
CONTACT INFORMATION	Biological Sciences 2901 Main Street Lubbock, TX 79409 806-834-5750 (office)	Texas Tech University matt.johnson@ttu.edu website: mossmatters.com
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EDUCATION	Ph.D. Duke University, Durham, NC	May, 2013
	Dissertation: “Evolution of Mating Systems in <i>Sphagnum</i> peatmosses”	

	B.S. with distinction , Duke University, Durham, NC	May 2006
	Honors Thesis: “Genetic relationships within <i>Sphagnum cribrosum</i> Lind. “wave form” and “normal form” in southeastern North Carolina using three anonymous nuclear genes.”	

PROFESSIONAL APPOINTMENTS	Assistant Professor Biological Sciences Texas Tech University	September 2017 to present
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	Director E.L. Reed Herbarium (TTC)	September 2017 to present
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	Postdoctoral Research Associate Plant Science and Conservation Research Center Chicago Botanic Garden Supervisor: Norman Wickett, Ph.D	June 2013 to August 2017
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PUBLICATIONS	Journal Articles (30 total, 10 first-author, 1 last-author) Google Scholar Profile
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1. Ribeiro, C. L., Conde, D., Balmant, K. M., Dervinis, C., **Johnson, M. G.**, McGrath, A. P., Szewczyk, P., Unda, F., Finegan, C. A., Schmidt, H. W., Miles, B., Drost, D. R., Novaes, E., Gonzalez-Benecke, C. A., Peter, G. F., Burleigh, J. G., Martin, T. A., Mansfield, S. D., Chang, G., Wickett, N. J. Kirst, M. (2020). The uncharacterized gene EVE contributes to vessel element dimensions in *Populus*. *Proceedings of the National Academy of Sciences of the United States of America*, 117(9), 5059–5066. doi:10.1073/pnas.1912434117
2. H. Hale, E.M. Gardner, J. Viruel, L. Pokorny, and **M.G. Johnson**. 2020. Strategies for reducing per-sample costs in target capture sequencing for phylogenomics and population genomics in plants. Invited Special Issue: *Low-cost methods in plant sciences Applications in Plant Sciences* e11337. doi:10.1002/aps3.11337.
3. A. Ghosh, **M.G. Johnson**, A.B. Osmanski, S. Louha, N.J. Bayona-Vasquez, T.C. Glenn, J. Gonorga, R.E. Green, S. Isberg, R.D. Stevens, and D.A. Ray. 2020. A high-quality reference genome assembly of the saltwater crocodile, *Crocodylus porosus*, reveals patterns of selection in Crocodylidae. *Genome Biology and Evolution* 12(1), 3635–3646. doi:10.1093/gbe/evz269.
4. S. Dodsworth[†], L. Pokorny[†], **M.G. Johnson[†]**, J.T. Kim, O. Maurin, N.J. Wickett, F. Forrest, and W.J. Baker. 2019. Hyb-Seq for Flowering Plant Systematics. *Trends in Plant Science* doi:10.1016/j.tplants.2019.07.011

5. R. Medina, **M.G. Johnson**, Y. Liu, N. Wickett, A.J. Shaw, and B. Goffinet. Phylogenomic delineation of Physcomitrium (Bryophyta: Funariaceae) based on targeted sequencing of nuclear exons and their flanking regions rejects the retention of Physcomitrella, Physcomitridium and Aphanorrhegma. *J. Systematics and Evolution* 57(4): 404-417. doi:10.1111/jse.12516
6. Y. Liu[†], **M.G. Johnson**[†], C.J. Cox, R. Medina, N. Devos, A. Vanderpoorten, L. Hedenas, N. Bell, J.R. Shevock, B. Aguero, D. Quandt, N.J. Wickett, A.J. Shaw, and B. Goffinet. 2019. Resolution of the ordinal phylogeny of mosses using targeted exons from organellar and nuclear genomes. *Nature Communications* 10, Article number: 1485. doi:10.1038/s41467-019-09454-w
7. **M.G. Johnson**[†], L. Pokorny[†], S. Dodsworth[†], L.R. Botigue, R.S. Cowan, A. Devault, W.L. Eiserhardt, N. Epiawalage, F. Forest, J.T. Kim, J.H. Leebens-Mack, I.J. Leitch, O. Maurin, D.E. Soltis, P.S. Soltis, G.K. Wong, W.J. Baker, and N.J. Wickett. A Universal Probe Set for Targeted Sequencing of 353 Nuclear Genes from Any Flowering Plant Designed Using k-medoids Clustering. *Systematic Biology* 68(5): 594-606. doi:10.1093/sysbio/syy086
8. T. Villaverde, L. Pokorny, S. Olson, M. Rincon, **M.G. Johnson**, E.G. Gardner, N.J. Wickett, J. Molero, R. Riina, and I. Sanmartin. 2018. Bridging the micro-macro evolutionary gap: target sequencing with chloroplast skimming resolves phylogenetic relationships within the Rand Flora *Euphorbia balsamifera*. *New Phytologist* 220:636-650. doi:10.1111/nph.15312
9. K. LaRicca, **M.G. Johnson**, E.G. Gardner, D. Ragone, N. Zyrega, and N.J. Wickett. 2018. A transcriptome screen for positive selection in domesticated breadfruit and its wild relatives (*Artocarpus* spp.). *American Journal of Botany* 105(5): 915-926. doi:10.1002/ajb2.1095
10. P.G. Wolf, T.A. Robison, **M.G. Johnson**, M.A. Sundue, W.L. Testo, and C.J. Rothfels. 2018. Target Sequence Capture of Nuclear-Encoded Genes for Phylogenetic Analysis in Ferns *Applications in Plant Science* e01148. doi:10.1002/aps3.1148
11. H.R. Kates[†], **M.G. Johnson**[†], E.G. Gardner, N. Zyrega, and N.J. Wickett. 2018. Allele phasing has minimal impact on phylogenetic reconstruction from targeted nuclear gene sequences in a case study of *Artocarpus* (Moraceae) *American Journal of Botany* 105(3):404-416 *Invited Special Issue: Using and Navigating the Plant Tree of Life* doi:10.1002/ajb2.1068
12. M.R. McKain[†], **M.G. Johnson**[†], S. Uribe-Convers[†], D. Eaton[†], and Y. Yang. 2018[†]. Practical considerations for plant phylogenomics. *Applications in Plant Sciences* 6(3):e01038. *Invited Special Issue: Methods for Exploring the Plant Tree of Life* doi:10.1002/aps3.1038
13. R. Medina, **M.G. Johnson**, Y. Liu, N. Wilding, T.A. Hedderson, N.J. Wickett, and B. Goffinet. 2018. Evolutionary Dynamism in Bryophytes: Phylogenomic Inferences Confirm Rapid Radiation in the Moss Family Funariaceae. *Molecular Phylogenetics and Evolution* 120:240-247. doi:10.1016/j.ympev.2017.12.002.
14. D.J. Weston, M.R. Turetsky, **M.G. Johnson**, G. Granath, Z. Lindo, L.R. Belyea, S.K. Rice, D.T. Hanson, K.A.M. Engelhardt, J. Schmutz, E. Dorrepaal, E.S. Euskirchen, H.K. Stenoiien, P. Szovenyi, M. Jackson B.T. Piatkowski, W. Muchero, R.J. Norby, J.E. Kostka, J.B. Glass, H. Rydin, J. Limpens, E. Tuittila, K.K. Ulrich, A. Carrell, B.W. Benscoter, J. Chen, T.A. Oke, M.B. Nilsson, P. Ranjan, D. Jacobson, E.A. Lileskov, R.S. Clymo, and A.J. Shaw. 2018. The Sphagnum Project: Enabling Ecological and Evolutionary Insights through a Genus-Level Sequencing Project. *New Phytologist* 217 (1):16-25.

15. **M.G. Johnson**, E.M. Gardner, Y. Liu, R. Medina, B. Goffinet, A.J. Shaw, N.J.C. Zerega, and N.J. Wickett. 2016. HybPiper: Extracting coding sequence and introns for phylogenetics from high-throughput sequencing reads using target enrichment. *Applications in Plant Sciences*. 4(7):1600016 doi:10.3732/apps.1600016.
16. E.M. Gardner, **M.G. Johnson**, D. Ragone, N.J. Wickett, and N.J.C. Zerega. 2016. Low-coverage, whole-genome sequencing of *Artocarpus camansi* (Moraceae) for phylogenetic marker development and gene discovery. *Applications in Plant Sciences* 4(7):1600017. doi:10.3732/apps.1600017.
17. N. Brandley, **M.G. Johnson**, and S. Johnsen. 2016. Aposematic signals in North American black widows are more conspicuous to predators than to prey. *Behavioral Ecology*. 27(4):1104-1112. doi:10.1093/beheco/arw014
18. **M.G. Johnson** and A.J. Shaw. 2016. The effects of quantitative fecundity in the haploid stage on reproductive success and diploid fitness in the aquatic peat moss *Sphagnum macrophyllum*. *Heredity*. 116:523-530. doi:10.1038/hdy.2016.13.
19. **M.G. Johnson**, C. Malley, A.J. Shaw, B. Goffinet, and N.J. Wickett. 2016. A phylotranscriptomic analysis of gene family expansion and evolution in the largest order of pleurocarpous mosses (Hypnales, Bryophyta). *Molecular Phylogenetics and Evolution*. 98:29-40. doi:10.1016/j.ympev.2016.01.008
20. N. Devos, P. Szovenyi, D. Weston, C. Rothfels, **M.G. Johnson**, and A.J. Shaw. 2016. Analyses of transcriptome sequences reveal multiple ancient large-scale duplication events in the ancestor of Sphagnopsida (Bryophyta). *New Phytologist* 211(1):300-318. doi:10.1111/nph.13887.
21. **M.G. Johnson**, K. Lang, P. Manos, G.H. Golet, and K.A. Schierenbeck. 2016. Evidence for genetic pollution of a California native tree, *Platanus racemosa*, via recent, ongoing introgressive hybridization with an introduced ornamental species." *Conservation Genetics*. 17(3):593-602. doi:10.1007/s10592-015-0808-z.
22. **M.G. Johnson** and A.J. Shaw. 2015. Genetic diversity, sexual condition, and microhabitat preference determine mating patterns in *Sphagnum* (Sphagnaceae) peat-mosses. *Biological Journal of the Linnean Society*. 115(1):96-113. doi:10.1111/bij.12497
23. **M.G. Johnson**, G. Granath, T. Tahvanainen, R. Pouliot, H. Stenoien, L. Rochefort, H. Rydin, and A.J. Shaw. 2015. Evolution of niche preference in *Sphagnum* peat mosses" *Evolution*. 69(1) 90-103. doi:10.1111/evo.12547
24. E. Mikulaskova, M. Hajek, A. Veleba, **M.G. Johnson**, T. Tomas, and A.J. Shaw. 2015. Local adaptations in bryophytes revisited: the genetic structure of the calcium-tolerant peatmoss *Sphagnum warnstorffii* along geographic and pH gradients. *Ecology and Evolution*. 5(1) 229-242. doi:10.1002/ece3.1351
25. A.J. Shaw, B. Shaw, **M.G. Johnson**, N. Devos, H. Stenoien, K.I. Flatberg, and B.E. Carter. 2015. Phylogenetic structure and biogeography of the Pacific Rim clade of *Sphagnum* subgen. *Subsecunda*: haploid and allopolyploid taxa. *Biological Journal of the Linnean Society*. 116(2): 295-311. doi:10.1111/bij.12586
26. A.J. Shaw, B. Shaw, **M.G. Johnson**, M. Higuchi, T. Arikawa, Y. Hirayama, and N. Devos. 2013. Origins, genetic structure, and systematics of the narrow endemic peatmosses (*Sphagnum*): *S. triseriporum* and *S. calymmatophyllum* (Sphagnaceae). *American Journal of Botany*. 100(6) 1202-1220. doi:10.3732/ajb.1200630
27. **M.G. Johnson**, B. Shaw, P. Zhou, and A.J. Shaw. 2012. Genetic analysis of the peatmoss *Sphagnum cribrosum* indicates indepent origins of an extreme infra-specific morphology shift. *Biological Journal of the Linnean Society*. 106(1):137-153. doi:10.1111/j.1095-8312.2012.01842.x

28. A.J. Shaw, K.I. Flatberg, P. Szovenyi, M. Ricca, **M.G. Johnson**, H. Stenoëin, and B. Shaw. 2012. Systematics of the *Sphagnum fimbriatum* complex: phylogenetic relationships, morphological variation, and allopolyploidy. *Systematic Botany*. 37:36-50. doi:10.1600/036364412X616585
 29. M. Ricca, P. Szovenyi, E. Temsch, **M.G. Johnson**, and A.J. Shaw. 2011. Interploidal hybridization and mating patterns in *Sphagnum subsecundum* complex. *Molecular Ecology*. 20(15): 3202-3218. doi:10.1111/j.1365-294X.2011.05170.x
 30. M. Ramaliya*, **M.G. Johnson**, J. Heinrichs, J. Hentschel, M. von Konrat, P. Davison, B. Shaw, and A.J. Shaw. 2010. Morphologically cryptic biological species within the liverwort *Frullania asagrayana*. *American Journal of Botany*. 97:1707-1718. doi:10.3732/ajb.1000171
- (†Authors Contributed Equally; *Undergraduate Student)

IN REVIEW AND REVISION

1. L.L. Bechen, **M.G. Johnson**, G. Broadhead, R. A. Levin, R.P. Overson, T. Jogesh, J.B. Fant, R.A. Raguso, K.A. Skogen, and N.J. Wickett. Differential gene expression associated with a floral scent polymorphism in the evening primrose *Oenothera harringtonii* (Onagraceae) *BMC Genomics* (in revision)
 2. E.M. Gardner, **M.G. Johnson**[†], J.T. Pereira, A.S.A. Puad, D. Arifiani, S. Sahromi, N.J. Wickett, and N.J.C. Zerega. Paralogs and off-target sequences improve phylogenetic resolution in a densely-sampled study of the breadfruit genus (*Artocarpus*, Moraceae). *Systematic Biology* (in review)
- (†Authors Contributed Equally)

EXTERNAL RESEARCH GRANTS

Principal Investigator: Collaborative Research: Diversity of *Physcomitrium pyriforme* in North America and Europe: significance of autopolyploidy within a phylogenomic and experimental framework. *National Science Foundation Division of Environmental Biology*. 2018-2021. Awarded Amount: \$417,685. DEB-1753800

Subaward: Progress toward solving the silvery-thread moss issue in cool-season putting greens. *United States Golf Association*. 2019-2021. Total Awarded Amount: \$119,991. Sub-award: \$12,000. Lead Principal Investigator: Lloyd Stark, University of Nevada Las Vegas. Collaborator: Zane Raudenbush, Ohio State University.

Subaward: Digitization TCN: Collaborative: American Crossroads: Digitizing the Vascular Flora of the South-Central United States. *National Science Foundation*. 2019-2021. Total Awarded Amount: \$1,497,043. Sub-award: \$29,775. Lead Principal Investigator: Peter Fritsch, Botanical Research Institute of Texas.

AWARDS AND FELLOWSHIPS

Harold Sanford Perry Prize (\$5,500)	May 2013
– Annual departmental cash award for the best dissertation in Plant Sciences.	
– Students are nominated and selected by Duke Biology faculty.	
Duke Biology Department Grant-in-Aid of Research (\$500)	June 2012
E. Bayard Halsted Scholarship (\$19,836)	August 2010
Sigma Xi Grant-in-Aid of Research (\$1,000)	December 2009

PRESENTATIONS

Invited Seminars

On the potential of Angiosperms353 for Population Genomics
Botanical Society of America July 2020
 Invited Symposium Speaker: Angiosperms353: A new essential tool for plant systematics

Making sense of plant biodiversity using targeted DNA sequencing
Angelo State University Tri-Beta *October 2020*

Intergeneric allopolyploidy in Funariaceae revealed through targeted sequencing
Plant and Animal Genomes XXVII, Polyploidy Session *January 2019*

Embracing the Conflict: Phylogenomics and the Diversification of Mosses
American Bryological and Lichenological Society Annual Meeting *August 2018*
 Invited Keynote Speaker

Including herbarium specimens in targeted sequencing projects: data analysis challenges and solutions.
Botanical Society of America *July 2018*
 Invited Colloquium Speaker: Herbaria in the Genomics Age

One Set of Markers to Rule them All: Advances in Targeted Sequencing for Phylogenetics from Populations to Phyla
Wichita State University *April 2018*

Phylogenomic insights into the radiation of bryophytes.
Utah State University *October 2017*

Phylotranscriptomic analysis reveals widespread gene duplication associated with the radiation of pleurocarpous mosses
XIX International Botanical Congress, Shenzhen, China *July 2017*

Building a better tree and using it wisely: Phylogenomic approaches in non-model organisms
Chicago Plant Science Symposium, Field Museum *April 2017*

Building a better tree and using it wisely: Phylogenomic approaches in non-model organisms
University of Connecticut Biology Forum *March 2017*

Targeted Exon Sequencing in Non-Model Organisms: Best Practices for Probe Design and Data Analysis with HybPiper
PAG XXV, MycroArray Session *January 2017*

Introns, Paralogs, and Ditching the Bootstrap: Targeted Sequencing with HybPiper
University of Florida PopBio Seminar Series *September 2016*

Phylotranscriptomic insights into the radiation of mosses
2nd International Symp. on Pleurocarpous Mosses. Bonn, Germany *June 2016*

Evolution of niche preferences in *Sphagnum*
New Phytologist Sphagnum genomics meeting, invited participant *April 2016*

Ecological genomics in peatlands: the rise of *Sphagnum* as a model system
University of Chicago Darwin's Weekly Seminar Series *February 2016*

Reconstructing the ancestral gene set of bryophytes from comparative transcriptomes
PAG XXIV, Non-Seed Plant Section, San Diego, CA *January 2016*

Another abominable mystery: using phylogenomics to explore the radiation of mosses
University of Wisconsin Biology Colloquium *March 2015*

Scaling evolution from genomes to ecosystem in peatmosses (*Sphagnum*)
NESCent Catalysis Meeting, invited participant *October 2014*

What can phylogenetics teach us about peatland ecology?
Symposium: The evolution and ecology of aquatic bryophytes.
American Bryological and Lichenological Society *Botany Conference, July 2014*

Scientific Meetings

- Botanical Society of America, Tuscon, AZ July 2019
Oral Paper: Phylogenomic delineation of Physcomitrium based on targeted sequencing rejects the retention of Physcomitrella and other genera
Oral Paper: A phylogenomic approach to decode contentious relationships across all angiosperm families
- Texas Plant Conservation Conference, Fort Worth, TX September 2018
Lightning Talk: The Genetic Time Machine: Investigating the Response to Climate Change and Land Management Via a 50-Year-Old Herbarium Collection from Guadalupe Mountains National Park
- International Moss (iMOSS), Tampa, FL June 2018
Oral Paper: Intergeneric allopolyploidy in Funariaceae revealed through targeted sequencing
- Botanical Society of America, Savannah, GA July 2016
Colloquium Presentation: A re-evaluation of ancient horizontal transfer in bryophytes using comparative transcriptome data.
- Botanical Society of America, Edmonton, AB July 2015
Oral Paper: Phylotranscriptomic insights into the radiation of pleurocarpous mosses.
- Botanical Society of America, Boise, ID July 2014
Oral Paper: Constructing phylogenetic datasets with bait-capture data without a genome: strategies and challenges.
- Botanical Society of America, New Orleans, LA July 2013
Oral Paper: The relationship between mating patterns, sexual condition, and microhabitat preference in *Sphagnum*
- American Society of Human Genetics, San Francisco, CA November 2012
Poster: Comparison of phylogenetic and haplotype methods for the study of genotype-phenotype association in genome-wide studies.
- Botanical Society of America, Columbus, OH July 2012
Poster: Evolution of microhabitat preference in *Sphagnum*
- Evolution Meeting, Norman, OK June 2011
Oral Paper: Fitness and fecundity variance in a natural *Sphagnum* population: potential for sexual selection?

Co-authored Presentations by Mentees

- Botanical Society of America, Tuscon, AZ July 2019
Poster Conservation genomics of plant populations in Guadalupe Mountains National Park using herbarium specimens.
Presented by: Madeline Slimp, Honors URS, Texas Tech University
Poster The effect of life-history strategies on stomatal characteristics using herbarium specimens from Guadalupe Mountains National Park.
Presented by: Zachary Bailey, Honors URS, Texas Tech University
Oral Paper Phylogenetic information in seed morphology and seed germination for shortgrass prairie species.
Presented by: Yanni Chen, Ph.D. Student, Texas Tech University
Oral Paper Developing a cost-effective workflow for targeted sequencing of herbarium

specimens using Angiosperms353.
 Presented by: Haley Hale, Technician III, Texas Tech University

TEACHING EXPERIENCE	Professor , Texas Tech University	2017 - present
	Biology of Plants (BIOL 1401)	<i>Non-majors course</i> Typical enrollment: 120-144
	Phylogenetics (BIOL 6304)	<i>Graduate course</i> Typical enrollment: 8-10
	Evolution of Plants (BOT 3404)	<i>Majors-level lab course</i> Typical enrollment: 16-20
	Bioinformatics User Group Series (BIOL 4101-003)	
	<i>Seminar course, co-instructor with Dr. Amanda Brown</i>	Typical Enrollment: 10-15
	Co-instructor , Northwestern University	2013-2016
	Field and Lab Methods in Plant Biology and Conservation (PSC 450)	
	<i>Phylogenetics and Genomics Section</i>	
	Nyree Zerega, Course Coordinator	
	Teaching Assistant , Duke University Biology Department	
	BIO 212L Microbiology	Spring 2009, Fall 2012, Spring 2013
	BIO 26L Organismal Diversity	Summer 2010
MENTORING AND ADVISING	Graduate Major Advisor	
	– Yanni Chen, Texas Tech University	Ph.D. Student 2018-
	– Aman Pruthi, Texas Tech University	M.S. Student 2019-
	Co-advisor: Zhixin Xie	
	– Lindsay Williams, Texas Tech University	Ph.D. Student 2020-
	Graduate Research Advisor	
	– Kira Buckowing, Texas Tech University	M.S. Student 2019-
	Department: Biotechnology and Bioinformatics	
	– Katie Holt, Texas Tech University	M.S. 2019
	Department: Museum Science	
	Thesis Committees: Active	
	– Kelly McMillen, Texas Tech University	M.S. Student
	Advisor: Natasja VanGestel	
	– Morgan Long, Texas Tech University	M.S. Student
	Advisor: Dylan Schwilk	
	– Austin Osmanski, Texas Tech University	Ph.D. Student
	Advisor: David Ray	
	– Jennifer Korstian, Texas Tech University	Ph.D. Candidate
	Advisor: David Ray	
	– Nan Hu, Texas Tech University	Ph.D. Student
	Advisor: Matt Olson	
	– Shiva Aghdam, Texas Tech University	Ph.D. Student
	Advisor: Amanda Brown	
	– Minghao Guo, Texas Tech University	Ph.D. Student
	Advisor: Matt Olson	
	– Colby Witherup, Northwestern University	Ph.D. Candidate
	Advisor: Norman Wickett	
	Thesis Committees: Past	
	– Claire Malley, Northwestern University	M.S. 2015
	Advisor: Norman Wickett	
	– Shariful Islam, Texas Tech University	Ph.D. Student 2018-2019
	Advisor: Zhixin Xie	
	– Hendra Siaholo, Texas Tech University	Ph.D. Student 2019
	Advisor: Amanda Brown	

Undergraduate Researchers

- Cassidy Coker, Honors College (URS) *Herbarium* 2019-present
- Madeline Slimp, Honors College (URS) *Herbarium* 2018- present
- Kristina Robinson *Herbarium* 2018-2019
- Lauren Winfrey, Independent Research *Herbarium* 2018-2019
- Zachary Bailey, Honors College (URS) *Herbarium* 2017-2019

Past Students Mentored

- Elliot Gardner, Northwestern University Ph.D. 2017
- Marissa Ashner, Illinois Institute of Technology REU 2016
- Lindsey Bechen, Amherst College REU 2015
- Kristen Laricchia, Northwestern University M.S. 2014

PROFESSIONAL AFFILIATIONS

Departmental

- *Director, E.L. Reed Herbarium* 2017-present
- *Chair, Seminar Committee* 2019-present
- *Member, Space Committee* 2018-present
- *Elected Member, Initiatives Committee* 2020-present
- *Search Committee Member, Quantitative Biologist* 2018

Professional

- *Applications in Plant Sciences*, Guest Special Issue Editor: Angiosperms353 2020
- *Technology Committee Member*, Botanical Society of America 2019-present

- *Reviewer: Analytical Biochemistry, American Journal of Botany, Applications in Plant Sciences, Botanical Journal of the Linnean Society, Ecology and Evolution, Frontiers in Plant Science, Molecular Biology and Evolution, Molecular Phylogenetics and Evolution, New Phytologist, Perspectives in Plant Ecology Evolution and Systematics, Restoration Ecology, Reviews in Plant Science, PeerJ, Bioinformatics*

Other Service

Freely available bioinformatics pipelines and programming tutorials

<http://github.com/mossmatters>