

CURRICULUM VITAE

Tracy A. Heath

Department of Ecology, Evolution & Organismal Biology
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CURRENT POSITION

Assistant Professor

Department of Ecology, Evolution, & Organismal Biology

Iowa State University

Ames, IA

January 2015 – present

EDUCATION

Ph.D. in Ecology, Evolution, and Behavior

August 2008
Advisor: David Hillis

University of Texas

Austin, TX

B.A. in Biology

May 2000

Boston University

Boston, MA

RESEARCH POSITIONS

Associate Research Specialist

Department of Integrative Biology

University of California, Berkeley

Berkeley, CA

December 2010 - December 2014

Postdoctoral Researcher

Department of Ecology and Evolutionary Biology

University of Kansas

Lawrence, KS

June 2013 - December 2014

Postdoctoral Research Fellow

NSF Fellowship in Biological Informatics
Supervisors: Mark Holder & John Huelsenbeck

University of Kansas

University of California, Berkeley

September 2008 - November 2010

Graduate Research Trainee

Integrative Graduate Education and Research Traineeship (IGERT)
Computational Phylogenetics and Applications to Biology

University of Texas

Austin, TX

2003 - 2005 & 2007 - 2008

Visiting Researcher

Biomathematics Research Centre
The Allan Wilson Centre for Molecular Ecology and Evolution

University of Canterbury

Christchurch, NZ

2007

Graduate Research Assistant

School of Biological Sciences

University of Texas

Austin, TX

CIPRES: Modeling and Simulation	2005 - 2007
Tree Set Visualization: Program Documentation and Web Page	2004
Tree Set Visualization: Analysis and Visualization of Tree Space	2003
Genetic Algorithms for Maximum Likelihood Inference (GAML)	2002

Laboratory Manager **Boston University**
 Department of Biology, DNA Sequencing Facility Boston, MA
 Supervisor: Michael Sorenson 2000 - 2001

Research Assistant **Boston University**
 Department of Biology, Evolutionary Genetics Lab Boston, MA
 Mentor: Christopher Schneider 2000

TEACHING

Workshop Instructor
 Wellcome Trust-EMBL-EBI-EMBO Course: Computational Molecular Evolution 2013 – 2015
 Workshop on Molecular Evolution, Woods Hole, MA 2012 – 2015
 Bodega Applied Phylogenetics Workshop, Bodega Bay, CA 2011 – 2015
 NESCent Academy Course: Phylogenetic Analysis Using RevBayes 2014
 Workshop on Molecular Evolution, Český Krumlov, Czech Republic 2013

*For teaching materials see: <http://treethinkers.org/tracy-heath-workshop-materials/>

Teaching Assistant/Laboratory Instructor **University of Texas**
 School of Biological Sciences Austin, TX
 Advanced Systematics (computer lab course) 2002 & 2007
 Vertebrate Natural History (lab/field course) 2002
 Limnology and Oceanography (lab/field course) 2001

PUBLICATIONS AND MANUSCRIPTS

- 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. (invited book chapter; <http://www.crcpress.com/product/isbn/9781466500792>)
- 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 (development team member; <http://revbayes.github.io>)
- DPPDiv (C++) – Bayesian estimation of species divergence times under a Dirichlet process prior (developer; <https://github.com/tracy7/FDPPDIV>)
- FossilGen (C++) – A program for simulating phylogenies and fossil occurrence times under the serial-sampled birth-death process (developer; <https://github.com/tracy7/FossilGen>)
- datelife (R/Python) – A web service that synthesizes divergence time estimates from published studies—a Phylotastic service (co-developer; <http://www.datelife.org>, <http://phylostatic.org>)
- TreeSetViz (Java) – Multidimensional scaling for visualizing and summarizing large sets of phylogenetic trees (contributor; <http://comet.lehman.cuny.edu/treeviz>)

INVITED TALKS

The European Bioinformatics Institute, EMBL-EBI External Seminar Series	2014
University of California, Berkeley, UCMP Fossil Coffee Seminar Series	2014
University of Connecticut, Ecology & Evolutionary Biology Seminar Series	2014
Smithsonian Institution National Museum of Natural History, PhyloPizza	2014
Brown University, Center for Computational Molecular Biology Seminar Series	2013
Phyloseminar.org Series on Integrating Fossils into Phylogenies (video link)	2013
Brigham Young University, Biology Department Seminar Series	2013
Cornell University, Ecology & Evolutionary Biology Weekly Seminar Series	2013
France-Berkeley Fund Symposium on Fossils & Phylogenetics, Berkeley, CA	2013

Bowdoin College, Biology Department Seminar Series	2013
California Academy of Sciences, Research Seminar Series	2012
University of California, Davis Center for Population Biology Seminar Series	2012
Symposium on Molecular Dating, Hennig XXXI, Riverside, CA	2012
Symposium on Bayesian Inference of Phylogeny, Berkeley, CA	2011
SSB Symposium, Evolution 2010, Portland, OR	2010
CIPRES Symposium & Workshop on Evolutionary Simulation, Philadelphia, PA, USA	2006

CONFERENCE PRESENTATIONS

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*	2014
Evolution 2013, Snowbird, UT, USA*	2013
Evolution 2012, Ottawa, Ontario, Canada*	2012
Evolution 2011, Norman, OK, USA	2011
Evolution 2009, Moscow, ID, USA	2009
Evolution 2007, Christchurch, New Zealand	2007
The Annual New Zealand Phylogenetics Meeting – Doom07, Whakapapa, NZ	2007
Evolution 2006, Stony Brook, NY, USA	2006
NSF IGERT Project Meeting (poster), Arlington, VA, USA	2006
Evolution 2004, Fort Collins, CO, USA	2004

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

GRANTS AND AWARDS

- NESCent Academy Course: Phylogenetic Analysis Using RevBayes — PI: T. Heath; Co-PIs: B. Boussau, S. Höhna, J. Huelsenbeck, M. Landis, B. Moore, F. Ronquist, T. Stadler (Summer 2014)
- NSF DEB-1256993: “Integrating Fossil Data into Likelihood-based Phylogenetic Analyses with Trilobites as a Model System” (<http://phylo.bio.ku.edu/fossil>) — PI: M. Holder, Co-PI: B. Lieberman, Postdoc/coauthor: T. Heath (2013 – 2016)
- NSF Postdoctoral Fellowship in Biological Informatics (2008 – 2010)
- University of Kansas/Haskell Indian Nations University NIH Institutional Research and Academic Career Development Award (IRACDA) Postdoctoral Fellowship (2008; declined)
- University of Texas Ecology, Evolution, and Behavior Program Hartman Merit Fellowship (2008)
- NSF, Integrative Graduate Education and Research Traineeship (IGERT) for graduate training in computational phylogenetics and applications to biology (2003 - 2008)
- NSF, Integrative Graduate Education and Research Traineeship (IGERT) Travel Award (2007)
- Allan Wilson Centre for Molecular Ecology & Evolution Summer Studentship, Biomathematics Research Centre, University of Canterbury, Christchurch, NZ (2007)
- University of Texas Ecology, Evolution, and Behavior Program Hamilton Fellowship (2006)
- Summer Institute in Statistical Genetics Scholarship, North Carolina State University (2004)

WORKSHOP AND HACKATHON PARTICIPATION

AIM-UP! Workshop on “Museums and Climate Change”, Pacific Grove, CA (February 2014)
 NESCent BEAST Developers Working Group; Durham, NC (December 2013)
 France-Berkeley Fund Workshop on Integrating Molecular Phylogenies and the Fossil Record;
 Organizers: H. Morlon, T. Quental, C. Marshall; Berkeley, CA (2013)
 AdaCamp Unconference for Women in Open Technology, San Francisco, CA (2013)
 AIM-UP! All Hands Meeting (www.aim-up.org), Cambridge, MA (2013)
 NESCent Hackathon: *Phylotastic! Making the Tree of Life Accessible for Automated Re-use*, Durham,
 NC (2012)
 Workshop on Molecular Evolution, Marine Biological Laboratory, Woods Hole, MA (2007)
 Cass Workshop, “Random models in phylogenetics and resolving ancient divergences”, Biomathematics
 Research Centre, University of Canterbury, Arthur’s Pass, New Zealand (2007)
 Summer Institute in Statistical Genetics, North Carolina State University, Raleigh, NC (2004)

PROFESSIONAL SERVICE & OUTREACH

Evolution 2015 SSB Symposium Organizer – “Breaking Barriers: Empirical, Theoretical, and Gender
 Issues in Phylogenetics”; with C. Moreau, B. O’Meara, & S. Perkins (Brazil, June 2015)
 SACNAS Professional Development Session Organizer – *Cracking the (bio)Code: How to Start a
 Research Career in Computational Biology* – 2014 SACNAS National Conference, Los Angeles, CA;
 with F. Zapata, E. Huerta-Sanchez, & C. Sandefur (October 18, 2014)
 Blog contributor: <http://treethinkers.org/blog> (March 2013 – present)
Society of Systematic Biologists Elected Council Member (2013 – 2015)
iEvoBio 2013 Organizing Committee Member (2012 – 2013)
 Mentor for the Undergraduate Diversity at SSE/SSB Program (Evolution 2011 and Evolution 2012)
 Reviewer:

- *Systematic Biology* Editorial Board Member (2011 – present)
- *Bioinformatics*, *BMC Evolutionary Biology*, *Evolution*, *Gene*, *Journal of Systematics & Evolution*,
Molecular Biology & Evolution, *Proceedings B*, *Systematic Biology*, *Trends in Ecology & Evolution*
- The Graduate Women in Science 2012 National Fellowships Program
- The Society of Systematic Biologists Graduate Student Research Award Competition (2012, 2014)

 Invited Panelist/Speaker:

- Girls Who Code Summer Program, @Twitter, San Francisco, CA (www.girlswhocode.com; 2013)
- The Women in Science and Engineering Residential Program Seminar, UC–Berkeley (2011)
- The Initiative for Maximizing Student Development (IMSD) Graduate Fellows Program Workshop,
 UC–Berkeley (2011)

 Society/Organization Membership: Society of Systematic Biologists, Society for Advancement of
 Chicanos and Native Americans in Science (SACNAS), Society of Vertebrate Paleontology