

# 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*

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## RESEARCH INTERESTS

- Statistical phylogenetics
- Models of character evolution
- Bayesian inference
- Machine learning

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## 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

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## 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

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**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

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**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

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**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

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**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

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**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

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**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

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**Graduate Student Fellowship**, National Evolutionary Synthesis Center *Fall 2013*  
**Google Summer of Code**, National Evolutionary Synthesis Center *Summer 2012*