<center>CURRICULUM VITAE</center>

Tracy A. Heath

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EDUCATION

Ph.D.	2008	University of Texas at Austin, Ecology, Evolution, & Behavior
B.A.	2000	Boston University, Biology

ACADEMIC POSITIONS

2015–present	**Assistant Professor**
	Dept. of Ecology, Evolution, & Organismal Biology, Iowa State University
2010–2015	*Associate Research Specialist*
	Dept. of Integrative Biology, University of California, Berkeley
2013–2015	*Postdoctoral Researcher*
	Dept. of Ecology & Evolutionary Biology, University of Kansas
2008–2010	*NSF Postdoctoral Fellow in Biological Informatics*
	University of Kansas & University of California, Berkeley
2003–2008	*NSF IGERT Graduate Research Trainee*
	Computational Phylogenetics, University of Texas at Austin
2007	*Visiting Scholar*
	Biomathematics Research Centre, Christchurch, NZ
2002–2007	*Graduate Research Assistant*
	School of Biological Sciences, University of Texas at Austin
2000–2001	*DNA Sequencing Facility Manager*
	Department of Biology, Boston University
2000	*Research Assistant*
	Department of Biology, Boston University

PUBLICATIONS

Citations (Google Scholar, February 2018): 1,695 • Erdös Number: 3

Stadler, T., A. Gavryushkina, R.C.M. Warnock, A.J. Drummond, **T.A. Heath**. 2017. The fossilized birth-death model for the analysis of stratigraphic range data under different speciation concepts. *Journal of Theoretical Biology*, 447:41-55.

Barido-Sottani, J., V. Bošková, L. du Plessis, D. Kühnert, C. Magnus, V. Mitov, N.F. Müller, J. Pečerska, D.A. Rasmussen, C. Zhang, A.J. Drummond, **T.A. Heath**, O.G. Pybus, T.G. Vaughan, T. Stadler. 2018. Taming the BEAST – A community teaching material resource for BEAST 2. *Systematic Biology*, 67:170–174.

Höhna, S., M.J. Landis, and **T.A. Heath**. Phylogenetic inference using RevBayes. 2017. *Current Protocols in Bioinformatics*, 57:6.16.1–6.16.34.

Gavryushkina, A., **T.A. Heath**, D.T. Ksepka, T. Stadler, D. Welch, and A.J. Drummond. 2017. Bayesian total evidence dating reveals the recent crown radiation of penguins. *Systematic Biology*, 66:57–73.

Höhna, S., M.J. Landis, **T.A. Heath**, B. Boussau, N. Lartillot, B.R. Moore, J.P. Huelsenbeck, and F. Ronquist. 2016. RevBayes: Bayesian phylogenetic inference using graphical models and an interactive model-specification language. *Systematic Biology*, 65:726–736.

Zhang, C., T. Stadler, S. Klopfstein, **T.A. Heath**, and F. Ronquist. 2016. Total-evidence dating under the fossilized birth-death process. *Systematic Biology*, 65:228–249.

Cook, J.A., S.V. Edwards, E.A. Lacey, R.P. Guralnick, P.S. Soltis, D.E. Soltis, C.K. Welch, K.C. Bell, K.E. Galbreath, C. Himes, J.M. Allen, **T.A. Heath**, A.C. Carnival, K.L. Cooper, M. Liu, J. Hanken, and S. Ickert-Bond. 2014. Natural history collections as emerging resources for innovative education. *Bioscience*, 64:725–734.

Heath, T.A., J.P. Huelsenbeck, and T. Stadler. 2014. The fossilized birth-death process for coherent calibration of divergence-time estimates. *Proceedings of the National Academy of Sciences*, 111(29):E2957–E2966.

Höhna, S., **T.A. Heath**, B. Boussau, M.J. Landis, F. Ronquist, and J.P. Huelsenbeck. 2014. Probabilistic graphical model representation in phylogenetics. *Systematic Biology*, 63:753–771

Heath, T.A. and B.R. Moore. 2014. Bayesian inference of species divergence times. In: Chen, M.-H., L. Kuo, and P.O. Lewis (editors). *Bayesian Phylogenetics: Methods, Algorithms, and Applications*. Chapman & Hall/CRC.

Stoltzfus, A., H. Lapp, N. Matasci, H. Deus, B. Sidlauskas, C.M. Zmasek, G. Vaidya, E. Pontelli, K. Cranston, R. Vos, C.O. Webb, L.J. Harmon, M. Pirrung, B. O'Meara, M.W. Pennell, S. Mirarab, M.S. Rosenberg, J.P. Balhoff, H.M. Bik, **T.A. Heath**, P.E. Midford, J.W. Brown, E.J. McTavish, J. Sukumaran, M. Westneat, M.E. Alfaro, A. Steele, and G. Jordan 2013. Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. *BMC Bioinformatics*, 14:158.

Darriba, D., A. Aberer, T. Flouri, **T.A. Heath**, F. Izquierdo-Carrasco, and A. Stamatakis. 2013. Boosting the performance of Bayesian divergence time estimation with the Phylogenetic Likelihood Library. *IEEE 27th International Symposium on Parallel & Distributed Processing* doi:10.1109/IPDPSW.2013.267. (peer-reviewed conference proceedings)

Heath, T.A. 2012. A hierarchical Bayesian model for calibrating estimates of species divergence times. *Systematic Biology*, 61:793-809.

Heath, T.A., M.T. Holder, and J.P. Huelsenbeck. 2012. A Dirichlet process prior for estimating lineage-specific substitution rates. *Molecular Biology and Evolution*, 29:939-955.

Heath, T.A., S.M. Hedtke, and D.M. Hillis. 2008. Taxon sampling and the accuracy of phylogenetic analyses. *Journal of Systematics and Evolution*, 46:239-257.

Heath, T.A., D.J. Zwickl, J. Kim, and D.M. Hillis. 2008. Taxon sampling affects inferences of macroevolutionary processes from phylogenetic trees. *Systematic Biology* 57:160-166.

Hillis, D.M., **T.A. Heath**, and K. St. John. 2005. Analysis and visualization of tree space. *Systematic Biology*, 54(3):471-482. (cover article)

Wilcox, T.P., D.J. Zwickl, **T.A. Heath**, and D.M. Hillis. 2002. Phylogenetic relationships of the dwarf boas and a comparison of Bayesian and bootstrap measures of phylogenetic support. *Molecular Phylogenetics and Evolution*, 25(2):361-371.

Software

RevBayes (C/C++) – Bayesian phylogenetic inference using probabilistic graphical models and an interpreted language (developer; http://revbayes.com)

DPPDiv (C++) – Bayesian estimation of species divergence times under a Dirichlet process prior (developer; https://github.com/trayc7/FDPPDIV)

FossilGen (C++) – A program for simulating phylogenies and fossil occurrence times under the serial-sampled birth-death process (developer; https://github.com/trayc7/FossilGen)

`datelife (R/Python)` – A web service that synthesizes divergence time estimates from published studies–
a Phylotastic service (contributor; http://www.datelife.org, http://phylotastic.org)

`varphylogen (C++)` – Tree topology simulation under a variable birth-death process (developer; Heath et
al. 2008 *Syst. Biol.* 57:160-166)

`TreeSetViz (Java)` – Multidimensional scaling for visualizing and summarizing large sets of phylogenetic
trees (contributor; Hillis et al. 2005 *Syst. Biol.* 54:471-482)

INVITED PRESENTATIONS AND SEMINARS

CONFERENCES & SYMPOSIA

2018 The Molecular Tree of Life Symposium, Jiangsu Normal University, Xuzhou, China
2017 SMBE Symposium, Society for Molecular Biology & Evolution, Austin, TX
2016 Bird 10K Genome Project Workshop, Beijing, China
2016 Jacques Monod Conference on Molecular Evolution, Roscoff, France
2013 Phyloseminar.org Series on Integrating Fossils into Molecular Phylogenies (video)
2013 France-Berkeley Fund Symposium on Fossils & Phylogenetics, Berkeley, CA
2012 Symposium on Molecular Dating, Hennig XXXI, Riverside, CA
2011 Symposium on Bayesian Inference of Phylogeny, Berkeley, CA
2011 Bay Area Biosystematists Meeting, Berkeley, CA
2010 SSB Symposium, Evolution 2010, Portland, OR
2006 CIPRES Symposium & Workshop on Evolutionary Simulation, Philadelphia, PA

DEPARTMENTAL SEMINARS

2018 Montana State University, Department of Earth Sciences Seminar
2018 University of New Mexico, Biology Department Seminar
2017 University of Michigan, UMMZ Hubbell Invited EEB Speaker
2016 University of Idaho, Institute for Bioinformatics and Evolutionary Studies Seminar
2016 American Museum of Natural History, Comparative Biology Seminar
2016 Indiana University, Dept. of Biology EEB Seminar
2015 University of Missouri, EEB Seminar
2015 University of Minnesota, EEB Seminar
2014 The European Bioinformatics Institute, EMBL-EBI External Seminar Series
2014 University of California, Berkeley, Museum of Paleontology Seminar
2014 University of Connecticut, Ecology & Evolutionary Biology Seminar
2014 Smithsonian Institution National Museum of Natural History, PhyloPizza Seminar
2014 Auburn University, Department of Biological Sciences Seminar
2014 North Carolina State University, Bioinformatics Seminar
2014 University of Alabama, Department of Biological Sciences Seminar
2014 UCLA, Division of Life Sciences Faculty Mentorship Colloquium
2013 Iowa State University, Ecology, Evolution, & Organismal Biology Seminar
2013 Brown University, Center for Computational Molecular Biology Seminar
2013 Brigham Young University, Biology Department Seminar
2013 Cornell University, Ecology & Evolutionary Biology Seminar
2013 University of Washington PopGenLunch Seminar
2013 Bowdoin College, Biology Department Seminar
2013 Texas Tech University, Department of Biological Sciences Seminar
2012 California Academy of Sciences, Research Seminar

2012 University of California, Davis, Center for Population Biology Seminar

CONTRIBUTED PRESENTATIONS

2015 Iowa State University, EEB Spring Symposium
2014 Society for Vertebrate Paleontology (education/outreach poster), Berlin, Germany
2014 SACNAS 2014 (professional development session), Los Angeles, CA, USA*
2014 iEvoBio 2014, Raleigh, NC, USA*
2013 Evolution 2013, Snowbird, UT, USA*
2012 Evolution 2012, Ottawa, Ontario, Canada*
2011 Evolution 2011, Norman, OK, USA
2009 Evolution 2009, Moscow, ID, USA
2007 Evolution 2007, Christchurch, New Zealand
2007 The Annual New Zealand Phylogenetics Meeting – Doom07, Whakapapa, NZ
2006 Evolution 2006, Stony Brook, NY, USA
2006 NSF IGERT Project Meeting (poster), Arlington, VA, USA
2004 Evolution 2004, Fort Collins, CO, USA

*slides available at http://www.slideshare.net/trayc7

NATIONAL AND INTERNATIONAL WORKSHOPS

2017 Introduction to Bayesian inference of phylogenies using molecular and fossil data in RevBayes, International Biogeography Society, Bengaluru, India
2017 Phylogenetic Inference Using RevBayes, NIMBios, Knoxville, TN USA
2017 Taming the BEAST – Workshop on Bayesian Evolutionary Analysis by Sampling Trees, Waiheke Island, New Zealand
2017 Workshop on Phylogenomics, Český Krumlov, Czechia
2017 RevBayes: Analysis of Fossil and Molecular Data, SSB Meeting, Baton Rouge, LA USA
2016 Taming the BEAST – Workshop on Bayesian Evolutionary Analysis by Sampling Trees, Engelberg, Switzerland
2015 Model-Based Molecular Systematics Workshop at Evolution 2015, Guarujá, Brazil
2015 Workshop on Bayesian Divergence Time Estimation at Society of Systematic Biologists Meeting 2015, Ann Arbor, MI USA
2014–2016 Advanced Course on Computational Molecular Evolution, European Molecular Biology Organization, Institute of Marine Biology, Biotechnology and Aquaculture, Hellenic Centre for Marine Research, Heraklion, Greece
2014 NESCent Academy Course: Phylogenetic Analysis Using RevBayes, National Evolutionary Synthesis Center (NESCent), Durham, NC USA
2013–2016 Advanced Course on Computational Molecular Evolution, Wellcome Trust and European Bioinformatics Institute, Hinxton, UK
2013 Workshop on Molecular Evolution, Český Krumlov, Czechia
2012–2018 Workshop on Molecular Evolution, Marine Biological Laboratory, Woods Hole, MA USA
2011–2015 Bodega Applied Phylogenetics Workshop, Bodega Bay, CA USA

PROFESSIONAL SERVICE

2018 Organizer, SSB Ernst Mayr Award Symposium, Evolution Meetings, Montpellier, France

2017–2020	Diversity Committee Member, American Society of Naturalists
2017	*ad hoc* Reviewer, National Science Foundation (DEB)
2017	Organizer, SSB Ernst Mayr Award Symposium, Evolution Meetings, Portland, OR
2017	Panelist, National Science Foundation (DEB), Arlington, VA
2016–2019	Awards Director, Society of Systematic Biologists Executive Council
2016	Organizer, Scientific Symposium on "(Day and) Night at the Museum: Exploring Research in Ecology and Evolution behind the Scenes of Natural History Museums", SACNAS National Conference, Long Beach, CA
2016	Ph.D. Defense External Evaluator, Louis du Plessis, ETH Zürich
2016	Organizer, SSB Spotlight Session on "Next-generation Phylogenetic Inference", Evolution Meetings, Austin, TX
2016	Organizer, SSB Ernst Mayr Award Symposium, Evolution Meetings, Austin, TX
2016	Ph.D. Thesis Reviewer, Australian National University
2015	Organizer, SSB Symposium on "Breaking Barriers: Empirical, Theoretical, and Gender Issues in Phylogenetics", Evolution Meetings, Guarujá, Brazil
2015	Judge, Ernst Mayr SSB Graduate Student Presentation Award, Evolution Meetings, Guarujá, Brazil
2015	Textbook Chapter Reviewer for *Life: The Science of Biology*
2015	Panelist, National Science Foundation (DEB), Arlington, VA
2013–2015	Elected Council Member, Society of Systematic Biologists
2014	Session Chair and Organizer, Professional Development Session on Computational Biology at the SACNAS National Conference (crackingthebiocode.github.io)
2013	Organizing Committee Member, *iEvoBio 2013* Conference, Snowbird, UT
2012 & 2014	Proposal Reviewer, The Society of Systematic Biologists Graduate Student Research Award Competition
2012	Proposal Reviewer, The Graduate Women in Science 2012 National Fellowships Program
2008–present	Editorial Board Member, *Systematic Biology*
2006–present	Reviewer for: *Bioinformatics*, *BMC Evolutionary Biology*, *Ecology Letters*, *Evolution*, *Gene*, *Journal of Systematics & Evolution*, *Molecular Biology & Evolution*, *Nature Ecology & Evolution*, *Philosophical Transactions B*, *Proceedings B*, *PNAS*, *Systematic Biology*, *Trends in Ecology & Evolution*, *Trends in Genetics*

PROFESSIONAL AFFILIATIONS

- Society of Systematic Biologists
- Society for Advancement of Chicanos and Native Americans in Science (SACNAS)
- American Society of Naturalists

OUTREACH ACTIVITIES

2015–present	Member, Iowa State University SACNAS Chapter
2015–2017	Recruitment, Attended SACNAS National Conference as a representative of Iowa State University Graduate Programs
2016	Panelist, GEN 110 Faculty Panel, Iowa State University
2016	Field Trip Leader, The Rancho Santa Ana Botanic Garden, SACNAS National Conference, Long Beach, CA
2016	Social Media Street Team Member, SACNAS National Conference, Long Beach, CA
2016	Mentor for the Preparing Future Faculty Program at Iowa State University

2016	Invited Speaker, Biological Sciences Club (undergraduate student organization), Iowa State University
2015	Panelist, BIOL 110 Faculty Panel, Iowa State University
2015	Social Media Street Team Member, SACNAS National Conference, Washington, DC
2015	Panelist for large-format discussion on "iEvoBio: How to start software development in evolutionary biology" at the Soc. of Systematic Biologists Meeting, Ann Arbor, MI
2013–2015	Participant, AIM-UP!–Advancing Integration of Museums into Undergraduate Programs (NSF RCN-UBE DEB-0956129)
2014	Session Chair and Organizer, Professional Development Session on Computational Biology at the SACNAS National Conference (crackingthebiocode.github.io)
2013	Speaker, Girls Who Code Summer Program @Twitter, San Francisco, CA
2013	Participant, AdaCamp Unconference for Women in Open Technology, San Francisco, CA
2012–2014	Mentor for the Undergraduate Diversity at SSE/SSB Program
2011	Panelist, The Women in Science and Engineering Residential Program Seminar, U.C. Berkeley
2011	Panelist, The Initiative for Maximizing Student Development (IMSD) Graduate Fellows Program Workshop, U.C. Berkeley

MAJOR GRANTS

2018–2022	**National Science Foundation.** (DBI-1759909 & DBI-1759811) "Collaborative Research: ABI Development: Improving the stability, usability, and speed of the RevBayes platform for phylogenetic analysis" (start date: July 1, 2018) PIs: Tracy Heath and John Huelsenbeck (UC Berkeley)
2016–2020	**National Science Foundation.** (DEB-1556853) "Multilocus analyses of co-diversification and phylogenetic incongruence between highly coevolved figs and fig wasps" (start date: June 1, 2016) PI: John Nason, Co-PIs: Tracy Heath, Allen Herre (Smithsonian)
2016–2019	**National Science Foundation.** (DEB-1556615 & DEB-1556701) "Collaborative Research: Advancing Bayesian phylogenetic methods for synthesizing paleontological and neontological data" (start date: May 1, 2016) PI: Tracy Heath & Robert Meredith (Montclair State University), Co-PI: Daniel Ksepka (Bruce Museum).
2008–2010	**National Science Foundation.** (DBI-0805631) "Complex models of substitution rate variation and a comparison of Bayesian methods for estimating species divergence times" NSF PostDoctoral Research Fellowship in Biology