

# Scott Allen Funkhouser

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CONTACT INFORMATION	474 S Shaw Lane, Room 1205C East Lansing, MI 48823 Website: <a href="http://scottafunkhouser.com">http://scottafunkhouser.com</a>	Phone: 253-720-2797 Email: <a href="mailto:funkhou9@msu.edu">funkhou9@msu.edu</a>
EDUCATION	<b>Michigan State University</b> , East Lansing, MI Ph.D., Genetics and Quantitative Biology, Expected Summer 2019 <ul style="list-style-type: none"><li>• <b>Thesis Title:</b> Utilizing alternative metrics and intermediate phenotypes to understand the genetic basis for complex traits</li><li>• Advisor: Catherine Ernst, Ph.D</li></ul> <b>University of Washington</b> , Seattle, WA B.S., Biochemistry, June 2011	
RESEARCH EXPERIENCE	<b>Applying local Bayesian regressions to decipher sex-specific genetic architectures</b> Thesis Research — May 2016-Present Utilizing novel Bayesian GWA methods to discover new sex-specific effects using the UK Biobank. <ul style="list-style-type: none"><li>• Quantitative Genetics: Theory concerning population parameters.</li><li>• Statistical Genetics: Methods for inference and prediction.</li><li>• Big Data: Techniques for leveraging large sample sizes and predictors.</li></ul> <b>Determining the genetic basis of RNA editing and higher order phenotypes</b> Thesis Research — May 2015-Present Using whole genome regressions to estimate the heritability of RNA editing. <ul style="list-style-type: none"><li>• Functional genomics: Inferring loci that impact gene regulation.</li><li>• Software design: Building new bioinformatics tools.</li></ul> <b>Estimating global and local breed composition</b> Summer 2014-2016 Implementing fast methods to estimate breed composition using pig genetic data <ul style="list-style-type: none"><li>• R Package design: Design of statistical software.</li><li>• Industry experience: Collaborated with NSR, a pig breeding company</li></ul> <b>Investigated the role of a heme exporter, FLVCR, in the development of T lymphocytes</b> January 2012 - August 2013 Immunological experiments using mouse models. <ul style="list-style-type: none"><li>• Immunology: High-throughput analysis using flow cytometry.</li><li>• Mouse handling: Injections, blood draws, transplants.</li></ul> <b>Studied novel binding partners to G-Protein coupled receptors</b> 2010-2011 Undergraduate research	
AWARDS / GRANTS	<b>NSIF Graduate Student Award</b> Fall 2018 — <b>\$500</b> Prize for graduate work “Novel statistical methods using common SNPs”. <b>USDA NIFA Pre-doctoral Fellowship</b> Fall 2017 - Summer 2019 — <b>\$95,000</b> Principle Investigator for “RNA editing: discovering hidden genomic variants and investigating their function among mammalian genomes” <b>ISAG Travel Award</b> Summer 2016 — <b>\$2,000</b> <b>NSIF Graduate Student Travel Award</b> Fall 2016 — <b>\$500</b>	

**Fred and Lucille Stamper Academic College Scholarship**  
2007-2011 — **\$16,256**

MEMBERSHIPS / **ASHG Trainee Member**  
MANAGEMENT / Fall 2018 - Present  
TEACHING

**GSA Trainee Member**  
Fall 2018 - Present

**Co-organizer for the 2017 MSU Genetics Mini-symposium**  
Symposium theme: Impact and Applications of Genome Editing Technologies

**Teaching assistant for Zoology 341: Fundamentals of Genetics**  
Fall 2014

**Software Carpentry Instructor**  
Learning assistant for Software Carpentry Workshop, U Mich 2017

**Genetics Student Organization Officer**  
Fall 2014-Present

- 2017-2018: Genetics Representative for Dean's student council
- 2016 - 2017: President
- 2015 - 2016: Third-year Representative and Social Chair
- 2014 - 2015: Second-year Representative

SKILLS

**General programming**  
The R Language, C++, Bash, Fortran, Python, Java

**Web design**  
Markdown, HTML, CSS

**Bioinformatics**  
Bowtie, Tophat, Picard, SAMTools, bcftools, Variant Effect Predictor, UCSC Genome Browser

**Software development**  
Git, Github, R Studio, GNU Make

PUBLICATIONS

1. **Funkhouser SA**, Vazquez A, de los Campos G. *Applying local Bayesian regressions to decipher sex-specific genetic architectures*. In prep.
2. **Funkhouser SA**, Steibel JP, Bates RO, Raney NE, Sargolzaei M, Ernst CW. *Utility of the Affymetrix Axiom Porcine Genotyping Array for genome-wide studies*. In prep.
3. **Funkhouser SA**, Steibel JP, Bates RO, Raney NE, Schenk D, Ernst CW. *Evidence for transcriptome-wide RNA editing among *Sus scrofa* PRE-1 SINE elements*. BMC Genomics. 2017;18: 360. doi:10.1186/s12864-017-3766-7
4. **Funkhouser SA**, Bates RO, Ernst CW, Newcom D, Steibel JP. *Estimation of genome-wide and locus-specific breed composition in pigs*. Trans Anim Sci. 2017. doi:10.2527/tas2016.0003
5. Zhao D, Hamilton JP, Hardigan M, Yin D, He T, Vaillancourt B, Reynoso M, **Funkhouser SA** et al. *Analysis of ribosome-associated mRNAs in rice reveals the importance of transcript size and GC content in translation*. G3 (Bethesda). 2016;7: 203219. doi:10.1534/g3.116.0360
6. Philip M, **Funkhouser SA**, Chiu EY, Phelps SR, Delrow JJ, Cox J, et al. *Heme Exporter FLVCR Is Required for T Cell Development and Peripheral Survival*. J Immunol. 2015. doi:10.4049/jimmunol.1402172

CONFERENCE  
PRESENTATIONS /  
POSTERS

1. **Funkhouser SA.** *Frameworks for utilizing common SNPs: Estimating breed composition and genetic effect heterogeneity.* 2018. Oral presentation given at the NSIF Meeting as the recipient of the 2018 NSIF Graduate Student Award.
2. **Funkhouser SA,** de los Campos G. 2018. *Deciphering sex-specific genetic architectures using Bayesian methods.* Poster presented at the ASHG Annual Meeting.
3. **Funkhouser SA,** de los Campos G. 2018. *Mapping sex differences using local Bayesian regressions.* Oral presentation given at the MSU Institute for Quantitative Health Sciences Retreat.
4. **Funkhouser SA,** de los Campos G. 2018. *Deciphering sex-specific genetic architectures using Bayesian methods.* Poster presented at the 2018 GSA Population, Evolution, and Quantitative Genetics Conference.
5. **Funkhouser SA,** Steibel JP, Bates RO, Raney NE, Ernst CW. 2017. *Evidence for transcriptome-wide RNA editing among *Sus scrofa* PRE-1 SINE elements.* 2017. Poster presented at the Gordon Conference on RNA Editing.
6. **Funkhosuer SA,** Bates RO, CW Ernst, Newcom D, Steibel JP. 2016. *Estimation of the composition of four U.S. swine breeds using genomic data.* ePoster presented at the ASDA/AAS Joint Annual Meeting.
7. **Funkhouser SA,** Steibel JP, Bates RO, Raney NE, Ernst CW. 2016. *RNA editing in swine is associated with PRE-1 retrotransposons.* ePoster presented at the 2016 International Society for Animal Genetics Conference.
8. **Funkhouser SA,** Steibel JP, Bates RO, Raney NE, Ernst CW. 2015. *Evidence of RNA editing in pig longissimus dorsi muscle.* Oral presentation given at the American Dairy Science / American Society of Animal Science Midwest Conference.