

MICHAEL J. LANDIS
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EDUCATION

Ph.D. Integrative Biology

Designated Emphasis in Computational Biology
University of California, Berkeley, CA

September 2010 - Present

B.S. Computer Science

California State University, Long Beach, CA

July 2005

RESEARCH INTERESTS

Statistical phylogenetics
Models of character evolution
Bayesian inference
Machine learning

PUBLICATIONS

- Landis***, M. J., Schraiber*, J. G., & Liang, M. (2013). Phylogenetic analysis using Lvy processes: finding jumps in the evolution of continuous traits. *Systematic Biology*, 62(2), 193204. doi:10.1093/sysbio/sys086
- Landis, M. J.**, Matzke, N. J., Moore, B. R., & Huelsenbeck, J. P. (2013). Bayesian analysis of biogeography when the number of areas is large. *Systematic Biology*, 62(6), 789804. doi:10.1093/sysbio/syt040
- Landis, M. J.**, & Bedford, T. (2013). Phylowood: interactive web-based animations of biogeographic and phylogeographic histories. *Bioinformatics*, 30(1), 123124. doi:10.1093/bioinformatics/btt635
- Höhna, S., Heath, T. A., Boussau, B., **Landis, M. J.**, Ronquist, F., & Huelsenbeck, J. P. (2013). Probabilistic Graphical Model Representation in Phylogenetics. *Submitted to Systematic Biology*.

* – authors contributed equally

PRESENTATIONS

- 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 Montreal.
- 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. *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*.

* – authors contributed equally

RESEARCH EXPERIENCE

Huelsenbeck Lab, *University of California*, Berkeley, CA

Jul 2009 - Present

- Implemented numerous statistical methods in C++, Python, R, and RevBayes with particular experience with Bayesian methods using MCMC with data augmentation.

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.

TEACHING EXPERIENCE

IB200A: Principles of Phylogenetics, UC Berkeley

Spring 2012

- Topics: Theory and methods for phylogenetic inference
- Professors: David Lindberg, Brent Mishler, Kip Williams

IB164: Human Genetics and Genomics, UC Berkeley

Fall 2011

- Topics: Human genome variation, molecular evolution, population genetics
- Professors: Doris Bachtrog, Rasmus Nielsen, Monty Slatkin

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++, Python, R, RevBayes, C, Java, MPI, Javascript, D3.js, HTML/CSS, bash, git, LaTeX

IT: Windows, Mac OS X, Linux, UNIX, Cisco, VMWare

LEADERSHIP ACTIVITIES

Co-chair, Integrative Biology Graduate Student Assembly

Sep 2012 - May 2013

Co-organizer, Museum of Vertebrate Zoology and Center for Theoretical Evolutionary Genomics Joint Meeting

Fall 2012

Co-organizer, PhD Student Recruitment

Mar 2011 - Sep 2011

Organizer, Paleostatistics Reading Group

Fall 2012

Organizer, Classic Papers in Evolutionary Biology

Fall 2010

OUTREACH

Mentor, UC Undergraduate Research Apprentice Program

- Jaya Narasimhan, *Computer Science*. Phylogenetic transcriptome evolution.

Fall 2012 - Present

Tutor, 826 Valencia volunteer for English Language Learners

Summer 2009, 2010

FELLOWSHIPS & AWARDS

Graduate Student Fellowship, National Evolutionary Synthesis Center

Fall 2013

Google Summer of Code, National Evolutionary Synthesis Center

Summer 2012