

Stephen A. Smith

University of Michigan
2071A Kraus Natural Science Building
830 North University
Ann Arbor, MI 48109-1048

Phone: 734.764.7923
eebsmith@umich.edu
<http://blackrim.org>

Education

Ph.D. Evolutionary Biology, Yale University, Major Advisor: Michael Donoghue, 2008

M.S. Evolutionary Biology, Yale University, 2005

B.A. Liberal Arts, Sarah Lawrence College, 2003

Professional Experience

Assistant Professor 2012–
University of Michigan Ann Arbor, MI
Phylogenetic methods and theory, especially large scale. Evolutionary and especially biogeographic methods and analyses.

iPlant Postdoctoral Researcher 2010–2011
Casey Dunn & Alexandros Stamatakis Brown University
Developing tools for constructing large phylogenetic datasets, comparative analyses, and examining the utility of new sequencing technologies for phylogenetics.

NESCent Postdoctoral Fellow 2008–2010
NESCent Duke University
National Evolutionary Synthesis Center postdoctoral fellow examining the evolution of angiosperms with comparative analyses and large datasets.

CIPRES Graduate Student 2004–2008
Michael Donoghue Yale University
CIPRES: Cyberinfrastructure for Phylogenetic Research graduate student collaborating on database and other subprojects.

Programmer 2004–2006
Tree of Life projects Yale University
TOLKIN: Tree of Life Knowledge and Information Network.

Teaching Experience

Instructor – Bodega Bay Workshop in Applied Phylogenetics, Spring 2009

Instructor – NESCent Computational Phyloinformatics Course: Java Component, Summer 2007

Lecturer – MB&B 230 Rainforest Expedition and Laboratory: Phyloinformatics Workshop, Yale University, Yale University, Spring 2007 and Summer 2008

Teaching Assistant – Plant Diversity and Evolution, Yale University, 2004-2007

Publications

2011

Izquierdo-Carrasco F, **S. A. Smith**, A. Stamatakis. 2011. Algorithms, Data Structures, and Numerics for Likelihood-based Phylogenetic Inference of Huge Trees. *BMC Bioinformatics*. 12(1):470.

Smith, S. A., N. G. Wilson, F. E. Goetz, C. Feehery, S. C. S. Andrade, G. W. Rouse, G. Giribet, C. W. Dunn. 2011. Resolving the evolutionary relationships of molluscs with phylogenomic tools. *Nature*. doi:10.1038/nature10526.

Siebert, S., M. Robinson, S. Tintori, F. Goetz, R. Helm, **S. A. Smith**, N. Shaner, S. Haddock, C. Dunn. 2011. Differential Gene Expression in the Siphonophore *Nanomia bijuga* (Cnidaria) Assessed with Multiple Next-Generation Sequencing Workflows. *PLoS ONE*. e22953. doi:10.1371/journal.pone.0022953

Soltis, D. E., **S. A. Smith**, N. Cellinese, et al. 2011. Angiosperm phylogeny: 17 genes, 640 taxa. *American J. of Botany*. 98: 704

Smith, S. A., J. Beaulieu, A. Stamatakis, & M. J. Donoghue. 2011. Understanding angiosperm diversification using large and small phylogenies. *American J. of Botany*. 98: 404-414.

2010

Goldberg, E. E., J. R. Kohn, R. Lande, K. A. Robertson, **S. A. Smith** & B. Iqic. 2010. Species Selection Maintains Self-Incompatibility. *Science*. 328: 587-591.

Smith, S. A. & M. J. Donoghue. 2010. Informing large-scale biogeography with niche models in *Lonicera* (Caprifoliaceae, Dipsacales) subgenus *Caprifolium*. *Systematic Biology*. 59(3): 322-341.

Edwards, E., C. P. Osborne, C. A. E. Stromberg, **S. A. Smith** & C4 Grasses Consortium. 2010. The Evolutionary Origins of C4 Grasslands. *Science*. 328: 587-591.

Smith, S. A., J. Beaulieu & M. J. Donoghue. 2010. An uncorrelated relaxed-clock analysis suggests an earlier origin for flowering plants. *PNAS*. 107: 5897-5902.

Edwards, E. & **S. A. Smith**. 2010. Phylogenetic analyses reveal the shady history of C4 grasses. *PNAS*. 107: 2532-2538.

2009

Smith, S. A. & J. Beaulieu. 2009. Life history influences rates of climatic niche evolution in flowering plants. *Proc Roy Soc B*. DOI: 10.1098/rspb.2009.1176. 276: 4345-4352. (*USAToday article*)

Smith, S. A. & B. C. O'Meara. 2009. Morphogenera, monophyly, and macroevolution. *PNAS*. 106: E97-E98. (*in response to Jablonski & Finarelli, 2009*)

Smith, S. A., J. Beaulieu & M. J. Donoghue. 2009. Mega-phylogenies for comparative biology: an alternative to supertree and supermatrix approaches. *BMC Evol Bio*. 9: 37. (*NYTimes article*)

Smith, S. A. 2009. Taking into account phylogenetic and divergence-time uncertainty in a parametric biogeographic analysis of the Northern Hemisphere plant clade Caprifoliaceae. *Journal of*

Biogeography. DOI: 10.1111/j.1365-2699.2009.02160.x.

Cellinese, N., **S. A. Smith**, E. J. Edwards, S. T. Kim, R. C. Haberle, M. Avramakis & M. J. Donoghue. 2009. Historical biogeography of the endemic Campanulaceae of Crete. *Journal of Biogeography*. 36: 1253-1269.

Evans, M. E., **S. A. Smith**, R. E. Flynn & M. J. Donoghue. 2009. Climate, niche evolution, and diversification of the "bird-cage" evening primroses (*Oenothera*, sections *Anogra* and *Kleinia*). *American Naturalist*. 173: 225-240.

2008

Smith, S. A. & M. J. Donoghue. 2008. Rates of molecular evolution are linked to life history in flowering plants *Science*. 322: 86-89.

Smith, S. A. & C. Dunn. 2008. Phyutility: a phyloinformatics utility for trees, alignments, and molecular data. *Bioinformatics* 24: 715-716.

Ree, R. H. & **S. A. Smith**. 2008. Maximum-likelihood Inference of Geographic Range Evolution by Dispersal, Local Extinction, and Cladogenesis. *Systematic Biology* 57: 400-414.

Dunn, C. W., A. Hejnal, D. Q. Matus, K. Pang, W. E. Browne, **S. A. Smith**, et al. 2008. Broad taxon sampling improves resolution of the Animal Tree of Life in phylogenomic analyses. *Nature* 452: 745-749.

Smith, S. A. et al. 2008. Bioactive Endophytes Warrant Intensified Exploration and Conservation. *PLoS ONE* 3(8): e3052. (*product of Phyloinformatics Workshop*)

2007-older

Roulston, T. H., **S. A. Smith** & A. L. Brewster. 2007. Comparison of Pan Trap and Intensive Net Sampling Techniques for Documenting a Bee (Hymenoptera: Apiformes) Fauna. *Journal Kansas Entomological Society*. (*product of REU*)

Moore, B. R., **S. A. Smith** & M. J. Donoghue. 2006. Increasing Data Transparency and Estimating Phylogenetic Uncertainty in Supertrees: Approaches Using Nonparametric Bootstrapping. *Systematic Biology* 55: 662-676.

Donoghue, M. J. & **S. A. Smith**. 2004. Patterns in the assembly of temperate forests around the Northern Hemisphere. *Philosophical Transactions of the Royal Society: Biological Sciences*. 359: 1633-1644.

Publications accepted or in review

Invited Presentations

Smith, S. A.¹ 2011. Invited speaker for LIFE SCIENCES COLLOQUIUM (Smith College, Northampton, Massachusetts).

¹presenter *

- Smith, S. A.*** 2011. Invited speaker for Biology 2011 (University of Zurich, Zurich, Switzerland).
- Smith, S. A.*** 2011. Large scale phylogenetics and the exploration of evolutionary patterns. Invited speaker for the Dept. Plant Biology (MSU, Lansing, MI)
- Smith, S. A.*** 2010. The challenges of large scale biogeographic analyses: examples in angiosperms. (SSB Symposium: The Future of Historical biogeography: Conceptual and methodological challenges, Evolution 2010, Portland, OR).
- Smith, S. A.*** 2009. Large-scale angiosperm phylogenies uncover broad evolutionary patterns. (A. Watson Armour Research Seminar Series, Field Museum, Chicago, IL).
- Smith, S. A.*** 2009. Large-scale angiosperm phylogenies uncover broad evolutionary patterns. (Seminar Series, North Carolina State University, Raleigh, NC).
- Smith, S. A.***, J. Beaulieu & M. J. Donoghue. 2009. Large-scale phylogenies uncover large-scale evolutionary patterns. (BSA Past-President's Symposium, Snowbird, UT).
- Smith, S. A.*** 2009. Mega-phylogeny: an alternative to supertree and supermatrix approaches. (Symposium on Advances in Tree Reconstruction from Complex Data Matrices, Evolution 2009, Moscow, ID)
- Smith, S. A.*** 2007. A novel method for estimating the rate of evolution of niches: an example from desert evening primroses (*Oenothera*, Sections *Anogra* and *Kleinia*). (Museum National d'Histoire Naturelle, Paris).
- Ree, R. H.* & **S. A. Smith**. 2007. Stochastic models of geographic range evolution and likelihood-based inference of ancestral ranges. *Origin and Evolution of Biota in Mediterranean Climate Zones*, (Zurich, Switzerland).
- Donoghue, M.J.*, **S. A. Smith**, S. Carlson, & B. Moore. 2007. Phylogenetic Biogeography: Past, Present, and Future. *Origin and Evolution of Biota in Mediterranean Climate Zones*, (Zurich, Switzerland).
- Ree, R. H.*, M. J. Donoghue, B. R. Moore & **S. A. Smith**. 2005. Likelihood-based inference of historical biogeography. *52nd Annual Systematics Symposium*, (Missouri Botanical Garden).
- Smith, S. A.***, R. H. Ree, M. J. Donoghue & B. R. Moore. 2005. Computer Demonstration: Likelihood-based inference of historical biogeography. *52nd Annual Systematics Symposium*, (Missouri Botanical Garden).
- Smith, S. A.*** 2004. New methods for Biogeography. *Sarah Lawrence College Science Seminar*, (Sarah Lawrence College, NY).
- Donoghue, M.J.*, **S. A. Smith**, R. C. Winkworth, & R. Ree. 2004. Assembly of temperate deciduous forests of the Northern Hemisphere. *Plant phylogeny and the origin of major biomes*, Royal Society Scientific Discussion Meeting, (London, UK).

Contributed Presentations

- Beaulieu, J.*, **S. A. Smith** & M. J. Donoghue. 2009. (Moscow, ID) Angiosperm Radiations Aren't Where We Thought They Were, But They're Close.
- Smith, S. A.***, M. Evans, R. Flynn & M. J. Donoghue. 2007. (Chicago, IL) Rates of climatic niche evolution in *Oenothera* sect. *Anogra* and *Kleinia* (Onagraceae).

Cellinese, N.*, **S. A. Smith**, E. Edwards, S. Kim, & M. J. Donoghue. 2007. (Chicago, IL) Dating the Campanulaceae: implications for the biogeography of Cretan campanulas.

Ree, R. H.* & **S. A. Smith**. 2007. (Chicago, IL) Likelihood models for inferring the evolution of geographic ranges on phylogenetic trees.

Ree, R. H.* & **S. A. Smith**. 2007. (Christchurch, NZ) Maximum-likelihood inference of geographic range evolution.

Smith, S. A..* 2005. (Austin, TX) Likelihood methods for inference of geographic ranges.

Smith, S. A..*, M. J. Donoghue, R. Beaman. 2004. (Snowbird, UT) Comparison of predictive distribution modeling in a *Viburnum* species complex from Mexico and Central America. (poster)

Current Scientific Software

lagrange – Biogeographic likelihood reconstruction and stochastic mapping (in collaboration with Richard Ree) - code.google.com/p/lagrange

pebls – pebls evolutionary biology libraries - code.google.com/p/pebls

PHLAWD – (pronounced flawd) allows for the creation of large (mega) phylogenies using NCBI databases - code.google.com/p/phlawd

phyutility – Phylogenetic utilities and analyses - code.google.com/p/phyutility (over 1600 users)

tolkin – Tree of Life Knowledge and Information Network (in collaboration with Reed Beaman and Nico Cellinese) - tolkin.org

Service

Mentor – Google Summer of Code, student Nick Matzke, 2009

Reviewer – Science, PLoS Biology, BMC Evolutionary Biology, National Science Foundation (NSF), Systematic Biology, Molecular Phylogenetics and Evolution, Molecular Biology and Evolution, Systematic Botany, Functional Ecology, New Phytologist, and Bioinformatics.

Panelist – National Science Foundation (NSF)

Advisory – National Science Foundation (NSF)

Organizer – Bayesian Invasion, Bayesian Phylogenetics Conference (with B. Moore), 2006

Honors and Awards

Scientist to Watch, "The Botanist Hacker" in the magazine The Scientist March, 2010 *link to article*

John Spangler Nicholas prize for outstanding doctoral candidate at Yale University, 2009

NSF Postdoctoral Research Fellowship in Biology, 2008 (declined; accepted NESCent fellowship)

The Edward Cogan Prize for Mathematics and Science, Sarah Lawrence College, 2003

Young Botanist of the Year, Certificate of Special Achievement, Botanical Society of America, 2003

NSF REU Fellowship, Univ. of VA, 2002

Funding

iPlant Collaborative – *Member* Assembling the Tree of Life to Enable the Plant Sciences

NESCent – *Co PI* for Working group on Phylogenetics and biogeographic evolution of C4 grasses (with Erika Edwards)

Other Funded Activities

CIPRES – *Graduate Student* Cyberinfrastructure for Phylogenetic Research
NESCent – *Member* Evolution of C4 grasses catalysis meeting
NESCent – *Collaborator* Floral Evolution Working Group
NESCent – *Member* Northern Hemisphere Phytogeography Working Group
NESCent – *Member* Developing an Integrative Algorithmic Method for Historical Biogeography
Tree of Life – *Member* Angiosperms

Collaborations

Reed Beaman (University of Florida)
Jeremy Beaulieu (Yale University)
Nico Cellinese (University of Florida)
Michael Donoghue (Yale University)
Casey Dunn (Brown University)
Erika Edwards (Brown University)
Margaret Evans (Yale University)
Amaury Lambert (Ecole Normale Superieure)
Brian Moore (University of California, Davis)
Thomas Near (Yale University)
Brian O’Meara (University of Tennessee)
Richard Ree (Chicago Field Museum)
Douglas Soltis (University of Florida)
Pamela Soltis (University of Florida)
Alexandros Stamatakis (Technische Universitat Munchen)

Professional Societies

Society for the Study of Evolution
Society of Systematic Biologists
American Society of Plant Taxonomists

References

Dr. Michael Donoghue (PhD advisor)
G. Evelyn Hutchinson Professor
Department of Ecology and Evolutionary Biology
Yale University
P.O. Box 208118
New Haven, CT 06520-8118
203.432.3753
michael.donoghue@yale.edu

Dr. Casey Dunn (current Postdoc advisor)
Assistant Professor
Department Ecology and Evolutionary Biology
Brown University
Providence, RI 02912

401.863.6275
casey_dunn@brown.edu

Dr. Alexandros Stamatakis (current Postdoc advisor)
Assistant Professor
Department of Computer Science
Technische Universität München
D-85748 Garching b. München
+49 162 8541515 (Mobile)
+49 89 28919434 (Office)
stamatak@cs.tum.edu

Dr. Todd Vision (previous Postdoc advisor)
Assistant Professor
Department of Biology
University of North Carolina at Chapel Hill
Chapel Hill, NC 27599
919.843.4507
tjv@email.unc.edu

Dr. Richard Ree (collaborator)
Curator of Botany Field Museum of Natural History
1400 S Lake Shore Drive
Chicago, IL 60605
312.665.7857
rree@fieldmuseum.org