

MICHAEL J. LANDIS

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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

Donoghue Lab, *Yale University*, New Haven, CT

April 2016–present

- Develop Bayesian methods for historical biogeographic inference.

Heath Lab, *Iowa State University*, Ames, IA

Feb 2016–April 2016

- Developed methods for divide-and-conquer supertree analysis using a graphical model framework.

Huelsenbeck Lab, *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.

Dean Lab, *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.

FELLOWSHIPS & AWARDS

NSF Postdoctoral Research Fellowship, Yale University

Winter 2016 – Winter 2018

Ernst Mayr Award, Society of Systematic Biologists

Summer 2016

Donnelley Gaylord Fellowship, Yale Institute for Biospheric Studies

Spring 2016 – Winter 2016

Graduate Student Fellowship, National Evolutionary Synthesis Center

Fall 2013 – Winter 2013

Google Summer of Code, National Evolutionary Synthesis Center

Summer 2012

PUBLICATIONS

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

PRESENTATIONS

- Landis, M. J.** 2016. Finding space for biogeography in phylogenetic inference. Evolution Conference, Austin, Texas.
- Landis, M. J.** 2015. Divergence time estimation using biogeographic processes. Evolution Conference, Guarujá, Brazil.
- 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.**, 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.
- 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 EXPERIENCE

Teaching Assistant , Molecular Evolution Workshop, Woods Hole, MA	<i>Summer 2014, 2015, 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>

PROFESSIONAL EXPERIENCE

Systems Engineer, *Varsity Technologies**July 2005–October 2008*

- Technical 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 (incl. D3.js), MPI, bash, git**IT:** Linux, Mac OS X, Windows, Cisco, VMWareLEADERSHIP ACTIVITIES

Co-chair, Integrative Biology Graduate Student Assembly *Sep 2012–May 2013***Organizer**, Paleostatistics Reading Group *Fall 2012***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*MENTORING & OUTREACH

Mentor, UC Undergraduate Research Apprentice Program

- Jaya Narasimhan, *Computer Science*. Comparative transcriptome evolution. *2012–2014*
- Bryan Wang, *Pure Mathematics*. Partition distances. *2013–2015*

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*RESEARCH SOFTWARE

RevBayes, phylogenetic inference using graphical models revbayes.github.io**Phylowood**, biogeographic animations mlandis.github.io/phylowood**BayArea**, biogeographic inference code.google.com/p/bayarea**creepy-jerk**, inference of evolutionary jumps in traits github.com/mlandis/creepy-jerk**quant_trait_coalescent**, mutation-coalescent QTs github.com/Schraiber/quant_trait_coalescent