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 interspecfic 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

Landis, M. J. and Schraiber, J. G. Pulsed evolution shaped modern vertebrate body sizes. *Proceedings of the National Academy of Sciences*, 2017. (*bioRxiv* preprint, doi:10.1101/151175)

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

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`

INVITED TALKS

Landis, M. J. Inference of phylogenetic biogeography using models of range evolution. Swedish Museum of Natural History, 2017.

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

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

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

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

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

Contributed Talks

Landis, M. J. and Schraiber, J. G. Rapid adaptive shifts are a common mode of macroevolution. Evolution Conference, Portland, Oregon, 2017.

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

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

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

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

Landis, M. J., Matzke, N. J., Moore, B. R., Huelsenbeck, J. P. Statistical Analysis of Biogeography when the Number of Areas is Large. Evolution Conference, Ottawa, Canada, 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, Systematic Biology (ed. board member), Trends in Ecology & Evolution*

Teaching & Mentoring

Instructor, Biogeography with RevBayes, Society of Systematic Biologists 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, *Computer Science.* Comparative transcriptome evolution.	*2012—2014*
• Bryan Wang, *Pure Mathematics.* Partition distances.	*2013—2015*

Professional Experience

Systems Engineer, *Varsity Technologies* 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

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 Rohlfs) 2014, 2015

Guest Lecturer, Bay Area Scientists in Schools 2014

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