






# Brandon Monier

Curriculum Vitae  
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## Education

- 2018 **Ph.D. Department of Biology and Microbiology**  
South Dakota State University
- 2013 **M.S. Department of Agronomy, Horticulture and Plant Science**  
South Dakota State University
- 2008 **B.S. Microbiology**  
South Dakota State University

## Research Experience

**Cornell University** | Postdoc | 2018-2023

- **Advisor** Edward Buckler
- **Delivered:**
  - Worked with research institutions across African, Caribbean, Latin, and North American countries to develop cloud computing infrastructure and breeding pipelines leveraging gene activity predictors for sorghum, cow-pea, cassava, rice, and maize.
  - Created R packages to interface TASSEL and practical haplotype graph software with the R programming language.
  - Developed methods to efficiently evaluate 1.8 million gene models across 26 diverse maize assemblies. This involved assembling the gene space of ca. 400 grass species in the Andropogoneae tribe and aligning it to maize. Using this data, I helped lead a highly collaborative team to develop a series of machine learning models to predict if a gene model was to produce a functional protein by analyzing the structural characteristics of aligned transcripts.
  - Created methods and pipelines for both genome- and transcriptome-wide association studies to evaluate water use efficiency and photosynthetic traits in sorghum bioenergy panels.
  - Designed a database that efficiently stores and queries ca. 1 billion genome-wide association study results in maize leveraging graph theory and data structures for semantic querying and evaluation. This was used to evaluate the biological relevance in pleiotropy and the effect of variation in upstream open reading frames on protein abundance in maize.

**South Dakota State University** | Visiting Scholar | 2017-2018

- **Advisor** Qin Ma
- **Delivered:**
  - Created a web server for cloud-based expression data analysis leveraging the Shiny framework, Javascript, and commonly used bioinformatic libraries.
  - Developed an R package to generate rapid, information-rich visualizations for the interpretation of differential gene expression results from multiple widely-used libraries for RNA-seq analysis.

**South Dakota State University** | Graduate Research Assistant | 2013-2018

- **Advisors** Heike Bücking and Jose Gonzalez-Hernandez
- **Delivered**
  - Examined the variability of microbial community structures across next generation lignocellulosic feedstocks in the Upper Midwest regions of the United States. This was accomplished by implementing high-throughput amplicon sequencing and metagenomics approaches.
  - Conducted RNA-seq analyses to determine the effect of arbuscular mycorrhiza on differential expression in prairie cordgrass, switchgrass, and *Brachypodium distachyon* under varying nutrient conditions.
  - Investigated the impact of arbuscular mycorrhizal communities on lignocellulosic feedstock biomass production under varying nutrient supply conditions. This was conducted through evaluations at both the greenhouse and field level.

**South Dakota State University** | Graduate Research Assistant | 2009-2013

- **Advisor** Jose Gonzalez-Hernandez
- **Delivered:**
  - Helped establish a germplasm collection of the potential bioenergy crop, prairie cordgrass. Samples were collected from across the Midwest region of the United States. From this collection, I analyzed cytotypic variation through flow cytometry.
  - Created the first bacterial artificial chromosome library and protocols for prairie cordgrass.

## Publications

### In preparation

1. Vath, R. L., B., F. S., Monier, B., Głowacka, K., Pederson, T. L., Bernacchi, C. J., Ferguson, J., & Kromdijk, J. (n.d.). *Revealing the genetic architecture of nonphotochemical quenching in sorghum through high-throughput screening of dynamic photoprotection.*

### Research Articles

1. Khaipho-Burch, M., Ferebee, T., Giri, A., Ramstein, G., Monier, B., Yi, E., Romain, M. C., & Buckler, E. S. (2023). Elucidating the patterns of pleiotropy and its biological relevance in maize. *PLOS Genetics*, 19(3), 1–28. <https://doi.org/10.1371/journal.pgen.1010664>
2. Sun, X., Xiang, Y., Dou, N., Zhang, H., Pei, S., Franco, A. V., Menon, M., Monier, B., Ferebee, T., Liu, T., Liu, S., Gao, Y., Wang, J., Terzaghi, W., Yan, J., Hearne, S., Li, L., & Li, M., Fengand Dai. (2023). The role of transposon inverted repeats in balancing drought tolerance and yield-related traits in maize. *Nature Biotechnology*, 41(1), 120–127. <https://doi.org/10.1038/s41587-022-01470-4>
3. Monier, B., Casstevens, T. M., Bradbury, P. J., & Buckler, E. S. (2022). rTASSEL: An r interface to TASSEL for analyzing genomic diversity. *Journal of Open Source Software*, 7(76), 4530. <https://doi.org/10.21105/joss.04530>
4. Bradbury, P. J., Casstevens, T., Jensen, S. E., Johnson, L. C., Miller, Z. R., Monier, B., Romain, M. C., Song, B., & Buckler, E. S. (2022). The Practical Haplotype Graph, a platform for storing and using pangenomes for imputation. *Bioinformatics*, 38(15), 3698–3702. <https://doi.org/10.1093/bioinformatics/btac410>
5. Gage, J. L., Mali, S., McLoughlin, F., Khaipho-Burch, M., Monier, B., Bailey-Serres, J., Vierstra, R. D., & Buckler, E. S. (2022). Variation in upstream open reading frames contributes to allelic diversity in protein abundance. *Proceedings of the National Academy of Sciences*. <https://doi.org/10.1073/pnas.2112516119>
6. Ferguson, J. N., Fernandes, S. B., Monier, B., Miller, N. D., Allen, D., Dmitrieva, A., Schumaker, P., Lozano, R., Val-luru, R., Buckler, E. S., Gore, M. A., Brown, P. J., Spalding, E. P., & Leakey, A. D. (2021). Machine learning-enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions. *Plant Physiology*, 187(3), 1481–1500. <https://doi.org/10.1093/plphys/kiab346>
7. Gage, J. L., Monier, B., Giri, A., & Buckler, E. S. (2020). Ten years of the maize nested association mapping population: Impact, limitations, and future directions. *The Plant Cell*, 32(7), 2083–2093. <https://doi.org/10.1105/tpc.19.00951>
8. Monier, B., McDermaid, A., Wang, C., Zhao, J., Miller, A., Fennell, A., & Ma, Q. (2019). IRIS-EDA: An integrated RNA-seq interpretation system for gene expression data analysis. *PLoS Computational Biology*, 15(2), e1006792. <https://doi.org/10.1371/journal.pcbi.1006792>
9. McDermaid, A., Monier, B., Zhao, J., Liu, B., & Ma, Q. (2019). Interpretation of differential gene expression results of RNA-seq data: Review and integration. *Briefings in Bioinformatics*, 20(6), 2044–2054. <https://doi.org/10.1093/bib/bby067>
10. Monier, B., McDermaid, A., Zhao, J., Fennell, A., & Ma, Q. (2018). IRIS-DGE: An integrated RNA-seq data analysis and interpretation system for differential gene expression. *bioRxiv*, 283341. <https://doi.org/10.1101/283341>
11. McDermaid, A., Monier, B., Zhao, J., & Ma, Q. (2018). ViDGER: An r package for integrative interpretation of differential gene expression results of RNA-seq data. *bioRxiv*, 268896. <https://doi.org/10.1101/268896>

### Book Chapters

1. Monier, B., Peta, V., Mensah, J., & Bücking, H. (2017). Inter- and intraspecific fungal diversity in the arbuscular mycorrhizal symbiosis. In *Mycorrhiza-Function, Diversity, State of the Art* (pp. 253–274). Springer, Cham. [https://doi.org/10.1007/978-3-319-53064-2\\_12](https://doi.org/10.1007/978-3-319-53064-2_12)

### PhD Dissertation

1. Monier, B. (2018). *Microbial communities and their impact on bioenergy crops in dynamic environments* [PhD thesis, South Dakota State University]. <https://openprairie.sdstate.edu/etd/2659>

### Master's Thesis

1. Monier, B. (2013). *The analysis of cytotypic variation and construction of a BAC library of midwestern prairie cordgrass (spartina pectinata link) genotypes* [Master's thesis, South Dakota State University]. <https://openprairie.sdstate.edu/etd/1624>

## Software

### R Packages

1. Monier, B. (2023). *MGJars: An r package for distributing TASSEL and PHG API libraries* (Version 0.0.3) [Computer software]. <https://github.com/maize-genetics/MGJars>
2. Monier, B., Casstevens, T. M., Bradbury, P. J., & Buckler, E. S. (2022). *rTASSEL: An r-based front-end for TASSEL interactivity* (Version 0.9.29) [Computer software]. <https://maize-genetics.github.io/rTASSEL/>
3. Monier, B., Bradbury, P. J., Casstevens, T. M., Jannick, J.-L., & Buckler, E. S. (2022). *rPHG: An r-based front-end for the practical haplotype graph* (Version 0.1.14) [Computer software]. <https://maize-genetics.github.io/rPHG/>
4. Monier, B. (2019). *ask4r: R methods for querying askDB* (Version 0.1.3) [Computer software]. <https://bitbucket.org/bucklerlab/ask4r/src/master/>
5. Yu, Z., Ma, A., Monier, B., & Ma, Q. (2019). *BRIC: A novel biclustering method for detecting gene regulatory signals (GRSs) within single cells* (Version 1.0) [Computer software]. <https://github.com/OSU-BMBL/BRIC>
6. Monier, B., McDermaid, A., Zhao, J., & Ma, Q. (2018). *vidger: Create rapid visualizations of RNASeq data in r* (Version 1.20) [Computer software]. <https://bioconductor.org/packages/release/bioc/html/vidger.html>
7. Monier, B. (2017). *ggDESeq: A visualization suite for DESeq related data frames that implements ggplot2 aesthetics* (Version 1.0) [Computer software]. <https://github.com/btmonier/ggDESeq>

### Web Applications and Databases

1. Monier, B. (2020). *Biokotlin Playground: A compiler server for showcasing BioKotlin API in HTML code blocks* (Version 0.1) [Computer software]. [https://bitbucket.org/bucklerlab/biokotlin\\_compiler\\_server/src/master/](https://bitbucket.org/bucklerlab/biokotlin_compiler_server/src/master/)
2. Monier, B. (2020). *askDB: Andropogoneae systems knowledge DataBase* (Version 0.1) [Computer software]. <https://bitbucket.org/bucklerlab/askdb/src/master/>
3. Monier, B., McDermaid, A., Wang, C., Zhao, J., Miller, A., Fennell, A., & Ma, Q. (2019). *IRIS-EDA: Integrated RNA-seq data analysis and interpretation system* (Version 1.0) [Computer software]. <https://bmbis.bmi.osumc.edu/IRIS/>

### Kotlin

1. Casstevens, T. M., Lynn, J., Miller, Z., Monier, B., Morse, J., Gupta, V., Bradbury, P. J., & Buckler, E. S. (2020). *BioKotlin: A high performance bioinformatics library written in kotlin* (Version 0.6) [Computer software]. <https://www.biokotlin.org/>

### Perl

1. Monier, B. (2018). *PerlSeq: Perl routines for common bioinformatics tasks with FASTA data* (Version 0.1) [Computer software]. <https://github.com/btmonier/perlseq>

## Teaching and Outreach

- 2023 | **Taught two in-person classes** as part of the *Thomas Wyatt Turner Lecture Series* to 7 students at Cornell University. These classes covered the R programming language and how we can use this for the biological sciences.
- 2022 | **Taught two in-person workshops** as part of the *Feed the Future Innovation Lab for Crop Improvement (ILCI) Annual Meeting* to 22 researchers in Senegal. These workshops entailed an overview of cloud computing infrastructure developed for the ILCI program along with an intro to the R package, rTASSEL.
- 2022 | **Taught three virtual workshops** as part of the *Feed the Future Innovation Lab for Crop Improvement (ILCI) JupyterHub Workshop* to 26 researchers at centers across Africa, Latin America, and the Caribbean Islands. These workshops entailed an overview of cloud computing methods, computational notebooks, and an introductory course for data analyses in R.
- 2020 | **Guest lectured one virtual class** as part of a *Computational Biology* class to 25 graduate students at Cornell University. For this class, I gave an overview of topics in machine learning and how the Buckler Lab applies these to current research. This also included running example models to predict transcription factor binding and expression for biologically relevant data.
- 2019 | **Taught one in-person workshop** as part of the *Workshop on Cereal Genomics* to xx researchers at Cold Spring Harbor Laboratories. During this workshop, I aided in the lecture and walkthrough of the rTASSEL software and how this can be applied to genome-wide association models.
- 2019 | **Taught a week long in-person workshop** as part of the *Wheat Coordinated Agriculture Project (CAP) Workshop* to xx researchers at Cornell University. During this workshop, I aided in the lecture and walkthrough of the Practical Haplotype Graph Software and R package (rPHG) developed in the Buckler Lab.
- 2018 | **Graduate Teaching Assistant** for *Plant Physiology*. The assistantship entailed teaching three lab sections to a total of xx students at South Dakota State University, creating lab materials (quizzes, lectures, slides), overseeing lab group research projects, and grading exams and reports.

- 2016 | **Graduate Teaching Assistant** for *General Biology II*. The assistantship entailed teaching three lab sections to a total of xx students at South Dakota State University, creating lab materials (quizzes, lectures, slides), facilitating anatomical dissections, and grading exams and reports.
- 2015 | **Graduate Teaching Assistant** for *General Botany II*. The assistantship entailed teaching four lab sections to a total of xx students at South Dakota State University, creating lab materials (quizzes, lectures, slides), running experiments, facilitating tree and plant tours, and grading exams.
- 2014 - 2017 | **Graduate Teaching Assistant** for *General Biology I*. The assistantship entailed teaching 3 lab sections to a total of xx students over four years at South Dakota State University. In this class, I created lab materials (quizzes, lectures, slides), prepared and facilitated lab experiments, and graded exams and reports.
- 2011 | **Graduate Teaching Assistant** for *Diseases of Field Crops*. The assistantship entailed teaching 1 lab section to a total of xx students at South Dakota State University, preparing lab work stations for assignments and examinations. Additionally, I graded quizzes and exams.

## Skills

### Programming languages

Bash, C++, Java, Javascript, Kotlin, Lua, Perl, Python, and R.

### Web Development and Database Systems

HTML/CSS, Node.js, Shiny, React.js, Cypher/Neo4j, and SQL/mysql

### Machine Learning

Keras, Scikit-learn, and TensorFlow

### Reporting

Google Colab, Jupyter,  $\LaTeX$ , and Markdown

### Cloud Computing Services

Cornell High Performance Computing Services, Digital Ocean, and Heroku

### Quantitative Genetics and Bioinformatics

Association mapping (using mixed linear models, general linear models, matrix eQTL), genomic prediction (SNPs, RNA expression), imputation (Beagle, Practical Haplotype Graph), RNA and DNA sequence analysis and alignment, genome assembly and annotation, and metagenomics.

### Molecular experience

DNA and RNA extraction, PCR techniques (standard and quantitative real time), gel electrophoresis techniques (standard, PAGE, pulsed-field, and denaturing gradient), primer design, plasmid construction, bacterial artificial chromosome library construction, flow cytometry, and microscopy.

### Management and Mentoring

- Mentored 8 graduate and undergraduate students:
  - April DeMell, undergraduate (3 months, full-time), South Dakota State University, 2016
  - Clarissa Mercado, undergraduate (3 months, full-time), South Dakota State University, 2016
  - Jerry Cordero Sepulvéda, undergraduate (3 months, full-time) South Dakota State University, 2015
  - Winly Mai, undergraduate (3 months, full-time), South Dakota State University, 2015
  - Merritt Burch, undergraduate (3 months, full-time), South Dakota State University, 2014
  - Sabrina Bushlack, undergraduate (3 months, full-time), South Dakota State University, 2013
  - Linh Anh Cat, undergraduate (3 months, full-time), South Dakota State University, 2013
  - Vincent Peta, graduate (~9 months, full-time), South Dakota State University, 2013-2014
- Certified in a course called *Postdoc Leadership Program* sponsored by the Office of Postdoctoral Studies at Cornell University.

## Presentations

### Posters

1. Johnson, L. C., Agosto-Perez, F. J., Bradbury, P. J., Casstevens, T. M., Econopoulou, B. F., R., M. Z., Monier, B., Morse, J., Wiese, M., & Buckler, E. S. (2023). *Breeder genomics hub: A hub full of tools for analyzing genomic data*. Advances in Genome Biology; Technology Meeting, San Antonio, Texas.
2. Berthel, A., Bradbury, P. J., Casstevens, T. M., Econopoulou, B. F., Long, E., Johnson, L. C., Miller, Z. R., Monier, B., Romy, C. M., Song, B., Wiese, M., & Buckler, E. S. (2023). *The practical haplotype graph: A graph-based approach for imputing genotypes*. Advances in Genome Biology; Technology Meeting, San Antonio, Texas.

3. Hale, C. O., AuBuchon-Elder, T., Casstevens, T. M., Costa-Neto, G., Hsu, S.-K., Hufford, M. B., Johnson, L. C., Kellogg, E. A., La, T., Miller, Z. R., Monier, B., Romain, M. C., Schulz, A. J., Arun, S., & Buckler, E. S. (2023). *Characterizing cis-regulatory evolution at scale across hundreds of wild grass species*. Maize Genetics Meeting, St. Louis, Missouri.
4. Monier, B., Econopoulou, B. F., Casstevens, T. M., Agosto-Perez, F. J., Bradbury, P. J., Robbins, K. R., & Buckler, E. S. (2023). *Cloudifying reproducible breeding pipelines: Integrating TASSEL and the PHG with R and JupyterHub*. Maize Genetics Meeting, St. Louis, Missouri.
5. Monier, B., Econopoulou, B. F., Casstevens, T. M., Agosto-Perez, F. J., Bradbury, P. J., & Buckler, E. S. (2022). *Cloudifying reproducible genetic analyses: Integrating TASSEL and R with JupyterHub*. Crops Conference, Huntsville, Alabama.
6. Gage, J. L., Sujana, M., Fionn, M., Khaipho-Burch, M., Monier, B., Bailey-Seres, J., Vierstra, R. D., & Buckler, E. S. (2022). *Variation in upstream open reading frames contributes to allelic diversity in protein abundance*. Maize Genetics Meeting, St. Louis, Missouri.
7. Schulz, A. J., Long, E., Miller, Z. R., AuBuchon-Elder, T., Kellogg, E. A., La, T., Romain, M. C., Buckler, E. S., & Monier, B. (2022). *101 evolutions: Evaluating maize gene annotations with genome sequences across the andropogoneae*. Maize Genetics Meeting, St. Louis, Missouri.
8. Khaipho-Burch, M. B., Giri, A., Ramstein, Guillaume, Monier, B., Romain, M. C., & Buckler, E. S. (2021). *Elucidating the extent of pleiotropy in maize and its functional relevance towards trait prediction*. Maize Genetics Meeting, St. Louis, Missouri.
9. Bradbury, P. J., Casstevens, T. M., Jensen, S., Johnson, L. C., Miller, Z. R., Monier, B., Romain, S., M. C., & Buckler, E. S. (2021). *The maize PHG - a practical haplotype graph*. Maize Genetics Meeting, St. Louis, Missouri.
10. Monier, B., Casstevens, T. M., Bradbury, P. J., & S., B. E. (2021). *rTASSEL: An R interface to TASSEL for association mapping of complex traits*. Maize Genetics Meeting, St. Louis, Missouri.
11. Monier, B., Valluru, R., Casstevens, T. M., & S., B. E. (2019). *The development of computational resources for association studies in maize and sorghum*. Maize Genetics Meeting, St. Louis, Missouri.
12. Monier, B., DeMell, A., Khaipho-Burch, M., Gonzalez-Hernandez, J., & Bücking, H. (2017). *Impact of arbuscular mycorrhizal communities on the biomass production of prairie cordgrass – a potential bioenergy crop*. International Conference on Mycorrhiza, Prague, Czech Republic.
13. Monier, B., Gonzalez-Hernandez, J., & Bücking, H. (2017). *Transcriptome analysis of a model grass species reveals differential gene expression in arbuscular mycorrhizal symbiosis*. Day of Scholars, Brookings, South Dakota.
14. DeMell, A., Monier, B., Peta, V., & Bücking, H. (2016). *Influence of arbuscular mycorrhizal interactions on biomass and nutrient uptake in spartina pectinata*. SD EPSCor Research Symposium, Pierre, South Dakota.
15. Cordero-Sepulveda, J., Mai, W., Monier, B., Peta, V., & Bücking, H. (2016). *Optimizing biomass production in spartina pectinata through arbuscular mycorrhizal symbiosis*. SD EPSCor Research Symposium, Pierre, South Dakota.
16. Monier, B., Gonzalez-Hernandez, J., & Bücking, H. (2014). *Plant-microbe interactions show benefits for bioenergy crops*. American Society for Microbiology North Central Branch Meeting, Superior, Wisconsin.
17. Khaipho-Burch, M., Monier, B., Gonzalez-Hernandez, J., & Bücking, H. (2014). *Plant-microbe interactions affect biomass production of spartina pectinata, a potential bioenergy crop*. Sanford Undergraduate Research Symposium, Sioux Falls, South Dakota.
18. Khaipho-Burch, M., Monier, B., Gonzalez-Hernandez, J., & Bücking, H. (2014). *Plant-microbe interactions affect biomass production of spartina pectinata, a potential bioenergy crop*. SD EPSCor Research Symposium, Pierre, South Dakota.
19. Cat, L. A., Bushlack, S., Monier, B., & Bücking, H. (2013). *Mycorrhizae and biofuel crop yield: Variation in prairie cordgrass genotypes*. SD EPSCor Research Symposium, Pierre, South Dakota.
20. Monier, B., Gonzalez-Hernandez, J., Boe, A., Owens, V., & Stein, J. (2011). *Construction of a prairie cordgrass (S. Pectinata) BAC library*. Plant; Animal Genome Conference.

## Talks

1. Schulz, A. J., Hsu, S.-K., Wrightsman, T., Zhai, J., Miller, Z. R., AuBuchon-Elder, T., Kellogg, E. A., Seetharam, A., Hufford, M. B., La, T., Romain, M. C., Buckler, E. S., & Monier, B. (2023). *reelGene: Fishing for good gene models with evolution and machine learning*. Maize Genetics Meeting, St. Louis, Missouri.
2. Schulz, A. J., Hsu, S.-K., Wrightsman, T., Romain, M. C., La, T., Miller, Z. R., AuBuchon-Elder, T., Kellogg, E. A., Hufford, M. B., Seetharam, A., S., B. E., & Monier, B. (2022). *reelGene: A pipeline for robust evaluation through evolutionary leverage of gene models*. Zeaevolution Meeting, Ithaca, New York.

3. Schulz, A. J., Long, E., Miller, Z. R., AuBuchon-Elder, T., Kellogg, E. A., La, T., Romay, M. C., Buckler, E. S., & Monier, B. (2022). *101 evolutions: Evaluating maize gene annotations with genome sequences across the andropogoneae*. Crops Conference, Huntsville, Alabama.
4. Bradbury, P. J., Miller, Z. R., Johnson, L. C., Monier, B., & S., B. E. (2021). *The PHG as a web service*. Zeaevolution Meeting, Ithaca, New York.
5. Monier, B., Valluru, R., Casstevens, T. M., & S., B. E. (2019). *The development of computational resources for association studies in maize*. Zeaevolution Meeting, Ithaca, New York.
6. Monier, B. (2017). *Microbial communities and their impact on bioenergy crops in dynamic environments*. Life Science Seminar Series, Brookings, South Dakota.
7. Monier, B., Gonzalez-Hernandez, J., & Bücking, H. (2016). *An ancient accord between plants and fungi spells prosperity for bioenergy crops*. American Society of Plant Biologists Midwest Section Conference, Brookings, South Dakota.
8. Bücking, Heike, Gonzalez-Hernandez, J., E., L., & Monier, B. (2014). *Beneficial plant microbe interactions and their potential application to increase biomass production and environmental sustainability of prairie cordgrass*. North Central Regional Sun Grant Center Meeting, Brookings, South Dakota.