

MICHAEL J. LANDIS

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September 21, 2016

EDUCATION

Ph.D. Integrative Biology

December 2015

Designated Emphasis in Computational & Genomic Biology

University of California, Berkeley, CA

Dissertation: Phylogenetic Inference for Biogeographic and Quantitative Trait Evolution

B.S. Computer Science

July 2005

California State University, Long Beach, CA

RESEARCH INTERESTS

- Evolutionary biology
- Historical biogeography
- Statistical phylogenetics
- Bayesian inference

RESEARCH EXPERIENCE

Postdoctoral fellow, *Yale University*, New Haven, CT

April 2016 – present

- Developing Bayesian methods for historical biogeographic inference.
- Advised by Michael Donoghue.

Postdoctoral researcher, *Iowa State University*, Ames, IA

Feb 2016 – Apr 2016

- Developed methods for divide-and-conquer supertree analysis using a graphical model framework.
- Advised by Tracy Heath.

Graduate researcher, *University of California*, Berkeley, CA

Jul 2009 – Dec 2015

- Implemented numerous phylogenetic methods in C++, Python, R, and RevBayes with particular experience designing Bayesian methods using MCMC.
- Developed novel models of interspecific character evolution for biogeography and quantitative traits.
- Advised by John Huelsenbeck.

Bioinformatician, *Children's Hospital of Oakland*, Oakland, CA

Jan 2009 – Jun 2010

- Investigated the role of lateral gene transfer and recombination in the genetic diversity of *Chlamydia trachomatis* strains.
- Designed and configured a bioinformatics server to host clinical sequences and analysis tools.
- Advised by Deborah Dean.

FELLOWSHIPS & AWARDS

NSF Postdoctoral Research Fellowship

Winter 2016 – Winter 2018

National Science Foundation

Ernst Mayr Award

Summer 2016

Society of Systematic Biologists

Donnelley Postdoctoral Environmental Fellowship

Spring 2016 – Winter 2016

Yale Institute for Biospheric Studies

Summer Research Award

Spring 2015

Dept. of Integrative Biology, UC Berkeley

Travel Award

Spring 2015

Dept. of Computational Biology, UC Berkeley

Graduate Student Fellowship

Fall 2013 – Winter 2013

National Evolutionary Synthesis Center, Duke-affiliated

Travel Award, UC Berkeley

Spring 2012

Dept. of Integrative Biology, UC Berkeley

Google Summer of Code

Summer 2012

National Evolutionary Synthesis Center, Duke-affiliated

NSF Graduate Research Fellowship

Spring 2012

National Science Foundation

Honorable Mention

NSF Graduate Research Fellowship

Spring 2011

National Science Foundation

Honorable Mention

PUBLICATIONS

Höhna, S., **Landis, M. J.**, and Heath, T. A. Phylogenetic inference using RevBayes. Current Protocols in Bioinformatics. (2016) *Submitted*.

Landis, M. J. Biogeographic dating of divergence times using paleogeographically informed processes. (2016) Systematic Biology. *In press*.

Höhna, S., **Landis, M. J.**, and Huelsenbeck, J. P. Parallel power posterior analyses for fast computation of Bayes factors in phylogenetics. Bioinformatics. *Accepted*.

Höhna, S., **Landis, M. J.**, Heath, T. A., Boussau, B., Lartillot, N., Moore, B. R., Huelsenbeck, J. P, and Ronquist, F. (2016) RevBayes: Bayesian Phylogenetic Inference Using Graphical Models and an Interactive Model-Specification Language. Systematic Biology. *In press*.

Schraiber, J. G. and **Landis, M. J.** (2015) Sensitivity of quantitative traits to mutational effects and number of loci. Theoretical Population Biology. doi:10.1016/j.tpb.2015.03.005

Höhna, S., Heath, T. A., Boussau, B., **Landis, M. J.**, Ronquist, F., and Huelsenbeck, J. P. (2014). Probabilistic graphical model representation in phylogenetics. Systematic Biology, 63(5), 753-771. doi: 10.1093/sysbio/syu039

Landis, M. J. and Bedford, T. (2014). PhyloWood: interactive web-based animations of biogeographic and phylogeographic histories. Bioinformatics, 30(1), 123124. doi:10.1093/bioinformatics/btt635

Landis, M. J., Matzke, N. J., Moore, B. R., and Huelsenbeck, J. P. (2014). Bayesian Analysis of Biogeography when the Number of Areas is Large. Systematic Biology, 62(6), 789804. doi:10.1093/sysbio/syt040

Landis*, **M. J.**, Schraiber*, J. G., and Liang, M. (2013). Phylogenetic analysis using Lévy processes: finding jumps in the evolution of continuous traits. Systematic Biology, 62(2), 193204. doi:10.1093/sysbio/sys086

* – authors contributed equally

RESEARCH SOFTWARE

RevBayes , phylogenetic inference using graphical models	revbayes.github.io
PhyloWood , biogeographic animations	mldis.github.io/phyloWood
BayArea , biogeographic inference	github.com/mldis/bayarea
creepy-jerk , inference of evolutionary jumps in traits	github.com/mldis/creepy-jerk
quant_trait_coalescent , mutation-coalescent QTs	github.com/Schraiber/quant_trait_coalescent

INVITED TALKS

Landis, M. J. 2016. Phylogenetic inference of where the wild things were. Center for Computational Genetics and Genomics, Temple University.

Landis, M. J. 2015. Divergence time estimation using biogeographic processes. Society of Systematic Biologists Symposium on Parametric Biogeography, Evolution Conference, Guarujá, Brazil.

Landis, M. J., Schraiber, J. G.. 2013. Lévy processes as models of continuous trait evolution. Workshop on Mathematics for an Evolving Biodiversity, University of Montréal.

Landis, M. J., Schraiber, J. G., and Liang, M. 2013. Continuous trait evolution with fat tails: Lévy processes and mutations of large effect. Center for Population Genomics, UC Davis.

CONTRIBUTED TALKS

Landis, M. J. 2016. Finding space for biogeography in phylogenetic inference. Evolution Conference, Austin, Texas.

Landis, M. J., Matzke, N. J., Moore, B. R., Huelsenbeck, J. P. 2013. Bayesian inference of species range evolution for hundreds of discrete areas. Phylogenetics & Evolutionary Biology Seminar, North Carolina State University.

Landis, M. J., Matzke, N. J., Moore, B. R., and Huelsenbeck, J. P. 2013. Bayesian inference of biogeographical histories for hundreds of discrete areas. Evolution Conference, Snowbird, Utah.

Landis, M. J., Matzke, N. J., Moore, B. R., and Huelsenbeck, J. P. 2013. Bayesian inference of biogeographical histories for hundreds of discrete areas. Center for Theoretical Evolutionary Genomics, UC Berkeley.

Landis, M. J., Schraiber, J. G., and Liang, M. 2012. Lévy process models of continuous character evolution. Center for Theoretical Evolutionary Genomics, UC Berkeley.

Landis, M. J., Matzke, N. J., Moore, B. R., Huelsenbeck, J. P. 2012. Statistical Analysis of Biogeography when the Number of Areas is Large. Evolution Conference, Ottawa, Canada.

PROFESSIONAL REVIEWS

Journals: *Systematic Biology*, *Evolution*, *Molecular Biology & Evolution*, *Journal of Biogeography*, *Bioinformatics*, *Methods in Evolution & Ecology*, *Molecular Phylogenetics & Evolution*, *BMC Evolutionary Biology*, *Genome Biology & Evolution*

TEACHING & MENTORING

Teaching Assistant , Molecular Evolution Workshop, Woods Hole, MA	<i>Summer 2014 – 2016</i>
Invited Lecturer , BIOL1425, Phylogenetic Biology, Brown University, RI	<i>Spring 2016</i>
Instructor, Coordinator , RevBayes Workshop, UC Berkeley, CA	<i>Spring 2015</i>
Instructor , Bodega Phylogenetics Workshop, UC Davis, CA	<i>Spring 2014, 2015</i>
Instructor , Applied Phylogenetics Workshop, NESCent, NC	<i>Summer 2014</i>
Invited Lecturer , IB87, Bioinformatics, UC Berkeley, CA	<i>Summer 2014</i>
Invited Lecturer , EEB101, Macroevolution, UC Davis, CA	<i>Spring 2013</i>
Teaching Assistant , IB200A: Principles of Phylogenetics, UC Berkeley, CA	<i>Spring 2012</i>
Teaching Assistant , IB164: Human Genetics and Genomics, UC Berkeley, CA	<i>Fall 2011</i>
Mentor , UC Undergraduate Research Apprentice Program	
• Jaya Narasimhan, <i>Computer Science</i> . Comparative transcriptome evolution.	<i>2012 – 2014</i>
• Bryan Wang, <i>Pure Mathematics</i> . Partition distances.	<i>2013 – 2015</i>

PROFESSIONAL EXPERIENCE

Systems Engineer , <i>Varsity Technologies</i>	<i>2005 – 2008</i>
• Engineering lead for Managed Services department, serving non-profits	
• Designed, implemented, configured, and maintained diverse infrastructures, including: server domains, mail servers, networks, virtualization, disaster recovery.	

SKILLS

Programming: C/C++, Python, R, Java, Javascript, MPI, bash, git
IT: Linux, Mac OS X, Windows, Cisco, VMWare

LEADERSHIP ACTIVITIES

Co-chair , Integrative Biology Graduate Student Assembly	<i>Sep 2012–May 2013</i>
Organizer , Paleostatistics Reading Group	<i>Fall 2012</i>

Co-organizer, Evolutionary Theory and Museum Graduate Student Group

Fall 2012

Co-organizer, PhD Student Recruitment

Mar 2011–Sep 2011

Organizer, Classic Papers in Evolutionary Biology

Fall 2010

OUTREACH

Guest Lecturer, Berkeley High School Outreach (coordinated by Rori Rohlf)

2014 – 2015

Guest Lecturer, Bay Area Scientists in Schools

Spring 2014

Tutor, 826 Valencia volunteer for English Language Learners

Summer 2009 – 2010