

MICHAEL J. LANDIS

michael.landis@yale.edu

<http://mlandis.github.io>

November 27, 2018

EDUCATION

Ph.D. Integrative Biology

Dec 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

Jul 2005

California State University, Long Beach, CA

EMPLOYMENT

Assistant Professor

starts *Jul 2019*

Department of Biology

Washington University, St. Louis, MO

RESEARCH INTERESTS

- Evolutionary biology
- Statistical phylogenetics
- Historical biogeography
- Bayesian inference

RESEARCH EXPERIENCE

Postdoctoral fellow, *Yale University*, New Haven, CT

2016—Present

- Developing Bayesian methods for historical biogeographic inference.
- Producing novel inference methods for complex character evolution.
- Advised by Michael Donoghue.

Postdoctoral researcher, *Iowa State University*, Ames, IA

2016

- Developed methods for divide-and-conquer supertree analysis using a graphical model framework.
- Advised by Tracy Heath.

Graduate researcher, *University of California*, Berkeley, CA

2010—2015

- Developed 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.
- Advised by John Huelsenbeck.

Bioinformatician, *Children's Hospital of Oakland*, Oakland, CA

2009, 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.
- Advised by Deborah Dean.

FELLOWSHIPS & AWARDS

NSF Postdoctoral Research Fellowship

2017—2018

National Science Foundation

Ernst Mayr Award

2016

Society of Systematic Biologists

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|---|-------------------|
| Donnelley Postdoctoral Environmental Fellowship | 2016 |
| Yale Institute for Biospheric Studies | |
| Summer Research Award | 2015 |
| Dept. of Integrative Biology, UC Berkeley | |
| Travel Award | 2015 |
| Dept. of Computational Biology, UC Berkeley | |
| Graduate Student Fellowship | 2013 |
| National Evolutionary Synthesis Center, Duke-affiliated | |
| Travel Award | 2012 |
| Dept. of Integrative Biology, UC Berkeley | |
| Google Summer of Code | 2012 |
| National Evolutionary Synthesis Center, Duke-affiliated | |
| NSF Graduate Research Fellowship | 2011, 2012 |
| National Science Foundation | Honorable Mention |

MANUSCRIPTS – PUBLISHED

- Landis, M. J.**, Freyman, W. A., and Baldwin, B. G.. Retracing the Hawaiian silversword radiation despite phylogenetic, biogeographic, and paleogeographic uncertainty. *Evolution* 72: 2343–2359, 2018.
- Park B., Sinnott-Armstrong, M., Schlutius, C., Zuluaga, J.-C. P. Spriggs, B. L., Simpson, R. G., **Landis, M. J.**, Sweeney, P. W., Eaton, D. A. R., and Donoghue, M. J. Sterile marginal flowers increase visitation and fruit set in the hobblebush (*Viburnum lantanoides*, Adoxaceae) at multiple spatial scales. *Ann. Bot.*, 2018.
- Höhna, S., **Landis, M. J.**, and Huelsenbeck, J. P. Parallel power posterior analyses for fast computation of Bayes factors in phylogenetics. *Bioinformatics*, 2017. (*bioRxiv* preprint, doi:10.1101/104422)
- Landis, M. J.** and Schraiber, J. G. Pulsed evolution shaped modern vertebrate body sizes. *Proceedings of the National Academy of Sciences*, 114(50): 13224–13229, 2017.
- Höhna, S., **Landis, M. J.**, Heath, T. A. Phylogenetic inference using RevBayes. *Current Protocols in Bioinformatics*, 57:6.16.1–6.16.34, 2017.
- Landis, M. J.** Biogeographic dating of speciation times using paleogeographically informed processes. *Systematic Biology*, 66(2):128–144, 2017.
- 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. *Systematic Biology*, 65(4):726–736, 2016.
- Schraiber, J. G. and **Landis, M. J.** Sensitivity of quantitative traits to mutational effects and number of loci. *Theoretical Population Biology*, 102: 85–93, 2015.
- Höhna, S., Heath, T. A., Boussau, B., **Landis, M. J.**, Ronquist, F., and Huelsenbeck, J. P. Probabilistic graphical model representation in phylogenetics. *Systematic Biology*, 63(5), 753–771, 2014.
- Landis, M. J.** and Bedford, T. PhyloWood: interactive web-based animations of biogeographic and phylogeographic histories. *Bioinformatics*, 30(1), 123–124, 2014.
- Landis, M. J.**, Matzke, N. J., Moore, B. R., and Huelsenbeck, J. P. Bayesian Analysis of Biogeography when the Number of Areas is Large. *Systematic Biology*, 62(6), 789–804, 2013.
- Landis,* M. J.**, Schraiber,* J. G., and Liang, M. Phylogenetic analysis using Lévy processes: finding jumps in the evolution of continuous traits. *Systematic Biology*, 62(2), 193–204, 2013.

* – authors contributed equally

BOOK CHAPTERS – UNDER REVIEW

- Landis,* M. J.** Biogeographic dating of phylogenetic divergence times using priors and processes in *The Molecular Evolutionary Clock: Theory and Practice*. (S. Y. W. Ho. ed.) Springer.

RESEARCH SOFTWARE

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| RevBayes , phylogenetic inference using graphical models | revbayes.github.io |
| PhyloWood , interactive biogeographic animations | mlandis.github.io/phyloWood |
| BayArea , Bayesian biogeographic inference for many areas | github.com/mlandis/bayarea |
| pulsR , simulate and fit macroevolutionary trait models | github.com/Schraiber/pulsR |
| creepy-jerk , Bayesian inference of evolutionary jumps in traits | github.com/mlandis/creepy-jerk |
| qtc , quantitative trait evolution under the coalescent | github.com/Schraiber/quant_trait_coalescent |

PRESENTATIONS – INVITED

| | |
|---|------|
| Plant Biology Seminar, University of Georgia | 2018 |
| Evolution & Systematics Seminar, University of Connecticut | 2018 |
| Phyloseminar, http://phyloseminar.org/ | 2018 |
| Department of Biology Seminar, University of Oregon | 2018 |
| Department of Biology Seminar, Washington University at St. Louis | 2018 |
| Symposium on Computational Paleobiology, Geological Society of America Meeting in Seattle | 2017 |
| Systematics Seminar, Swedish Museum of Natural History | 2017 |
| Computational Genomics Seminar, Temple University | 2016 |
| Symposium on Parametric Biogeography, Evolution Conference in Guarujá, Brazil | 2015 |
| Phylogenetics & Evolutionary Biology Seminar, North Carolina State University | 2013 |
| Workshop on Mathematics for an Evolving Biodiversity, University of Montréal | 2013 |
| Center for Population Genomics Seminar, UC Davis | 2013 |

PRESENTATIONS – ASSORTED

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|---|------|
| External Advisory Board Meeting, Yale Institute of Biospheric Studies | 2017 |
| Evolution Conference in Portland | 2017 |
| Ernst Mayr Symposium, Evolution Conference in Austin | 2016 |
| Evolution Conference in Snowbird | 2013 |
| Center for Theoretical Evolutionary Genomics, UC Berkeley | 2013 |
| Center for Theoretical Evolutionary Genomics, UC Berkeley | 2012 |
| Evolution Conference in Ottawa | 2012 |

PROFESSIONAL REVIEWS

Journals: *Bioinformatics*, *BMC Evolutionary Biology*, *Evolution*, *Genome Biology & Evolution*, *Journal of Biogeography*, *Methods in Evolution & Ecology*, *Molecular Biology & Evolution*, *Molecular Phylogenetics & Evolution*, *Nature Communications*, *New Phytologist*, *Paleobiology*, *Proceedings of the Royal Society B*, *Systematic Biology* (ed. board member), *Trends in Ecology & Evolution*

TEACHING & MENTORING

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| Instructor , Molecular Evolution Workshop, Woods Hole, MA | 2018 |
| Instructor , Fossil tip-dating with RevBayes, GSA Meeting, Seattle, WA | 2017 |
| Instructor , Biogeography with RevBayes, SSB Meeting, Baton Rouge, LA | 2017 |
| Instructor , Introduction to RevBayes, Yale, New Haven, CT | 2017 |
| Teaching Assistant , Molecular Evolution Workshop, Woods Hole, MA | 2014–2016 |
| Invited Lecturer , BIOL1425, Phylogenetic Biology, Brown University, RI | 2016 |
| Instructor, Coordinator , RevBayes Workshop, UC Berkeley, CA | 2015 |

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| Instructor , Bodega Phylogenetics Workshop, UC Davis, CA | 2014—2015 |
| Instructor , Applied Phylogenetics Workshop, NESCent, NC | 2014 |
| Invited Lecturer , IB87, Bioinformatics, UC Berkeley, CA | 2014 |
| Invited Lecturer , EEB101, Macroevolution, UC Davis, CA | 2013 |
| Teaching Assistant , IB200A: Principles of Phylogenetics, UC Berkeley, CA | 2012 |
| Teaching Assistant , IB164: Human Genetics and Genomics, UC Berkeley, CA | 2011 |
| Mentor , UC Undergraduate Research Apprentice Program | |
| • Jaya Narasimhan, <i>Computer Science</i> . Comparative transcriptome evolution. | 2012—2014 |
| • Bryan Wang, <i>Pure Mathematics</i> . Partition distances. | 2013—2015 |

PROFESSIONAL EXPERIENCE

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|---|-----------|
| Systems Engineer , <i>Varsity Technologies</i> | 2005—2008 |
| • Engineering lead for Managed Services department, serving non-profits | |
| • Designed, implemented, configured, and maintained diverse infrastructures, including: server domains and policies, mail servers, networks, virtualization, disaster recovery. | |

SKILLS

Programming: C/C++, Python, R, Java, Javascript, MPI, bash, git, tex

SERVICE ACTIVITIES

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| Panel reviewer for Society of Systematic Biologists award applications | 2017 |
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LEADERSHIP ACTIVITIES

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| Organizer , Integrative Biology Computer Club | 2015 |
| Co-chair , Integrative Biology Graduate Student Assembly | 2012, 2013 |
| Organizer , Paleostatistics Reading Group | 2012 |
| Co-organizer , Evolutionary Theory and Museum Graduate Student Group | 2012 |
| Co-organizer , PhD Student Recruitment | 2011 |
| Organizer , Classic Papers in Evolutionary Biology | 2010 |

OUTREACH

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|---|------------|
| Guest Lecturer , Berkeley High School Outreach (coordinated by Rori Rohlf) | 2014, 2015 |
| Guest Lecturer , Bay Area Scientists in Schools | 2014 |
| Tutor , 826 Valencia volunteer for English Language Learners | 2009, 2010 |