

Brian C. O'Meara CV

bomeara@utk.edu

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Overview

- **Website:** brianomeara.info
- **Email:** bomeara@utk.edu
- **Github:** github.com/bomeara
- **Research:** Evolutionary biology, with a focus on phylogenetics and macroevolution
- **Teaching:** Macroevolution, Core Evolution, Phylogenetic Methods
- **Publications:** 66 publications, 9791 citations, h-index of 38
- **Funding:** \$2,702,060 in external funding from 9 grants
- **Mentoring:** Mentored 17 postdocs, 8 grad students (including 2 current), 5 undergrad students, 4 faculty, and served on numerous grad student committees
- **Service:** President of the Society of Systematic Biologists, Associate Head of EEB, Associate Director of NIMBioS, Code of Conduct for three evolution societies, and much more

Research

I address questions in evolutionary biology through development, implementation, and application of new phylogenetic methods. These include approaches for examining the process of continuous trait evolution (rate, optimal values, and other factors), species delimitation, phylogeography, diversification analyses, biogeography, and more. I collaborate extensively with empiricists, including some of my own students. Many of my approaches are made usable in popular software collaborators and I write; for example, my R packages have over 269,000 downloads.

Education

- University of California Davis: PhD (2008) in Population Biology. Advisors: Mike Sanderson, Phil Ward, Michael Turelli
- Harvard University: Bachelors (magna cum laude), with highest honors in Biology (2001)

Employment

- 2025-Present: **Interim Director**, National Institute for Modeling Biological Systems (NIMBioS), Knoxville, TN
- 2019-Present: **Professor**, Dept. of Ecology & Evolutionary Biology, University of Tennessee, Knoxville, TN
- 2016-2022: **Associate Head**, Dept. of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN
- 2016-2017: **Associate Director**, National Institute for Mathematical and Biological Synthesis (NIMBioS), University of Tennessee, Knoxville, TN
- 2015-2019: **Associate Professor**, Dept. of Ecology & Evolutionary Biology, University of Tennessee, Knoxville, TN
- 2009-2015: **Assistant Professor**, Dept. of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN
- 2007-2009: **Postdoc**, National Evolutionary Synthesis Center, Durham, NC

Publications

According to Google Scholar, my work has been cited 9791 times, and my h-index is 38. I use a stringent criterion for when I get authorship – I have to actively make a significant contribution to the research and writing to merit authorship (for example, not all postdoc or grad student projects in my lab have me as a coauthor, even if I helped with feedback or ideas – perhaps a bit annoying in the year people in my lab got three different *Science* papers without me as a coauthor, but still I think an honest way to do science).

Borstein, S. R., Hammer, M. P., O'Meara, B. C., & McGee, M. D. (2024). The macroevolutionary dynamics of pharyngognathia in fishes fail to support the key innovation hypothesis. *Nature Communications*, 15(1). <https://doi.org/10.1038/s41467-024-53141-4>

O'Meara, B. C., & Beaulieu, J. M. (2024). Noise leads to the perceived increase in evolutionary rates over short time scales. *PLOS Computational Biology*, 20(9), e1012458. <https://doi.org/10.1371/journal.pcbi.1012458>

Kates, H. R., O'Meara, B. C., LaFrance, R., Stull, G. W., James, E. K., Liu, S.-Y., Tian, Q., Yi, T.-S., Conde, D., Kirst, M., Ané, J.-M., Soltis, D. E., Guralnick, R. P., Soltis, P. S., & Folk, R. A. (2024). Author Correction: Shifts in evolutionary lability underlie independent gains and losses of root-nodule symbiosis in a single clade of plants. *Nature Communications*, 15(1). <https://doi.org/10.1038/s41467-024-50907-8>

Kates, H. R., O'Meara, B. C., LaFrance, R., Stull, G. W., James, E. K., Liu, S.-Y., Tian, Q., Yi, T.-S., Conde, D., Kirst, M., Ané, J.-M., Soltis, D. E., Guralnick, R. P., Soltis, P. S., & Folk, R. A. (2024). Shifts in evolutionary lability underlie independent gains and losses of root-nodule symbiosis in a single clade of plants. *Nature Communications*, 15(1). <https://doi.org/10.1038/s41467-024-48036-3>

Boyko, J. D., & O'Meara, B. C. (2024). dentist: Quantifying uncertainty by sampling points around maximum likelihood estimates. *Methods in Ecology and Evolution*, 15(4), 628–638. Portico. <https://doi.org/10.1111/2041-210x.14297>

Folk, R. A., Gaynor, M. L., Engle-Wrye, N. J., O'Meara, B. C., Soltis, P. S., Soltis, D. E., Guralnick, R. P., Smith, S. A., Grady, C. J., & Okuyama, Y. (2023). Identifying Climatic Drivers of Hybridization with a New Ancestral Niche Reconstruction Method. *Systematic Biology*, 72(4), 856–873. <https://doi.org/10.1093/sysbio/syad018>

Beaulieu, J. M., O'Meara, B. C., & Gilchrist, M. A. (2020). A Spatially Explicit Model of Stabilizing Selection for Improving Phylogenetic Inference. *Molecular Biology and Evolution*, 38(4), 1641–1652. <https://doi.org/10.1093/molbev/msaa318>

Vasconcelos, T., O'Meara, B. C., & Beaulieu, J. M. (2022). A flexible method for estimating tip diversification rates across a range of speciation and extinction scenarios. *Evolution*, 76(7), 1420–1433. Portico. <https://doi.org/10.1111/evo.14517>

Beaulieu, J. M., & O'Meara, B. C. (2022). Fossils Do Not Substantially Improve, and May Even Harm, Estimates of Diversification Rate Heterogeneity. *Systematic Biology*, 72(1), 50–61. <https://doi.org/10.1093/sysbio/syac049>

Jhwueng, D.-C., & O'Meara, B. C. (2020). On the Matrix Condition of Phylogenetic Tree. *Evolutionary Bioinformatics*, 16. <https://doi.org/10.1177/1176934320901721>

Nguyen, V. D., Nguyen, T. H., Tayeen, A. S. M., Laughinghouse, H. D., Sánchez-Reyes, L. L., Wiggins, J., Pontelli, E., Mozzherin, D., O'Meara, B., & Stoltzfus, A. (2020). Phylotastic: Improving Access to Tree-of-Life Knowledge With Flexible, on-the-Fly Delivery of Trees. *Evolutionary Bioinformatics*, 16. <https://doi.org/10.1177/1176934319899384>

Meireles, J. E., Cavender-Bares, J., Townsend, P. A., Ustin, S., Gamon, J. A., Schweiger, A. K., Schaepman, M. E., Asner, G. P., Martin, R. E., Singh, A., Schrodlt, F., Chlus, A., &

O'Meara, B. C. (2020). Leaf reflectance spectra capture the evolutionary history of seed plants. *New Phytologist*, 228(2), 485–493. Portico. <https://doi.org/10.1111/nph.16771>

McGee, M. D., Borstein, S. R., Meier, J. I., Marques, D. A., Mwaiko, S., Taabu, A., Kishe, M. A., O'Meara, B., Bruggmann, R., Excoffier, L., & Seehausen, O. (2020). The ecological and genomic basis of explosive adaptive radiation. *Nature*, 586(7827), 75–79. <https://doi.org/10.1038/s41586-020-2652-7>

Harvey, M. G., Bravo, G. A., Claramunt, S., Cuervo, A. M., Derryberry, G. E., Battilana, J., Seeholzer, G. F., McKay, J. S., O'Meara, B. C., Faircloth, B. C., Edwards, S. V., Pérez-Emán, J., Moyle, R. G., Sheldon, F. H., Aleixo, A., Smith, B. T., Chesser, R. T., Silveira, L. F., Cracraft, J., ... Derryberry, E. P. (2020). The evolution of a tropical biodiversity hotspot. *Science*, 370(6522), 1343–1348. <https://doi.org/10.1126/science.aaz6970>

Landerer, C., O'Meara, B. C., Zaretzki, R., & Gilchrist, M. A. (2020). Unlocking a signal of introgression from codons in *Lachancea kluyveri* using a mutation-selection model. *BMC Evolutionary Biology*, 20(1). <https://doi.org/10.1186/s12862-020-01649-w>

Sánchez Reyes, L. L., McTavish, E. J., & O'Meara, B. (2024). DateLife: Leveraging Databases and Analytical Tools to Reveal the Dated Tree of Life. *Systematic Biology*, 73(2), 470–485. <https://doi.org/10.1093/sysbio/syae015>

Beaulieu, J. M., & O'Meara, B. C. (2019). Diversity and skepticism are vital for comparative biology: a response to Donoghue and Edwards (2019). *American Journal of Botany*, 106(5), 613–617. Portico. <https://doi.org/10.1002/ajb2.1278>

Cope, A. L., O'Meara, B. C., & Gilchrist, M. A. (2020). Gene expression of functionally-related genes coevolves across fungal species: detecting coevolution of gene expression using phylogenetic comparative methods. *BMC Genomics*, 21(1). <https://doi.org/10.1186/s12864-020-6761-3>

Beaulieu, J. M., O'Meara, B. C., Zaretzki, R., Landerer, C., Chai, J., & Gilchrist, M. A. (2018). Population Genetics Based Phylogenetics Under Stabilizing Selection for an Optimal Amino Acid Sequence: A Nested Modeling Approach. *Molecular Biology and Evolution*, 36(4), 834–851. <https://doi.org/10.1093/molbev/msy222>

Borstein, S. R., & O'Meara, B. C. (2018). AnnotationBustR: an R package to extract subsequences from GenBank annotations. *PeerJ*, 6, e5179. Portico. <https://doi.org/10.7717/peerj.5179>

Beaulieu, J. M., & O'Meara, B. C. (2018). Can we build it? Yes we can, but should we use it? Assessing the quality and value of a very large phylogeny of campanulid angiosperms. *American Journal of Botany*, 105(3), 417–432. Portico. <https://doi.org/10.1002/ajb2.1020>

Caetano, D. S., O'Meara, B. C., & Beaulieu, J. M. (2018). Hidden state models improve state-dependent diversification approaches, including biogeographical models. *Evolution*, 72(11), 2308–2324. Portico. <https://doi.org/10.1111/evo.13602>

- Jackson, N. D., Morales, A. E., Carstens, B. C., & O'Meara, B. C. (2017). PHRAPL: Phylogeographic Inference Using Approximate Likelihoods. *Systematic Biology*, 66(6), 1045–1053. <https://doi.org/10.1093/sysbio/syx001>
- Carstens, B. C., Morales, A. E., Jackson, N. D., & O'Meara, B. C. (2017). Objective choice of phylogeographic models. *Molecular Phylogenetics and Evolution*, 116, 136–140. <https://doi.org/10.1016/j.ympev.2017.08.018>
- Morales, A. E., Jackson, N. D., Dewey, T. A., O'Meara, B. C., & Carstens, B. C. (2016). Speciation with Gene Flow in North American Myotis Bats. *Systematic Biology*, syw100. <https://doi.org/10.1093/sysbio/syw100>
- Jackson, N. D., Carstens, B. C., Morales, A. E., & O'Meara, B. C. (2016). Species Delimitation with Gene Flow. *Systematic Biology*, syw117. <https://doi.org/10.1093/sysbio/syw117>
- Bosco, J. M., Riechert, S. E., & O'Meara, B. C. (2017). The ontogeny of personality traits in the desert funnel-web spider, *Agelenopsis lisa* (Araneae: Agelenidae). *Ethology*, 123(9), 648–658. Portico. <https://doi.org/10.1111/eth.12639>
- Schwery, O., & O'Meara, B. C. (2016). MonoPhy: a simple R package to find and visualize monophyly issues. *PeerJ Computer Science*, 2, e56. Portico. <https://doi.org/10.7717/peerj-cs.56>
- Beaulieu, J. M., & O'Meara, B. C. (2016). Detecting Hidden Diversification Shifts in Models of Trait-Dependent Speciation and Extinction. *Systematic Biology*, 65(4), 583–601. <https://doi.org/10.1093/sysbio/syw022>
- O'Meara, B. C., Smith, S. D., Armbruster, W. S., Harder, L. D., Hardy, C. R., Hileman, L. C., Hufford, L., Litt, A., Magallón, S., Smith, S. A., Stevens, P. F., Fenster, C. B., & Diggle, P. K. (2016). Non-equilibrium dynamics and floral trait interactions shape extant angiosperm diversity. *Proceedings of the Royal Society B: Biological Sciences*, 283(1830), 20152304. <https://doi.org/10.1098/rspb.2015.2304>
- O'Meara, B. C., & Beaulieu, J. M. (2016). Past, future, and present of state-dependent models of diversification. *American Journal of Botany*, 103(5), 792–795. Portico. <https://doi.org/10.3732/ajb.1600012>
- O'Meara, B. (2016). Phylogenetic Comparative Method. *Encyclopedia of Evolutionary Biology*, 254–256. <https://doi.org/10.1016/b978-0-12-800049-6.00217-1>
- Zanne, A. E., Tank, D. C., Cornwell, W. K., Eastman, J. M., Smith, S. A., FitzJohn, R. G., McGlinn, D. J., O'Meara, B. C., Moles, A. T., Reich, P. B., Royer, D. L., Soltis, D. E., Stevens, P. F., Westoby, M., Wright, I. J., Aarssen, L., Bertin, R. I., Calaminus, A., Govaerts, R., ... Beaulieu, J. M. (2015). Correction: Corrigendum: Three keys to the radiation of angiosperms into freezing environments. *Nature*, 521(7552), 380–380. <https://doi.org/10.1038/nature14371>

- O'Meara, B. C., Graham, K. L., Pellis, S. M., & Burghardt, G. M. (2015). Evolutionary models for the retention of adult–adult social play in primates: The roles of diet and other factors associated with resource acquisition. *Adaptive Behavior*, 23(6), 381–391. <https://doi.org/10.1177/1059712315611733>
- Beaulieu, J. M., & O'Meara, B. C. (2015). Extinction can be estimated from moderately sized molecular phylogenies. *Evolution*, 69(4), 1036–1043. Portico. <https://doi.org/10.1111/evo.12614>
- Beaulieu, J. M., O'Meara, B. C., Crane, P., & Donoghue, M. J. (2015). Heterogeneous Rates of Molecular Evolution and Diversification Could Explain the Triassic Age Estimate for Angiosperms. *Systematic Biology*, 64(5), 869–878. <https://doi.org/10.1093/sysbio/syv027>
- Aldrovandi, M. S. P., Johnson, J. E., OMeara, B., Petersen, R. H., & Hughes, K. W. (2015). The Xeromphalina campanella/kauffmanii complex: species delineation and biogeographical patterns of speciation. *Mycologia*, 107(6), 1270–1284. <https://doi.org/10.3852/15-087>
- Zanne, A. E., Tank, D. C., Cornwell, W. K., Eastman, J. M., Smith, S. A., FitzJohn, R. G., McGlinn, D. J., O'Meara, B. C., Moles, A. T., Reich, P. B., Royer, D. L., Soltis, D. E., Stevens, P. F., Westoby, M., Wright, I. J., Aarssen, L., Bertin, R. I., Calaminus, A., Govaerts, R., ... Beaulieu, J. M. (2015). Zanne et al. reply. *Nature*, 521(7552), E6–E7. <https://doi.org/10.1038/nature14394>
- Zanne, A. E., Tank, D. C., Cornwell, W. K., Eastman, J. M., Smith, S. A., FitzJohn, R. G., McGlinn, D. J., O'Meara, B. C., Moles, A. T., Reich, P. B., Royer, D. L., Soltis, D. E., Stevens, P. F., Westoby, M., Wright, I. J., Aarssen, L., Bertin, R. I., Calaminus, A., Govaerts, R., ... Beaulieu, J. M. (2014). Erratum: Corrigendum: Three keys to the radiation of angiosperms into freezing environments. *Nature*, 514(7522), 394–394. <https://doi.org/10.1038/nature13842>
- Cornwell, W. K., Westoby, M., Falster, D. S., FitzJohn, R. G., O'Meara, B. C., Pennell, M. W., McGlinn, D. J., Eastman, J. M., Moles, A. T., Reich, P. B., Tank, D. C., Wright, I. J., Aarssen, L., Beaulieu, J. M., Kooyman, R. M., Leishman, M. R., Miller, E. T., Niinemets, Ü., Oleksyn, J., ... Zanne, A. E. (2014). Functional distinctiveness of major plant lineages. *Journal of Ecology*, 102(2), 345–356. Portico. <https://doi.org/10.1111/1365-2745.12208>
- Beaulieu, J. M., & O'Meara, B. C. (2014). Hidden Markov Models for Studying the Evolution of Binary Morphological Characters. *Modern Phylogenetic Comparative Methods and Their Application in Evolutionary Biology*, 395–408. https://doi.org/10.1007/978-3-662-43550-2_16
- Jhwueng, D.-C., Huzurbazar, S., O'Meara, B. C., & Liu, L. (2014). Investigating the performance of AIC in selecting phylogenetic models. *Statistical Applications in Genetics and Molecular Biology*, 13(4). <https://doi.org/10.1515/sagmb-2013-0048>
- O'Meara, B. C., & Beaulieu, J. M. (2014). Modelling Stabilizing Selection: The Attraction of Ornstein–Uhlenbeck Models. *Modern Phylogenetic Comparative Methods and Their Application in Evolutionary Biology*, 381–393. https://doi.org/10.1007/978-3-662-43550-2_15

- Banbury, B. L., & O'Meara, B. C. (2014). Reol: R interface to the Encyclopedia of Life. *Ecology and Evolution*, 4(12), 2577–2583. Portico. <https://doi.org/10.1002/ece3.1109>
- Williams, J. H., Taylor, M. L., & O'Meara, B. C. (2014). Repeated evolution of tricellular (and bicellular) pollen. *American Journal of Botany*, 101(4), 559–571. Portico. <https://doi.org/10.3732/ajb.1300423>
- Zanne, A. E., Tank, D. C., Cornwell, W. K., Eastman, J. M., Smith, S. A., FitzJohn, R. G., McGlinn, D. J., O'Meara, B. C., Moles, A. T., Reich, P. B., Royer, D. L., Soltis, D. E., Stevens, P. F., Westoby, M., Wright, I. J., Aarssen, L., Bertin, R. I., Calaminus, A., Govaerts, R., ... Beaulieu, J. M. (2013). Three keys to the radiation of angiosperms into freezing environments. *Nature*, 506(7486), 89–92. <https://doi.org/10.1038/nature12872>
- Beaulieu, J. M., O'Meara, B. C., & Donoghue, M. J. (2013). Identifying Hidden Rate Changes in the Evolution of a Binary Morphological Character: The Evolution of Plant Habit in Campanulid Angiosperms. *Systematic Biology*, 62(5), 725–737. <https://doi.org/10.1093/sysbio/syt034>
- Darrin Hulsey, C., Keck, B. P., Alamillo, H., & O'Meara, B. C. (2013). Mitochondrial genome primers for Lake Malawi cichlids. *Molecular Ecology Resources*, 13(3), 347–353. Portico. <https://doi.org/10.1111/1755-0998.12066>
- Soltis, D. E., Mort, M. E., Latvis, M., Mavrodiev, E. V., O'Meara, B. C., Soltis, P. S., Burleigh, J. G., & Rubio de Casas, R. (2013). Phylogenetic relationships and character evolution analysis of Saxifragales using a supermatrix approach. *American Journal of Botany*, 100(5), 916–929. Portico. <https://doi.org/10.3732/ajb.1300044>
- Stoltzfus, A., Lapp, H., Matasci, N., Deus, H., Sidlauskas, B., Zmasek, C. M., Vaidya, G., Pontelli, E., Cranston, K., Vos, R., Webb, C. O., Harmon, L. J., Pirrung, M., O'Meara, B., Pennell, M. W., Mirarab, S., Rosenberg, M. S., Balhoff, J. P., Bik, H. M., ... Jordan, G. (2013). Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. *BMC Bioinformatics*, 14(1). <https://doi.org/10.1186/1471-2105-14-158>
- O'Meara, B. C. (2012). Evolutionary Inferences from Phylogenies: A Review of Methods. *Annual Review of Ecology, Evolution, and Systematics*, 43(1), 267–285. <https://doi.org/10.1146/annurev-ecolsys-110411-160331>
- Beaulieu, J. M., Jhuang, D.-C., Boettiger, C., & O'Meara, B. C. (2012). MODELING STABILIZING SELECTION: EXPANDING THE ORNSTEIN-UHLENBECK MODEL OF ADAPTIVE EVOLUTION. *Evolution*, 66(8), 2369–2383. <https://doi.org/10.1111/j.1558-5646.2012.01619.x>
- Stoltzfus, A., O'Meara, B., Whitacre, J., Mounce, R., Gillespie, E. L., Kumar, S., Rosauer, D. F., & Vos, R. A. (2012). Sharing and re-use of phylogenetic trees (and associated data) to facilitate synthesis. *BMC Research Notes*, 5(1). <https://doi.org/10.1186/1756-0500-5-574>

Smith, S. A., & O'Meara, B. C. (2012). treePL: divergence time estimation using penalized likelihood for large phylogenies. *Bioinformatics*, 28(20), 2689–2690. <https://doi.org/10.1093/bioinformatics/bts492>

Stack, J. C., Harmon, L. J., & O'Meara, B. (2011). RBrownie: an R package for testing hypotheses about rates of evolutionary change. *Methods in Ecology and Evolution*, 2(6), 660–662. Portico. <https://doi.org/10.1111/j.2041-210x.2011.00112.x>

Stack, J. C., Harmon, L. J., & O'Meara, B. (2011). RBrownie: an R package for testing hypotheses about rates of evolutionary change. *Methods in Ecology and Evolution*, 2(6), 660–662. Portico. <https://doi.org/10.1111/j.2041-210x.2011.00112.x>

Abercrombie, J. M., O'Meara, B. C., Moffatt, A. R., & Williams, J. H. (2011). Developmental evolution of flowering plant pollen tube cell walls: callose synthase (CalS) gene expression patterns. *EvoDevo*, 2(1). <https://doi.org/10.1186/2041-9139-2-14>

Goff, S. A., Vaughn, M., McKay, S., Lyons, E., Stapleton, A. E., Gessler, D., Matasci, N., Wang, L., Hanlon, M., Lenards, A., Muir, A., Merchant, N., Lowry, S., Mock, S., Helmke, M., Kubach, A., Narro, M., Hopkins, N., Micklos, D., ... Stanzione, D. (2011). The iPlant Collaborative: Cyberinfrastructure for Plant Biology. *Frontiers in Plant Science*, 2. <https://doi.org/10.3389/fpls.2011.00034>

COLLAR, D. C., SCHULTE, J. A., O'MEARA, B. C., & LOSOS, J. B. (2010). Habitat use affects morphological diversification in dragon lizards. *Journal of Evolutionary Biology*, 23(5), 1033–1049. Portico. <https://doi.org/10.1111/j.1420-9101.2010.01971.x>

O'Meara, B. C. (2009). New Heuristic Methods for Joint Species Delimitation and Species Tree Inference. *Systematic Biology*, 59(1), 59–73. <https://doi.org/10.1093/sysbio/syp077>

Smith, S. A., & O'Meara, B. C. (2009). Morphogenera, monophyly, and macroevolution. *Proceedings of the National Academy of Sciences*, 106(36). <https://doi.org/10.1073/pnas.0906918106>

Collar, D. C., O'Meara, B. C., Wainwright, P. C., & Near, T. J. (2009). PISCIVORY LIMITS DIVERSIFICATION OF FEEDING MORPHOLOGY IN CENTRARCHID FISHES. *Evolution*, 63(6), 1557–1573. <https://doi.org/10.1111/j.1558-5646.2009.00626.x>

O'Meara, B. (2008). Using Trees: *Myrmecocystus* Phylogeny and Character Evolution and New Methods for Investigating Trait Evolution and Species Delimitation (PhD Dissertation). *Nature Precedings*. <https://doi.org/10.1038/npre.2008.2261.1>

O'Meara, B. C., Ané, C., Sanderson, M. J., & Wainwright, P. C. (2006). TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. *Evolution*, 60(5), 922. <https://doi.org/10.1554/05-130.1>

Driskell, A. C., Ané, C., Burleigh, J. G., McMahon, M. M., O'Meara, B. C., & Sanderson, M. J. (2004). Prospects for Building the Tree of Life from Large Sequence Databases. *Science*, 306(5699), 1172–1174. <https://doi.org/10.1126/science.1102036>

Farrell, B. D., Sequeira, A. S., O'Meara, B. C., Normark, B. B., Chung, J. H., & Jordal, B. H. (2001). THE EVOLUTION OF AGRICULTURE IN BEETLES (CURCULIONIDAE: SCOLYTINAE AND PLATYPODINAE). *Evolution*, 55(10), 2011–2027. <https://doi.org/10.1111/j.0014-3820.2001.tb01318.x>

Preprints

O'Meara, B. C., & Beaulieu, J. M. (2024). Noise leads to the perceived increase in evolutionary rates over short time scales. <https://doi.org/10.1101/2024.02.29.582777>

Boyko, J. D., & O'Meara, B. C. (2023). dentist: Computing uncertainty by sampling points around maximum likelihood estimates. <https://doi.org/10.1101/2023.01.10.523430>

Folk, R. A., Gaynor, M. L., Engle-Wrye, N. J., O'Meara, B. C., Soltis, P. S., Soltis, D. E., Guralnick, R. P., Smith, S. A., Grady, C. J., & Okuyama, Y. (2022). Identifying climatic drivers of hybridization in Heuchereae (Saxifragaceae). <https://doi.org/10.1101/2022.08.24.505154>

Vasconcelos, T., O'Meara, B. C., & Beaulieu, J. M. (2021). A flexible method for estimating tip diversification rates across a range of speciation and extinction scenarios. <https://doi.org/10.1101/2021.11.02.466977>

Beaulieu, J. M., & O'Meara, B. C. (2021). Fossils Do Not Substantially Improve, and May Even Harm, Estimates of Diversification Rate Heterogeneity. <https://doi.org/10.1101/2021.11.06.467550>

Reyes, L. L. S., McTavish, E. J., & O'Meara, B. (2019). DateLife: leveraging databases and analytical tools to reveal the dated Tree of Life. <https://doi.org/10.1101/782094>

Cope, A. L., O'Meara, B., & Gilchrist, M. A. (2019). Gene Expression of Functionally-Related Genes Coevolves Across Fungal Species: Detecting Coevolution of Gene Expression Using Phylogenetic Comparative Methods. <https://doi.org/10.1101/844472>

Evangelista, D. A., Gilchrist, M. A., Legendre, F., & O'Meara, B. (2019). The Implications of Over-Estimating Gene Tree Discordance on a Rapid-Radiation Species Tree (Blattodea: Blaberidae). <https://doi.org/10.1101/717660>

Caetano, D., O'Meara, B., & Beaulieu, J. (2018). Hidden state models improve the adequacy of state-dependent diversification approaches using empirical trees, including biogeographical models. <https://doi.org/10.1101/302729>

Beaulieu, J. M., & O'Meara, B. C. (2024). Navigating “tip fog”: Embracing uncertainty in tip measurements. <https://doi.org/10.1101/2024.08.19.608647>

Boyko, J., O'Meara, B., & Beaulieu, J. (2022). Jointly Modeling the Evolution of Discrete and Continuous Traits. <https://doi.org/10.32942/osf.io/fb8k7>

O'Meara, B., & Beaulieu, J. (2021). Potential survival of some, but not all, diversification methods. <https://doi.org/10.32942/osf.io/w5nvd>

Vasconcelos, T., O'Meara, B., & Beaulieu, J. (2021). Retiring “cradles” and “museums” of biodiversity. <https://doi.org/10.32942/osf.io/sxah8>

Schwery, O., & O'Meara, B. C. (2021). Age, Origin, and Biogeography: Unveiling the Factors Behind the Diversification of Dung Beetles. <https://doi.org/10.1101/2021.01.26.428346>

Schwery, O., & O'Meara, B. C. (2021). The Shape of Trees – Limits of Current Diversification Models. <https://doi.org/10.1101/2021.01.26.428344>

Schwery, O., & O'Meara, B. C. (2020). BoskR– Testing Adequacy of Diversification Models Using Tree Shape. <https://doi.org/10.1101/2020.12.21.423829>

Jhwueng, D.-C., & O'Meara, B. C. (2015). Trait Evolution on Phylogenetic Networks. <https://doi.org/10.1101/023986>

Teaching

Our standard load is to have three substantial courses and one small course (like a reading group) over a two year period (but teaching every semester). I have been teaching slightly over this (with my agreement) for the past few years.

Current

- Macroevolution (EEB 464): An undergraduate or early grad student course on “macroevolution” which includes everything from spandrels to genomes. I created this course as an assistant professor; its enrollment has grown and now has 40 students. I currently teach it every year; its modality is asynchronous online. I have a mixture of recorded lectures, readings, videos from others, software demos, and more.
- Core Evolution (EEB 509): An introduction to evolution: required for all grad students in UTK EEB, and often taken by students in related departments. It fulfills part of the background knowledge part of their candidacy exam. Each session is typically a mixture of a brief introductory lecture to a topic, then a longer full class discussion (including think-pair-share) of one or more papers previously assigned on that topic. Typically 10-20 students.

Past

- PhyloMeth: Partially supported by an NSF CAREER grant, a class that focuses on phylogenetics, with a focus on methods for using trees. The capstone was students developing a method (tuned to the starting level of the students). Materials are available on <phylometh.info>.

- Speciation reading group: Grad students, postdocs, and faculty meet weekly to discuss papers on speciation (or related topics).
- Introduction to Biology (BIO 130 or 150): Large (150-200 student) enrollment classes.
- Various workshops on comparative methods and R (e.g., at NIMBioS, NESCent, Friday Harbor, Mathematical Biosciences Institute (MBI), scientific conferences, etc.). Easily over a thousand students have taken these workshops.
- Group lab meetings (3-4 evolutionary biology labs meeting jointly), counted as a graduate seminar.

External Funding

While my lab infrastructure is fairly cheap (individual computers, computing clusters, whiteboards, and markers), paying humanely for people isn't. Fortunately, I have been able to secure \$2,702,060 funding for my institution (see below). As with my listing of publications, this does not include funding earned by students or postdocs in my lab (GRFPs, DDIGs, post-doc fellowships, research funds, etc.) – those go on their CVs. Funding indicated is that going to my institution, not necessarily the total amount of the grant.

- 2022-2025: “Collaborative Research: ORCC: The role of bioenergetic budgets in defining elevation limits and modeling geographic ranges of species.” NSF IOS. Xingli Giam PI (\$614,248), I’m research personnel on the grant.
- 2019-2024: “Collaborative Research: Novel framework for estimating continuously-varying diversification rates.” NSF DEB, Systematics & Biodiversity Science. \$193,401
- 2015-2021: “CAREER: Reducing barriers for comparative methods.” NSF DEB, Phylogenetic Systematics. \$738,297
- 2015-2019: “Collaborative Research: ABI Development: An open infrastructure to disseminate phylogenetic knowledge.” NSF DBI, Advances in Bioinformatics. \$148,101
- 2014-2019: “Population genetics-based codon models.” NSF DEB, Genetic Mechanisms, Information Technology Researc, Cross-BIO Activities, Systematics & Biodiversity Sci, Algorithmic Foundations. \$520,000
- 2013-2017: “Collaborative Research: Phylogeographic Inference Using Approximated Likelihoods.” NSF DEB, Phylogenetic Systematics. \$340,000.
- 2012-2017: “Historical naming traditions and cryptic speciation bias biodiversity estimates in transatlantic agaric fungi.” NSF DEB, Biodiversity: Discovery & Analysis. \$393,074
- 2012-2013: “rPlant”. Subaward from an NSF \$50,846,500 grant. \$98,252 to UTK
- 2011-2012: “iPlant: Trait evolution group, year 2”. Subaward from an NSF \$50,846,500 grant. \$138,590 to UTK
- 2010-2011: “iPlant: Trait evolution group, year 1”. Subaward from an NSF \$50,846,500 grant. \$132,345 to UTK

Mentoring

Here are some of the people I have mentored; I am not including graduate students on whose committees I have served (probably dozens by this point, across multiple departments at UTK and as an external member at other institutions).

Postdocs

Name	Duration	NIMBioS
Hugo Alamillo	2011- 2012	N
Barb Banbury	2010- 2012	N
David Bapst	2017- 2019	N
Jeremy Beaulieu	2012- 2016	Both
James Boyko	2022- 2023	N
Juanjuan (JJ) Crosskey (formerly Chai)	2011- 2013	Y
Dominic Evangelista	2018- 2018	Y
Nathan Jackson	2013- 2016	N
Tony Jhwueng	2009- 2011	Y
Sandy Kawano	2014- 2016	Y
Michelle Lawing	2012- 2014	Y
Ryan Martin	2012- 2013	Y
Nick Matzke	2013- 2015	Y
Megan Rua	2015- 2016	Y
Luna Sanchez Reyes	2017- 2019	N
Sergei Tarasov	2016- 2018	Y

Name	Duration NIMBioS
Jodie Wiggins	2018- N 2019

Grad students in my lab

These are students for whom I was their advisor or co-advisor. Note that I include just the time they were in my lab, not the time they were in the program. Our students must have one or more advisors when they enroll, but they may also add or replace advisors. All but one of the students below started in a different lab and then added me; so far, the reverse has not happened (but I encourage any of my students reading this CV to switch if it helps you with your goals).

Name	Stage	Time in Lab		Note
		PhD	Masters	
Sam Borstein	student	2014-		
Jenn Bosco	student	2019		Co-advised with Susan Riechert
Amanda Chandler	student	2012-	2017	
Krista De Cooke	student	2017	2024-	
Katie Massana	student	2020-	present	Co-advised with Dan Simberloff
Alivia Nytko	student	2023		
Orlando Schwery	student	2012-	2014-	Co-advised with Joe Bailey
Jenn Summers	student	2017	2020-	
		2020	2021	

Undergrad students in my lab

Name	Stage	Time in Lab		Note
		Undergrad	2019-2020	
Tyler-Christian Daniels				
Stephen Ray				Undergrad 2019-2020

Name	Stage	Lab	Note	Time in
Zach Tharpe				Undergrad 2019-2020
Christian Yarber				Undergrad 2015-2016
John Anderson				Undergrad 2021-present

Faculty

Our department creates a mentoring committee for each new faculty member. I have been on the mentoring committee for the following faculty members:

Name	Department
Liz Derryberry	EEB
Stephanie Kivlin	EEB
Laura Russo	EEB
Kimberly Sheldon	EEB

Service

Some of my service comes directly through publications (for example, DateLife allows people to easily get dated trees of life for teaching or research). Some comes through informal service (a colleague at a different institution reaching out for advice on a situation in their department, for example). Here I am listing more formal service.

- **Interim Director, NIMBioS:** I am taking over running NIMBioS, the National Institute for Modeling Biological Systems, at a time of transition as we plan for its future. NIMBioS has a long history of work at the interface of math and biology, and it's exciting to work for its future.
- **Associate Head for EEB:** One of two associate heads under Head Susan Kalisz, my focus was on grad students and overall equity in the department. I also split interim head duties during a semester when the head was on sabbatical. My work included working with our grad admissions and grad affairs committees (including chairing the former one year while also serving as associate head), working on covid policy for the department (making sure everyone in a lab approved its safety protocols before it reopened, for example), and working with university lawyers on various issues (to be clear, none with me as a respondent or anything of the sort).
- **Associate Director for NIMBioS:** My focus was on postdocs, including vocational mentoring and building their social interactions.

- **President of the Society of Systematic Biologists:** This involves three years of commitment, as president-elect, president, and past president. During that time, I was involved in decisions on named awards, leadership and support of the society's two journals, a mentorship program, and more. I also served as de facto representative on the joint meeting committee for the Evolution meetings. I used my [presidential address](#) to highlight four issues: how naming affects conservation; the need for and progress in handling misconduct in our field; issues with eponyms in our field; and our field's past and ongoing connection with eugenics (part of this included a new analysis of 122,096 papers and 141,284 unique authors).
- **Code of Conduct Committee for Evolution:** I have been on this committee since its inception. We built up support for an actionable code of conduct (I led an IRB-approved [study](#) on the topic), developed a working code in association with various lawyers and other experts, interviewed and selected safety officers, and wrote up transparency reports based on incidents at the meeting.
- **Code of Ethics for the three societies:** The Society of Systematic Biologists, the Society for the Study of Evolution, and the American Society of Naturalists together worked on a shared code of ethics (to handle misconduct in general, not just at meetings). I gave feedback at various stages in the process and then helped more substantially in the final stages of getting it approved and selecting an investigatory agent for two of the societies (SSB and SSE).
- **Liason between joint meeting committee and the meeting location committee:** The Evolution meetings (annual meetings of 3-4 evolution societies with 1500-2000 attendees) have long been guided by California's travel ban policy in choosing locations (though with the time lead required between choosing a location and the meeting, many things can change). A group was tasked with creating recommendations for how to choose meetings in the future, including doing a survey; I act as a liason between that group and the joint meeting committee, and made recommendations on making their product more actionable.
- **Internal service:** Reviews of proposals and fellowships for our office of research and the grad school, workshops on applying for the NSF GRFP, review of another department, serving on an enhanced post-tenure review committee, dean's advisory committee, head search committee, college strategic planning committee for graduate education, and more.