

# MICHAEL J. LANDIS

<http://mlandis.github.io>

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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

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. *Submitted*.

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

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## PRESENTATIONS

**Landis, M. J.** 2015. Biogeographic divergence 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. 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.

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## RESEARCH EXPERIENCE

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|---|--------------------------|
| <b>Huelsensbeck Lab</b> , <i>University of California</i> , Berkeley, CA  | <i>Jul 2009–Present</i>  |
| <ul style="list-style-type: none"><li>Implemented numerous phylogenetic methods in C++, Python, R, and RevBayes with particular experience designing Bayesian methods using MCMC.</li></ul>   |                          |
| <b>Dean Lab</b> , <i>Children's Hospital of Oakland</i> , Oakland, CA   | <i>Jan 2009–Jun 2010</i> |
| <ul style="list-style-type: none"><li>Investigated the role of lateral gene transfer and recombination in the genetic diversity of <i>Chlamydia trachomatis</i> strains.</li><li>Designed and configured a bioinformatics server to host clinical sequences and analysis tools.</li></ul> |                          |

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## TEACHING EXPERIENCE

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| <b>Instructor, Coordinator</b> , RevBayes Workshop, UC Berkeley, CA              | <i>Spring 2015</i>       |
| <b>Instructor</b> , Bodega Phylogenetics Workshop, UC Davis, CA                  | <i>Spring 2014, 2015</i> |
| <b>Teaching Assistant</b> , Molecular Evolution Workshop, Woods Hole, MA         | <i>2014–2015</i>         |
| <b>Instructor</b> , Applied Phylogenetic Workshop, NESCent, NC                   | <i>Summer 2014</i>       |
| <b>Invited Lecturer</b> , IB87, Bioinformatics, UC Berkeley, CA                  | <i>Summer 2014</i>       |
| <b>Invited Lecturer</b> , EEB101, Macroevolution, UC Davis, CA                   | <i>Spring 2013</i>       |
| <b>Teaching Assistant</b> , IB200A: Principles of Phylogenetics, UC Berkeley, CA | <i>Spring 2012</i>       |
| <b>Teaching Assistant</b> , IB164: Human Genetics and Genomics, UC Berkeley, CA  | <i>Fall 2011</i>         |

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## PROFESSIONAL EXPERIENCE

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| <b>Systems Engineer</b> , <i>Varsity Technologies</i>  | <i>July 2005–October 2008</i> |
| <ul style="list-style-type: none"><li>Technical lead for Managed Services department, serving non-profits</li><li>Designed, implemented, configured, and maintained diverse infrastructures, including: server domains, mail servers, networks, virtualization, disaster recovery.</li></ul> |                               |

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## SKILLS

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- Programming:** C/C++, Python, R, RevBayes, Java, Javascript (incl. D3.js), MPI, LaTeX
- IT:** Windows, Mac OS X, Linux, UNIX, Cisco, VMWare, bash, git

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## LEADERSHIP ACTIVITIES

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|---|--------------------------|
| <b>Co-chair</b> , Integrative Biology Graduate Student Assembly             | <i>Sep 2012–May 2013</i> |
| <b>Organizer</b> , Paleostatistics Reading Group                            | <i>Fall 2012</i>         |
| <b>Co-organizer</b> , Evolutionary Theory and Museum Graduate Student Group | <i>Fall 2012</i>         |
| <b>Co-organizer</b> , PhD Student Recruitment                               | <i>Mar 2011–Sep 2011</i> |
| <b>Organizer</b> , Classic Papers in Evolutionary Biology                   | <i>Fall 2010</i>         |

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## MENTORING & OUTREACH

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| <b>Mentor</b> , UC Undergraduate Research Apprentice Program  |                         |
| <ul style="list-style-type: none"><li>Jaya Narasimhan, <i>Computer Science</i>. Comparative transcriptome evolution. <i>Aug 2012–Mar 2014</i></li><li>Bryan Wang, <i>Pure Mathematics</i>. Partition distances. <i>Apr 2014–Present</i></li></ul> |                         |
| <b>Guest Lecturer</b> , Berkeley High School Outreach (coordinated by Rori Rohlf)   | <i>2014–2015</i>        |
| <b>Guest Lecturer</b> , Bay Area Scientists in Schools  | <i>Spring 2014</i>      |
| <b>Tutor</b> , 826 Valencia volunteer for English Language Learners   | <i>Summer 2009–2010</i> |

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## RESEARCH SOFTWARE

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| <b>RevBayes</b> , phylogenetic inference using graphical models | <a href="https://github.com/revbayes">revbayes.github.io</a>  |
| <b>Phylowood</b> , biogeographic animations                     | <a href="https://github.com/mlandis/phylowood">mlandis.github.io/phylowood</a>                                |
| <b>BayArea</b> , biogeographic inference                        | <a href="https://code.google.com/p/bayarea">code.google.com/p/bayarea</a>                                     |
| <b>creepy-jerk</b> , inference of evolutionary jumps in traits  | <a href="https://github.com/mlandis/creepy-jerk">github.com/mlandis/creepy-jerk</a>                           |
| <b>quant_trait_coalescent</b> , mutation-coalescent QTs         | <a href="https://github.com/Schraiber/quant_trait_coalescent">github.com/Schraiber/quant_trait_coalescent</a> |

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## FELLOWSHIPS & AWARDS

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| <b>Graduate Student Fellowship</b> , National Evolutionary Synthesis Center | <i>Fall 2013</i>   |
| <b>Google Summer of Code</b> , National Evolutionary Synthesis Center       | <i>Summer 2012</i> |