CURRICULUM VITAE
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Associate Professor in the Department of Ecology and Evolutionary Biology
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Education

PhD from the Institute for Cellular and Molecular Biology at the University of Texas at Austin. December, 2001. Dissertation: "Using a Complex Model of Sequence Evolution to Evaluate and Improve Phylogenetics Methods."

B.S. in Biochemistry/Genetics from Texas A&M University, College Station. December, 1994.

Employment

2017 – present: Associate research scientist. Biodiversity Institute, University of Kansas.

2013 – present: Associate professor. Ecology and Evolutionary Biology, University of Kansas.

2007 – 2013: Assistant professor. Ecology and Evolutionary Biology, University of Kansas.

2004 – 2007: Computer research specialist. Florida State University working with Dr. David Swofford.

2003 – 2004: Postdoctoral researcher. Florida State Univ. with Dr. David Swofford.

2001 – 2003: Postdoctoral researcher. Univ. of Connecticut with Dr. Paul Lewis.

Teaching

Undergraduate courses (KU):
  – BIOL 428 "Introduction to Systematics"
  – BIOL 370/570 "Introduction to Biostatistics" (co-taught with Dr. Helen Alexander, Dr. Maria Orive, Dr. Folashade Agusto, or Dr. Maggie Wagner).
  – BIOL/CHEM 598 "Research Methods" for the STEMTeachKU program.
  – BIOL 599 "Senior Seminar in Evolutionary Biology"

Graduate courses (KU):
  – BIOL 848 "Phylogenetic Methods"
  – BIOL 847 "Phylogenetics" (co-taught with Dr. Ed Wiley).
  – BIOL 701 "Topics in Programming for Ecology and Evolutionary Biology"
  – BIOL 801 "Current Research in Ecology and Evolutionary Biology" (seminar).
  – BIOL 701 "Topics in Likelihood Methods in Biology" (co-taught with Drs. Ballantyne and Kelly).
  – BIOL 648 "Systematics and Macroevolution" (co-taught Drs. Cartwright, Engel, Jensen, Lieberman, and Wm. Leo Smith).
  – BIOL701 "Advanced Topics in Biogeography" (co-taught with Drs. Peterson, Soberón,

Lieberman, Moyle, and Brown).

Teaching in workshops:

1. Synthesizing and dating phylogenies using the Open Tree of Life Workshop at the Society of Systematic Biologists (2023) at Universidad Nacional Autónoma de México (UNAM) in Mexico City.
2. Using Open Tree of Life for your Research Workshop at meeting of the Society of Systematic Biologists (2020).
3. Midwest Phylogenetics Workshop (2019)
4. Workshop on Molecular Evolution at the Marine Biological Laboratory, Woods Hole, Massachusetts (2003, 2005, 2008-2019; director 2018 & 2019).
5. The Molecular Phylogenetics module of the Summer Institute in Statistical Genetics (2006, 2007, 2009 – 2014, 2016)
6. Workshop in Applied Phylogenetics, Bodega Bay, CA (2014)
7. Software Carpentry assistant (2017-present) and co-instructor (2013).
8. Molecular Evolution Course at Centro de Ciêncies do Mar, Algarve, Portugal (2005).
9. Phylogenetics Workshop at the University of Wisconsin-Parkside (2005)

Publications

[1] McTavish, Emily Jane, Jeff A. Gerbracht, Mark T. Holder, Marshall J. Iliff, Denis Lepage, Pamela C. Rasmussen, Benjamin D. Redelings, Luna L. Sánchez Reyes, and Eliot T. Miller. A complete and dynamic tree of birds. *Proceedings of the National Academy of Sciences*, 122(18), 2025. ISSN 1091-6490. link.

[2] Moreno, Matthew Andres, Mark T. Holder, and Jeet Sukumaran. Dendropy 5: a mature python library for phylogenetic computing. *Journal of Open Source Software*, 9(101):6943, 2024. link.

[3] Redelings, Benjamin D. and Mark T. Holder. Speeding up iterative applications of the BUILD supertree algorithm. *PeerJ*, 12:e16624, 2024. ISSN 2167-8359. link.

[4] McTavish, Emily Jane, Luna Luisa Sanchez Reyes, and Mark T Holder. OpenTree: A Python package for Accessing and Analyzing data from the Open Tree of Life. *Systematic Biology*, 2021. ISSN 1063-5157. Syab033. link.

[5] Sukumaran, Jeet, Mark T. Holder, and L. Lacey Knowles. Incorporating the speciation process into species delimitation. *PLOS Computational Biology*, 17(5):1–19, 2021. link.

[6] Ghosh, Shyamolina, Lawrence W. Sheppard, Mark T. Holder, Terrance E. Loecke, Philip C. Reid, James D. Bever, and Daniel C. Reuman. Copulas and their potential for ecology. In *Advances in Ecological Research*, page *in press*. Elsevier, 2020.

[7] Gibson, Matthew JS, Daniel J Crawford, Mark T Holder, Mark E Mort, Benjamin Kerbs, Miguel Menezes de Sequeira, and John K Kelly. Genome-wide genotyping estimates mating system parameters and paternity in the island species *tolpis succulenta*. *American Journal of Botany*, 107(8):1189–1197, 2020.

[8] Redelings, Benjamin D. and Mark T. Holder. Taxonomic supertree construction with *incertae sedis* taxa. In Tandy Warnow, editor, *Bioinformatics and Phylogenetics*, pages 151–173. Springer, 2019.

[9] Redelings, Benjamin D. and Mark T. Holder. A supertree pipeline for summarizing phylogenetic and taxonomic information for millions of species. *PeerJ*, 5:e3058, 2017. ISSN 2167-8359. link.

[10] Holder, Mark T. and Emily Jane B. McTavish. Phylogenetic tree comparison. In *Encyclopedia of Evolutionary Biology*, pages 277–284. Elsevier, 2016.

[11] Lewis, Paul O, Mark T Holder, and David L Swofford. Phycas: Software for Bayesian phylogenetic analysis. *Systematic Biology*, 64(3):525–531, 2015. link.

[12] McTavish, Emily Jane, Mike Steel, and Mark T. Holder. Twisted trees and inconsistency of tree estimation when gaps are treated as missing data - the impact of model mis-specification in distance corrections. *Molecular Phylogenetics and Evolution*, 93:289–295, 2015a. link.

[13] McTavish, Emily Jane B, Cody E Hinchliff, James F Allman, Joseph W Brown, Karen A Cranston, Mark T Holder, Jonathan A Rees, and Stephen A Smith. Phylesystem: a git-based data store for community curated phylogenetic estimates. *Bioinfomatics*, 31(17):2794–2800, 2015b. link.

[14] Holder, Mark T., Paul O. Lewis, David L. Swofford, and David Bryant. Variable tree topology stepping-stone marginal likelihood estimation. In Ming-Hui Chen, Lynn Kuo, and Paul O. Lewis, editors, *Bayesian Phylogenetics: Methods, Algorithms, and Applications*, pages 95–112. CRC, Boca Raton, FL, USA, 2014.

[15] Oaks, Jamie R., Jeet Sukumaran, Jacob A. Esselstyn, Charles W. Linkem, Cameron D. Siler, Mark T. Holder, and Rafe M. Brown. Evidence for climate-driven diversification? a caution for interpreting ABC inferences of simultaneous historical events. *Evolution*, 67:991–1010, 2013. link.

[16] Ayres, Daniel L., Aaron Darling, Derrick J. Zwickl, Peter Beerli, Mark T. Holder, Paul O. Lewis, John P. Huelsenbeck, Fredrik Ronquist, David L. Swofford, Michael P. Cummings, Andrew Rambaut, and Marc A. Suchard. BEAGLE: an application programming interface and high-performance computing library for statistical phylogenetics. *Systematic Biology*, 61(1):170–173, 2012. link.

[17] Heath, Tracy A., Mark T. Holder, and John P. Huelsenbeck. A Dirichlet process prior for estimating lineage-specific substitution rates. *Molecular Biology and Evolution*, 29(3):939–955, 2012. link.

[18] Koch, Jordan M. and Mark T. Holder. An algorithm for calculating the probability of classes of data patterns on a genealogy. *PLOS Currents Tree of Life*, Dec 14 [last modified: 2012 Dec 14](1), 2012. link.

[19] Liberles, David A., Sarah A. Teichmann, Ivet Bahar, Ugo Bastolla, Jesse Bloom, Erich Bornberg-Bauer, Lucy J. Colwell, A. P. Jason de Koning, Nikolay V. Dokholyan, Julian Echave, Arne Elofsson, Dietlind L. Gerloff, Richard A. Goldstein, Johan A. Grahnen, Mark T. Holder, Clemens Lakner, Nicholas Lartillot, Simon C. Lovell, Gavin Naylor, Tina Perica, David D. Pollock, Tal Pupko, Lynne Regan, Andrew Roger, Nimrod Rubinstein, Eugene Shakhnovich, Kimmen Sjölander, Shamil Sunyaev, Ashley I. Teufel, Jeffrey L. Thorne, Joseph W. Thornton, Daniel M. Weinreich, and Simon Whelan. The interface of protein structure, protein biophysics, and molecular evolution. *Protein Science*, 21(6):769–785, 2012. link.

[20] Liu, Kevin, Tandy J. Warnow, Mark T. Holder, Serita Nelesen, Jiaye Yu, Alexandros Stamatakis, and C. Randal Linder. SATé-II: Very fast and accurate simultaneous estimation of multiple sequence alignments and phylogenetic trees. *Systematic Biology*, 61(1):90–106, 2012. link.

[21] Peterson, A. Townsend and Mark T. Holder. Phylogenetic assessment of Filoviruses: How many lineages of Marburg virus? *Ecology and Evolution*, 2(8):1826–1833, 2012. link.

[22] Vos, Rutger A., James P. Balhoff, Jason Caravas, Mark T. Holder, Hilmar Lapp, Wayne P. Maddison, Peter E. Midford, Anurag Priyam, Jeet Sukumaran, Xuhua Xia, and Arlin Stoltzfus. NeXML: rich, extensible, and verifiable representation of comparative data and metadata. *Systematic Biology*, 61(4):675–689, 2012. link.

[23] Edgcomb, Virginia, William Orsi, John Bunge, Sunok Jeon, Richard Christen, Chesley Leslin, Mark Holder, Gordon T. Taylor, Paula Suarez, Ramon Varela, and Slava Epstein. Protistan microbial observatory in the Cariaco Basin, Caribbean. I. species richness and endemicity. *ISME Journal*, 5(8):1344–1356, 2011. link.

[24] Holder, Mark T. and Mike Steel. Estimating phylogenetic trees from pairwise likelihoods and posterior probabilities of substitution counts. *Journal of Theoretical Biology*, 280(1):159–166, 2011. link.

[25] Lakner, Clemens, Mark T. Holder, Nick Goldman, and Gavin J. P. Naylor. What's in a likelihood? simple models of protein evolution and the contribution of structurally viable reconstructions to the likelihood. *Systematic Biology*, 60(2):161–174., 2011. link.

[26] Sukumaran, Jeet and Mark T. Holder. Ginkgo: spatially-explicit simulator of complex phylogeographic histories. *Molecular Ecology Resources*, 11(2):364–369, 2011. link.

[27] Allman, Elizabeth S., Mark T. Holder, and John A. Rhodes. Estimating trees from filtered data: Identifiability of models for morphological phylogenetics. *Journal of Theoretical Biology*, 263(1):108–119, 2010. link.

[28] Evans, Nathaniel M., Mark T. Holder, Marcos S. Barbeitos, Beth Okamura, and Paulyn Cartwright. The phylogenetic position of Myxozoa: Exploring conflicting signals in phylogenomic and ribosomal data sets. *Molecular Biology and Evolution*, 27(12):2733–2746, 2010. link.

[29] Holder, Mark T., Paul O. Lewis, and David L. Swofford. The Akaike information criterion will not choose the no common mechanism model. *Systematic Biology*, 59(4):477–485, 2010a. link.

[30] Holder, Mark T., Jeet Sukumaran, and Rafe M. Brown. Recent developments in Bayesian phylogenetics. In Dipak K. Dey, Samiran Ghosh, and Bani K. Mallick, editors, *Bayesian Modeling in Bioinformatics*, pages 193–232. Chapman & Hall/CRC, 2010b.

[31] Peterson, A. Townsend, Sandra Knapp, Robert Guralnick, Jorge Soberón, and Mark T. Holder. The big questions for biodiversity informatics. *Systematics and Biodiversity*, 8(2):159–168, 2010. link.

[32] Sukumaran, J and Mark T. Holder. DendroPy: a Python library for phylogenetic computing. *Bioinformatics*, 26(12):1569–1571, 2010. link.

[33] Holder, Mark T., Jeet Sukumaran, and Paul O. Lewis. A justification for reporting majority-rule consensus tree in Bayesian phylogenetics. *Systematic Biology*, 57(5):814–821, 2008a. link.

[34] Holder, Mark T., Derrick J. Zwickl, and Christophe Dessimoz. Evaluating the robustness of phylogenetic methods to among-site variability in substitution processes. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 363:4013–4012, 2008b. link.

[35] Holder, Kristina Kichler and Mark T. Holder. Phylogeography and population genetics. In Pamela T. Plotkin, editor, *Biology and Conservation of Ridley Sea Turtles*, pages 107–118. Johns Hopkins University Press, 2007.

[36] Lapp, Hilmar, Sendu Bala, James P. Balhoff, Amy Bouck, Naohisa Goto, Mark Holder, Richard Holland, Alisha Holloway, Toshiaki Katayama, Paul O. Lewis, Aaron Mackey, Brian I. Osborne, William H. Piel, Sergei L. Kosakovsky Pond, Art Poon, Wei-Gang Qiu, Jason E. Stajich, Arlin Stoltzfus, Tobias Thierer, Albert J. Vilella, Rutger A. Vos, Christian M. Zmasek, Derrick Zwickl, and Todd J. Vision. The 2006 NESCent phyloinformatics hackathon: A field report. *Evolutionary Bioinformatics*, 3:357–366, 2007. link.

[37] Alfaro, Michael E. and Mark T. Holder. The posterior and the prior in Bayesian phylogenetics. *Annual Review of Ecology, Evolution, and Systematics*, 37:19–42, 2006. link.

[38] Gelfand, Alan E, John A. Silander, Jr., Shan-shan Wu, Andrew M. Latimer, Paul O. Lewis, Anthony G. Rebelo, and Mark Holder. Explaining species distribution patterns through hierarchical modeling. *Bayesian Analysis*, 1:41–92, 2006. link.

[39] Holder, Mark T., Paul O. Lewis, David L. Swofford, and Bret Larget. Hastings ratio of the local proposal used in Bayesian phylogenetics. *Systematic Biology*, 54:961–965, 2005. link.

[40] Lewis, Paul O., Mark T. Holder, and Kent E. Holsinger. Polytomies and Bayesian phylogenetic inference. *Systematic Biology*, 54:241–253, 2005. link.

[41] Zwickl, Derrick J. and Mark T. Holder. Model parameterization, prior distributions and the general time-reversible model in Bayesian phylogenetics. *Systematic Biology*, 53:877–888, 2004. link.

[42] Holder, Mark T. and Paul O. Lewis. Phylogeny estimation: Traditional and Bayesian approaches. *Nature Reviews Genetics*, 43:275–284, 2003. link.

[43] Brauer, Matthew J., Mark T. Holder, Laurie A. Dries, Derrick J. Zwickl, Paul O. Lewis, and David M. Hillis. Genetic algorithms and parallel processing in maximum-likelihood phylogeny inference. *Molecular Biology and Evolution*, 19(10):1717–1726, 2002. link.

[44] Holder, Mark T., Jennifer A. Anderson, and Alisha K. Holloway. Difficulties in detecting hybridization. *Systematic Biology*, 50(6):978–982, 2001. link.

[45] Hillis, David M. and Mark T. Holder. Reconstructing the tree of life. In *New Technologies for the Life Sciences: A Trends Guide.*, volume *Supplement to Trends Journals*, pages 47–50. Elsevier, 2000.

[46] Holder, Mark T., Mark V. Erdmann, Thomas P. Wilcox, Roy L. Caldwell, and David M. Hillis. Two living species of coelacanths? *Proceedings of the National Academy of Sciences*, 96(22):12616–12620, 1999. link.

[47] Kichler, Kristina L., Mark T. Holder, Scott K. Davis, Rene Marquez, and David Owens. Detection of multiple paternity in the Kemp's ridley sea turtle with limited sampling. *Molecular Ecology*, 8:819–830, 1999. link.

[48] Burns, BM, JF Taylor, KL Herring, AD Herring, MT Holder, JS Collins, TM Guerra, JO Sanders, and SK Davis. Bovine microsatellite dinucleotide repeat polymorphisms at the texan11, texan12, texan13, texan14 and texan15 loci. *Animal Genetics*, 26(3):201–201, 1995a. link.

[49] Burns, BM, JF Taylor, KL Herring, AD Herring, MT Holder, JS Collins, TM Guerra, JO Sanders, and SK Davis. Bovine microsatellite mononucleotide and dinucleotide repeat polymorphisms at the texan6, texan7, texan8, texan9 and texan10 loci. *Animal Genetics*, 26(2):128–129, 1995b. link.

[50] Burns, BM, JF Taylor, KL Herring, AD Herring, MT Holder, DA Holder, JS Collins, JO Sanders, and SK Davis. Bovine microsatellite dinucleotide repeat polymorphisms at the texan16, texan17, texan18, texan19 and texan20 loci. *Animal Genetics*, 26(3):208–209, 1995c. link.

[51] Holder, DA, E. Arevalo, MT Holder, JF Taylor, and SK Davis. Bovine microsatellite dinucleotide repeat polymorphisms at the texan-1, texan-2, texan-3, texan-4 and texan-5 loci. *Animal Genetics*, 25(3):201–201, 1994. link.

Scholarly Presentations

* indicates the presenter if not MTH.

[1] Mark T. Holder. "Open Tree overview" BiCIKL Roundtable Meeting at GBIF. 27 April, 2023.

[2] Mark T. Holder, Emily Jane B. McTavish, Karen A. Cranston "The Need for Semantically Rich Notions of "Taxa" for Interoperability in Biodiversity Informatics". AGU meeting, San Francisco, CA, 10 December, 2019.

[3] Mark T. Holder "Open Tree of Life and Species Delimitation". University of Florida, Gainesville, 30 November, 2018.

[4] Mark T. Holder "Missing data in phylogenomics: when is it a problem?". Debate at Soc. Systematic Biologists meeting. Baton Rouge, LA. January, 2017.

[5] Benjamin D. Redelings* and Mark T. Holder "New methods for constructing the supertree of life". Evolution Meetings. Austin, TX, June 2016.

[6] Emily Jane McTavish* and Mark T. Holder "Continually updated phylogenies". SSB Spotlight Symposium at the Evolution Meetings. Austin, TX, June 2016.

[7] Mark T. Holder "Using peyotl and Open Tree of Life APIs". Lightning talk at the iEvoBio satellite conference to the Evolution meeting. Raleigh, NC. June, 2014.

[8] Mark Holder and Jordan M. Koch. "The statistical and informatics challenges posed by ascertainment biases in phylogenetic data collection". Lightning talk at the iEvoBio satellite conference to the Evolution meeting. Snowbird, UT. June, 2013.

[9] Mark Holder, Paul O. Lewis, David L. Swofford, and David Bryant. "Multitree Generalized Steppingstone Sampling - A New MCMC method for estimating the marginal likelihood of a model". Symposium on New Methods for Phylogenomics and Metagenomics. The University of Texas at Austin. February 16, 2013

[10] I. W. Gapp*, M. T. Holder, and B. S. Lieberman. 2012. "Comparing And Contrasting Parsimony And Maximum Likelihood Approaches To Paleontological Phylogenetics Using Trilobites As A Model System" Geological Society of America Annual Meeting, Charlotte, NC. November, 2012.

[11] Daniel Money*, Mark Holder. "Detecting and correcting alignment overcompression" Annual Meeting of the Society for Molecular Biology and Evolution. Dublin, Ireland. June, 2012.

[12] Steve Davis*, K. Taro Eldredge, and Mark T. Holder "Branch length estimates from morphological character data". Poster at the Joint Annual meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN), Ottawa, Ontario, Canada. July, 2012.

[13] Jordan M. Koch* and Mark T. Holder "Algorithms for Calculating Pattern Class Probabilities on Phylogenetic Trees" KU Undergraduate Research Symposium. Spring 2012.

[14] Derrick J. Zwickl* and Mark T. Holder "A simple insertion-deletion mixture model for phylogenetic inference." Frontiers in Phylogenetics Symposium, Smithsonian Institution. May 20, 2012.

[15] Mark T. Holder* "Some phylogenetic research projects in need of biophysical and structural insight." at a NESCent catalysis meeting titled "Modeling protein structural and energetic constraints on sequencing evolution" organized by David Liberles and Sarah Teichmann. October 20, 2011.

[16] I. W. Gapp*, M. T. Holder, and B. S. Lieberman. 2011. "Building phylogenetic trees for trilobites using maximum likelihood." Geological Society of America Annual Meeting, Minneapolis, MN. October, 2011.

[17] Derrick J. Zwickl* and Mark T. Holder "A simple insertion-deletion mixture model for phylogenetic inference." Joint Annual Meeting of the Society for the Study of Evolution, the Society of Systematic Biologists and the American Society of Naturalists, Norman, OK. June 19, 2011.

[18] Tracy A. Heath*, Mark T. Holder, and John P. Huelsenbeck. 2011. "Estimating lineage-specific substitution rates under a Dirichlet process prior". Evolution 2011, Norman, Oklahoma, USA.

[19] Mark T. Holder* "Incremental Phylogenetics" at the Next Generation Sequencing: Transformative Technology for Biodiversity Science workshop. held at the Smithsonian, National Museum of Natural History. April 18, 2011.

[20] Mark T. Holder* "ML tree inference using gap-coding" at the Workshop on Challenges for Large-scale Phylogeny and Alignment Estimation held at the National Evolutionary Synthesis Center, Durham, NC. March 31, 2011.

[21] Heath, Tracy A.*, John P. Huelsenbeck, and Mark T. Holder. "Dirichlet process models for estimating lineage-specific substitution rates and dating species divergences". Society of Systematic Biologists Symposium: Paleontological and neontological approaches to dating the Tree of Life, Evolution 2010, Portland, Oregon, USA. (invited presentation).

[22] Mark T. Holder*, Paul O. Lewis, and David L. Swofford "Estimating marginal likelihoods for phylogenetic models in Phycas" at the iEvoBio Meeting held with the Annual Meeting of the

Society for the Study of Evolution in Norman, OK. June, 2011.

[23] Jeet Sukumaran* and Mark T. Holder "Performance and Robustness of Phylogeographic Statistics under Complex Simulations". Joint Annual meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN), Portland, Oregon, USA June 2010.

[24] Jeet Sukumaran and Mark T. Holder* "Phylogenetic operations in Python with DendroPy" at iEvoBio Meeting held with the Annual Meeting of the Society for the Study of Evolution in Portland, OR. June, 2010.

[25] Jeet Sukumaran*, Mark T. Holder and Rafe Brown 2009. "Evaluating the Performance of Phylogeographic Test Statistics using Complex Simulations". Joint Annual meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN), Moscow, Idaho, USA, June 2009.

[26] Mark T. Holder* "Incremental phylogenetics – estimating trees by adding leaves to collections of previous estimates" at the Annual Meeting of the Society for the Study of Evolution in Moscow, ID. June 16, 2009.

[27] Mark T. Holder* "Evaluating the performance of phylogenetic inference methods on heterogeneous data" at the Royal Society of London Discussion Meeting on Statistical and Computational Challenges in Molecular Phylogenetics and Evolution. April 28-29, 2008.

[28] Mark T. Holder*, Jeet Sukumaran, and Paul O. Lewis, "Minimum Posterior Expected Loss Trees" at the Phylogenetics Programme hosted by the Isaac Newton Institute for Mathematical Sciences. December 03, 2007.

[29] Peter Beerli and Mark T. Holder*, "Maximum Likelihood and Bayesian Inference in Population Genetics and Phylogenetics," in the mini-symposium "Monte Carlo Computations in Biology and Materials Science" at the 2005 SIAM Conference on Computational Science and Engineering.

[30] Mark T. Holder* and Paul O. Lewis, "Examining the effects of branch length priors on clade support" at the Annual Meeting of the Society for the Study of Evolution in Chico, CA. 2003.

[31] Mark T. Holder*, Paul O. Lewis, and David L. Swofford, "Should we assume a common set of branch lengths for different sets of characters?" at the Annual Meeting of the Society for the Study of Evolution in Champaign/Urbana, Illinois. 2002.

[32] Mark T. Holder*, "Using a Complex Model of Sequence Evolution to Evaluate Phylogenetic Methods" at the Annual Meeting of the Society for the Study of Evolution in Knoxville, KY. 2001.

[33] Mark T. Holder* "Using branch flexibility to detect uncertainty in phylogenies" at the Annual Meeting of the Society for the Study of Evolution in Vancouver, BC. 1999.

[34] Mark T. Holder*, David Cannatella, A. Stanley Rand, Mike Ryan, and Adao Cardoso "Phylogeny of the frog genus *Physalaemus* with implications for evolution of call types in the group" at the Annual Meeting of the Society for the Study of Evolution in Boulder, CO. 1998.

Funding

using tapeworms and their shark and ray hosts". March, 2015 – Feb, 2018. NSF-DEB-1457776. Co-PI with K. Jensen at KU (approximately $315,000). Lead institution: U. Connecticut.

[3] "Integrating Fossil Data into Likelihood-based Phylogenetic Analyses with Trilobites as a Model System" NSF-DEB-1256993. May, 2013 – April, 2016 $450,000. Holder is the PI. Bruce Lieberman (also at KU) is the Co-PI. Tracy Heath was a co-author of the proposal and was listed as senior personnel on the award.

[4] "Collaborative Research Automated and community-driven synthesis of the tree of life" NSF-DEB-1208393 + supplemental award. June, 2012–May, 2017.(Collaborative grant with ten institutions. KU approximately $800,000).

[5] "Collaborative Research Large-scale simultaneous multiple alignment and phylogeny estimation." NSF-DEB-0732920. Oct. 1, 2007 – Sept. 30, 2012 (Collaborative award with research at U. Texas; U. Nebraska; U. Georga; and the Smithosnian. KU funds $668,640).

[6] CIPRES GRA subaward from the University of Texas from funds from the "Cyber Infrastructure for Phylogenetic Research." NSF ITR-0604212 award. August, 2007 – August, 2008 and Oct 1, 2008 - Sept 30, 2009. ($129,145)

[7] Postdoctoral Research Fellowship in Biological Informatics National Science Foundation. September, 2003 – August, 2004.

[8] Predoctoral Fellowship National Science Foundation. 1995 – 1998.

Mentoring

Postdoctoral researchers:

[1] Dr. Benjamin D. Redelings (2015-2023)
[2] Dr. June Walker (2017-2018; subsequently a postdoc. at Iowa State University)
[3] Dr. April M. Wright (2015-2016; now an Associate Prof. at Southeastern Louisiana U.)
[4] Dr. Jeet Sukumaran (2015-2017; now an Associate Prof. at San Diego State University)
[5] Dr. Emily Jane McTavish (2013-2016; now an Associate Prof. at U. C. Merced)
[6] Dr. Daniel P. Money (2011-2013; now a postdoc. at the University of Cambridge)
[7] Dr. Tracy Heath (2008-2010; now Associate Prof. at Iowa State University)
[8] Dr. Derrick Zwickl (2008-2014; now a research associate U. Arizona)
[9] Dr. Jiaye Yu (2008-2010; now employed by OmicSoft)
[10] Dr. Peter Midford (2007-2009; now a computational biologist at SRI International)

Graduate students:

[1] Dr. Jeet Sukumaran (2007-2012; co-advised with Dr. Rafe Brown; currently Associate Professor at San Diego State University)
[2] Dr. Jamie R. Oaks (2009-2013; co-advised with Dr. Rafe Brown; currently Associate Professor at Auburn University)
[3] Mr. Liam Heins (2014-2017; currently a software developer).
[4] Ms. Meg Nibbelink (2024–present;).

Software

Propinquity: supertree pipeline for Open Tree of Life project. https://github.com/OpenTreeOfLife/propinquity Authorship: Benjamin D. Redelings and Mark T. Holder

otcetera: C++ tree and supertree tools for Open Tree of Life project. https://github.com/OpenTreeOfLife/otcetera Authorship: Benjamin D. Redelings and Mark T. Holder

peyotl: Python phylogenetic utilities for Open Tree of Life project. http://opentreeoflife.

`github.io/peyotl/` Authorship: Mark T. Holder, Emily Jane B. McTavish, Jim Allman, Karen A. Cranston, Jonathan A. Rees, Joseph W. Brown, and Stephen A. Smith.

Phycas: software for Bayesian phylogenetic inference. `http://www.phycas.org` Authorship: Paul O. Lewis, Mark T. Holder and David L. Swofford

DendroPy: phylogenetic computing library `http://packages.python.org/DendroPy` Authorship: Jeet Sukumaran and Mark T. Holder

SATé: software for simultaneous tree and alignment estimation `http://phylo.bio.ku.edu/software/sate/sate.html` Authorship: Dr. Jiaye Yu, Mark T. Holder, Jeet Sukumaran, Siavash Mirarab, and Jamie Oaks.

Contributions to community software projects

NEXUS class library: a library for parsing the NEXUS file format used for systematics data `http://sourceforge.net/projects/ncl` Authorship: originally written by Paul Lewis. NCL is maintained by Mark T. Holder

libhmsbeagle: A general purpose library for evaluating the likelihood of sequence evolution on trees `http://code.google.com/p/beagle-lib` Lead authors: Marc Suchard, Andrew Rambaut, and Daniel Ayres.

Open Tree of Life: contributing author to some of the software packages hosted at: `https://github.com/organizations/OpenTreeOfLife` for the NSF-funded Open Tree of Life project.

Other: several other small programming projects are available on my GitHub page: `https://github.com/mtholder`

Other Relevant Activities

Working groups: Species File Group 2025 Workshop on Taxonomic Names (2–7 March, 2025) FuturePhy+OpenTree+Arbor "Clade" workshops (Feb. and Oct. 2016). Participant in the Phylotastic hackathon at NESCent (June 2012). Participant in NESCent Catalysis meeting on "Modeling protein structural and energetic constraints on sequence evolution" (Oct. 2011). Mentor in NESCent's Google Summer of Code program. Member of the iEvoBio Organizing Committee for 2011. BEAST working group (NESCent-sponsored; 2009-present). Isaac Newton Institute Programme on Phylogenetics (Nov. and Dec. 2007). NESCent Evolutionary Informatics Working Group (2007-2008). NESCent Phyloinformatics hackathon (Dec. 2006).

Associate editor: *Systematic Biology* (2008-2022) and *BMC Evolutionary Biology* (2011-March 2013).

Reviewer: Intelligent Systems for Molecular Biology (ISMB) Program Committee (2006, 2007, 2013). *Biology Letters*, *Bioinformatics*, *BMC Bioinformatics*, *Evolution*, *Evolutionary Bioinformatics*, *ISMB*, *Journal of Theoretical Biology*, *Molecular Biology and Evolution*, *Molecular Ecology*, *Molecular Phylogenetics and Evolution*, *PLoS Currents: Tree of Life*, *PLoS: ONE*, *PeerJ*, *Proceedings of the National Academy of Sciences (USA)*, *Systematic Biology*.

Society activities: Council member for the Society of Systematic Biologists.

Other mentoring: taught computational biology workshops for KU's chapter of Society for Advancement of Chicanos/Hispanics and Native Americans in Science (SACNAS). Also served as a mentor for the KU-Iowa State SACNAS grant writing workshops (in Lawrence 2017 and 2019; in Ames, Iowa 2018). One-on-one mentor at SACNAS meeting (2018)