 1040: Precalculus and Introductory Differential Calculus Fall 2016
  - MATH 1020: Introduction to Mathematical Analysis Fall 2015

**Professional Memberships**

- American Mathematical Society (AMS)

**References**

- Christopher McMahan, Clemson University. Contact: *mcmaha2@g.clemson.edu*.

- Andrew Brown, Clemson University. Contact: *ab7@g.clemson.edu*.