Michael J. Landis

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June 5, 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

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 interspecfic 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.

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. 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	*Summer 2014, 2015*
Instructor, Coordinator, RevBayes Workshop, UC Berkeley, CA	*Spring 2015*
Instructor, Bodega Phylogenetics Workshop, UC Davis, CA	*Spring 2014, 2015*
Instructor, Applied Phylogenetics Workshop, NESCent, NC	*Summer 2014*
Invited Lecturer, IB87, Bioinformatics, UC Berkeley, CA	*Summer 2014*
Invited Lecturer, EEB101, Macroevolution, UC Davis, CA	*Spring 2013*
Teaching Assistant, IB200A: Principles of Phylogenetics, UC Berkeley, CA	*Spring 2012*
Teaching Assistant, IB164: Human Genetics and Genomics, UC Berkeley, CA	*Fall 2011*

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, VMWare

LEADERSHIP 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 Rohlfs)	*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`

Fellowships

NSF Postdoctoral Research Fellowship, Yale University	*Winter 2016 – Winter 2018*
Donnelley Gaylord Fellowship, Yale Institute for Biospheric Studies	*Spring 2016 – Winter 2016*
Graduate Student Fellowship, National Evolutionary Synthesis Center	*Fall 2013*
Google Summer of Code, National Evolutionary Synthesis Center	*Summer 2012*