

MICHAEL J. LANDIS

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<http://mlandis.github.io>

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EDUCATION

Ph.D. Integrative Biology

Dec 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

Jul 2005

California State University, Long Beach, CA

RESEARCH INTERESTS

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

RESEARCH EXPERIENCE

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

2016—Present

- Developing Bayesian methods for historical biogeographic inference.
- Producing novel inference methods for complex character evolution.
- Advised by Michael Donoghue.

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

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

2010—2015

- Developed 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

2009, 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

2017—2018

National Science Foundation

Ernst Mayr Award

2016

Society of Systematic Biologists

Donnelley Postdoctoral Environmental Fellowship

2016

Yale Institute for Biospheric Studies

Summer Research Award

2015

Dept. of Integrative Biology, UC Berkeley

Travel Award	2015
Dept. of Computational Biology, UC Berkeley	
Graduate Student Fellowship	2013
National Evolutionary Synthesis Center, Duke-affiliated	
Travel Award	2012
Dept. of Integrative Biology, UC Berkeley	
Google Summer of Code	2012
National Evolutionary Synthesis Center, Duke-affiliated	
NSF Graduate Research Fellowship	2011, 2012
National Science Foundation	Honorable Mention

MANUSCRIPTS – ACCEPTED

Höhna, S., **Landis, M. J.**, and Huelsenbeck, J. P. Parallel power posterior analyses for fast computation of Bayes factors in phylogenetics. *Bioinformatics*, 2017. (*bioRxiv* preprint, doi:10.1101/104422)

MANUSCRIPTS – PUBLISHED

- Landis, M. J.** and Schraiber, J. G. Pulsed evolution shaped modern vertebrate body sizes. *Proceedings of the National Academy of Sciences*, 114(50): 13224-13229, 2017.
- Höhna, S., **Landis, M. J.**, Heath, T. A. Phylogenetic inference using RevBayes. *Current Protocols in Bioinformatics*, 57:6.16.1-6.16.34, 2017.
- Landis, M.J.** Biogeographic dating of speciation times using paleogeographically informed processes. *Systematic Biology*, 66(2):128–144, 2017.
- Höhna, S., **Landis, M. J.**, Heath, T. A., Boussau, B., Lartillot, N., Moore, B. R., Huelsenbeck, J. P, and Ronquist, F. RevBayes: Bayesian Phylogenetic Inference Using Graphical Models and an Interactive Model-Specification Language. *Systematic Biology*, 65(4):726-736, 2016.
- Schraiber, J. G. and **Landis, M. J.**. Sensitivity of quantitative traits to mutational effects and number of loci. *Theoretical Population Biology*, 102: 85-93, 2015.
- Höhna, S., Heath, T. A., Boussau, B., **Landis, M. J.**, Ronquist, F., and Huelsenbeck, J. P. Probabilistic graphical model representation in phylogenetics. *Systematic Biology*, 63(5), 753–771, 2014.
- Landis, M. J.** and Bedford, T. Phylowood: interactive web-based animations of biogeographic and phylogeographic histories. *Bioinformatics*, 30(1), 123–124, 2014.
- Landis, M. J.**, Matzke, N. J., Moore, B. R., and Huelsenbeck, J. P. Bayesian Analysis of Biogeography when the Number of Areas is Large. *Systematic Biology*, 62(6), 789–804, 2013.
- Landis,* M. J.**, Schraiber,* J. G., and Liang, M. Phylogenetic analysis using Lévy processes: finding jumps in the evolution of continuous traits. *Systematic Biology*, 62(2), 193–204, 2013.

* – authors contributed equally

RESEARCH SOFTWARE

RevBayes , phylogenetic inference using graphical models	revbayes.github.io
Phylowood , interactive biogeographic animations	mlandis.github.io/phylowood
BayArea , Bayesian biogeographic inference for many areas	github.com/mlandis/bayarea
pulsR , simulate and fit macroevolutionary trait models	github.com/Schraiber/pulsR
creepy-jerk , Bayesian inference of evolutionary jumps in traits	github.com/mlandis/creepy-jerk
qtc , quantitative trait evolution under the coalescent	github.com/Schraiber/quant_trait_coalescent

PRESENTATIONS – INVITED

Washington University at St. Louis, Department of Biology seminar 2018

Geological Society of America Meeting in Seattle, Symposium on Computational Paleobiology	2017
Swedish Museum of Natural History, Systematics seminar	2017
Temple University, Computational Genomics seminar	2016
Evolution Conference, Symposium on Parametric Biogeography	2015
North Carolina State University, Phylogenetics & Evolutionary Biology Seminar	2013
University of Montréal, Workshop on Mathematics for an Evolving Biodiversity	2013
University of California, Davis, Center for Population Genomics seminar	2013

PRESENTATIONS – ASSORTED

Yale Institute of Biospheric Studies, External Advisory Board Meeting	2017
Evolution Conference in Portland	2017
Evolution Conference in Austin, Ernst Mayr Symposium	2016
Evolution Conference in Snowbird	2013
UC Berkeley, Center for Theoretical Evolutionary Genomics	2013
UC Berkeley, Center for Theoretical Evolutionary Genomics	2012
Evolution Conference in Ottawa	2012

PROFESSIONAL REVIEWS

Journals: *Bioinformatics*, *BMC Evolutionary Biology*, *Evolution*, *Genome Biology & Evolution*, *Journal of Biogeography*, *Methods in Evolution & Ecology*, *Molecular Biology & Evolution*, *Molecular Phylogenetics & Evolution*, *New Phytologist*, *Systematic Biology* (ed. board member), *Trends in Ecology & Evolution*

TEACHING & MENTORING

Instructor , Fossil tip-dating with RevBayes, GSA Meeting, Seattle, WA	2017
Instructor , Biogeography with RevBayes, SSB Meeting, Baton Rouge, LA	2017
Instructor , Introduction to RevBayes, Yale, New Haven, CT	2017
Teaching Assistant , Molecular Evolution Workshop, Woods Hole, MA	2014–2016
Invited Lecturer , BIOL1425, Phylogenetic Biology, Brown University, RI	2016
Instructor, Coordinator , RevBayes Workshop, UC Berkeley, CA	2015
Instructor , Bodega Phylogenetics Workshop, UC Davis, CA	2014–2015
Instructor , Applied Phylogenetics Workshop, NESCent, NC	2014
Invited Lecturer , IB87, Bioinformatics, UC Berkeley, CA	2014
Invited Lecturer , EEB101, Macroevolution, UC Davis, CA	2013
Teaching Assistant , IB200A: Principles of Phylogenetics, UC Berkeley, CA	2012
Teaching Assistant , IB164: Human Genetics and Genomics, UC Berkeley, CA	2011
Mentor , UC Undergraduate Research Apprentice Program	
• Jaya Narasimhan, <i>Computer Science</i> . Comparative transcriptome evolution.	2012–2014
• Bryan Wang, <i>Pure Mathematics</i> . Partition distances.	2013–2015

PROFESSIONAL EXPERIENCE

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

SKILLS

Programming: C/C++, Python, R, Java, Javascript, MPI, bash, git, tex

SERVICE ACTIVITIES

Panel reviewer for Society of Systematic Biologists award applications *2017*

LEADERSHIP ACTIVITIES

Organizer, Integrative Biology Computer Club *2015*

Co-chair, Integrative Biology Graduate Student Assembly *2012, 2013*

Organizer, Paleostatistics Reading Group *2012*

Co-organizer, Evolutionary Theory and Museum Graduate Student Group *2012*

Co-organizer, PhD Student Recruitment *2011*

Organizer, Classic Papers in Evolutionary Biology *2010*

OUTREACH

Guest Lecturer, Berkeley High School Outreach (coordinated by Rori Rohlf) *2014, 2015*

Guest Lecturer, Bay Area Scientists in Schools *2014*

Tutor, 826 Valencia volunteer for English Language Learners *2009, 2010*