Michael J. Landis

michael.landis@wustl.edu

http://landislab.org

April 27, 2021

Education

Ph.D. Integrative Biology   *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   *2005*
California State University, Long Beach, CA

Employment

Assistant Professor   *2019—Present*
Department of Biology
Washington University in St. Louis, St. Louis, MO

Research Interests

· Evolutionary biology

· Phylogenetics and systematics

· Historical biogeography

· Probabilistic models and stochastic processes

· Inference methods

Research Experience

Postdoctoral fellow, *Yale University*, New Haven, CT   *2016—2019*

Postdoctoral researcher, *Iowa State University*, Ames, IA   *2016*

Graduate researcher, *University of California*, Berkeley, CA   *2010—2015*

Bioinformatician, *Children's Hospital of Oakland*, Oakland, CA   *2009—2010*

Fellowships & Awards

Yale Donnelley Postdoctoral Environmental Fellowship (resumed)   *2019*

NSF Postdoctoral Research Fellowship   *2017—2018*

Yale Donnelley Postdoctoral Environmental Fellowship   *2016*

Ernst Mayr Award (Society of Systematic Biologists)   *2016*

UC Berkeley, Integrative Biology Summer Research Award   *2015*

UC Berkeley, Computational Biology Travel Award   *2012, 2015*

National Evolutionary Synthesis Center Graduate Student Fellowship   *2013*

Google Summer of Code Student Fellowship   *2012*

MANUSCRIPTS – PUBLISHED

1. **Landis MJ**, Edwards EJ, and Donoghue MJ. 2021. Modeling phylogenetic biome shifts on a planet with a past. *Systematic Biology.* 70: 86–107.

2. **Landis MJ**, Eaton DAR, Clement WL, Park B, Spriggs EL, Sweeney PW, Edwards EJ, and Donoghue MJ. 2021. Joint phylogenetic estimation of geographic movements and biome shifts during the global diversification of *Viburnum. Systematic Biology.* 70: 67–85.

3. Braga MP, **Landis MJ**, Nylin S, Janz N, and Ronquist F. 2020. Bayesian inference of ancestral host-parasite interactions under a phylogenetic model of host repertoire evolution. *Systematic Biology* 69:1149—1162.

4. Field DJ, Berv JS, Hsiang AY, Lanfear J, Landis MJ, Dornberg A. 2020. Timing the extant avian radiation: The rise of modern birds, and the importance of modeling molecular rate variation. *Bulletin of the American Museum of Natural History* 440: 159–181.

5. Kim AS, Zimmerman O, Nelson CA, Basore K, Zhang R, Desai C, Bullock C, Durnell L, Deem SL, Oppenheimer J, Shapiro B, Wang T, Coyne CB, Handley SA, **Landis**† **MJ**, Fremont† DH, and Diamond† MS. 2020. A sequence insertion in the Mxra8 receptor of Bovinae family members confers resistance to alphavirus infection. *Cell Host & Microbe* 27:428-440.

6. Quintero I and **Landis MJ** 2019. Interdependent phenotypic and biogeographic evolution driven by biotic interactions. *Systematic Biology* 69, 739–755.

7. **Landis MJ**, Freyman WA, and Baldwin BG. 2018. Retracing the Hawaiian silversword radiation despite phylogenetic, biogeographic, and paleogeographic uncertainty. *Evolution* 72: 2343–2359.

8. Park B, Sinnott-Armstrong M, Schlutius C, Zuluaga, J-CP, Spriggs EL, Simpson RG, **Landis MJ**, Sweeney PW, Eaton DAR, and Donoghue MJ. 2018. Sterile marginal flowers increase visitation and fruit set in the hobblebush (*Viburnum lantanoides*, Adoxaceae) at multiple spatial scales. *Ann. Bot.* 123: 381-390.

9. Höhna S, **Landis MJ**, and Huelsenbeck JP. 2017. Parallel power posterior analyses for fast computation of Bayes factors in phylogenetics. *Bioinformatics.* (*bioRxiv* preprint, doi:10.1101/104422)

10. **Landis MJ** and Schraiber JG. 2017. Pulsed evolution shaped modern vertebrate body sizes. *Proceedings of the National Academy of Sciences* 114: 13224–13229.

11. Höhna S, **Landis MJ**, Heath TA. 2017. Phylogenetic inference using RevBayes. *Current Protocols in Bioinformatics* 57:6.16.1–6.16.34.

12. **Landis, MJ** Biogeographic dating of speciation times using paleogeographically informed processes. 2017. *Systematic Biology* 66:128–144.

13. Höhna S, **Landis MJ**, Heath TA, Boussau B, Lartillot N, Moore BR, Huelsenbeck JP, and Ronquist F. 2016. RevBayes: Bayesian phylogenetic inference using graphical models and an interactive model-specification language. *Systematic Biology* 65:726-736.

14. Schraiber JG and **Landis MJ**. 2015. Sensitivity of quantitative traits to mutational effects and number of loci. *Theoretical Population Biology* 102:85–93.

15. Höhna S, Heath TA, Boussau B, **Landis MJ**, Ronquist F, and Huelsenbeck JP. 2014. Probabilistic graphical model representation in phylogenetics. *Systematic Biology* 63:753–771.

16. **Landis MJ** and Bedford T. 2014. Phylowood: interactive web-based animations of biogeographic and phylogeographic histories. *Bioinformatics* 30:123–124.

17. **Landis MJ**, Matzke NJ, Moore BR, and Huelsenbeck JP. Bayesian analysis of biogeography when the number of areas is large. 2013. *Systematic Biology* 62:789–804.

18. **Landis*** **MJ**, Schraiber* JG, and Liang M. 2013. Phylogenetic analysis using Lévy processes: finding jumps in the evolution of continuous traits. *Systematic Biology* 62:193–204.

   *, shared first authorship; †, shared corresponding authorship

1. Braga MP, Janz N, Nylin S, Ronquist F, and **Landis MJ**. Evolution of butterfly-plant networks over time, as revealed by Bayesian inference of host repertoire. In review at *Ecology Letters*.

1. **Landis MJ**. Biogeographic dating of phylogenetic divergence times using priors and processes. 2020. In Ho SYW (ed.), *The Molecular Evolutionary Clock: Theory and Practice*. Springer.

RevBayes, phylogenetic inference using graphical models	`revbayes.github.io`
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`
Phylowood, interactive biogeographic animations	`mlandis.github.io/phylowood`
qtc, quantitative trait evolution under the coalescent	`github.com/Schraiber/quant_trait_coalescent`

Biology Seminar, University of Nebraska, Lincoln (Zoom)	*2021*
Statistics Seminar, Washington University in St. Louis (Zoom)	*2021*
Biology Seminar, University of Missouri, St. Louis (Zoom)	*2020*
Living Earth Collaborative Seminar, Washington University in St. Louis (Zoom)	*2020*
St. Louis Ecology, Evolution & Conservation Seminar, Lewis & Clark Community College	*2019*
Biological Sciences Seminar, Auburn University	*2019*
Plant Biology Seminar, University of Georgia	*2018*
Evolution & Systematics Seminar, University of Connecticut	*2018*
Phyloseminar, an online society-sponsored seminar (`http://phyloseminar.org/`)	*2018*
Department of Biology Seminar, University of Oregon	*2018*
Department of Biology Seminar, Washington University in 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 Guaruja, 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*

Midcontinent Paleobotanical Colloquium (Zoom)	*2020*
Evolution Conference in Providence	*2019*
Yale Institute for Biospheric Studies Seminar	*2019*
External Advisory Board Meeting, Yale Institute for 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*

Journals: *Annals of Botany, Bioinformatics, BMC Evolutionary Biology, Evolution, Genome Biology & Evolution, Journal of Biogeography, Methods in Evolution & Ecology, Methods in Ecology & Evolution, Molecular Biology & Evolution, Molecular Phylogenetics & Evolution, Nature Communications, New Phytologist, Paleobiology, Proceedings of the Royal Society B, Proceedings of the National Academy of Sciences USA, Systematic Biology, Trends in Ecology & Evolution*

Grants: *NSF reviewer, SSB Ernst Mayr applications, SSB graduate award grants*

Service Activities

Committee member for WUSTL Biology Curriculum Committee	*2019—Present*
Committee member for EEPB Steering Committee	*2019—Present*
Committee member for EEPB Admissions Committee	*2019—Present*
Symposium organizer for Society of Systematic Biologists on *The Bright Side of Phylogenetics*	*2019*
Council member for Society for Systematic Biologists	*2019*
Editorial board member for Systematic Biology	*2018*
Co-chair, Integrative Biology Graduate Student Assembly	*2012—2013*

Courses

Instructor, BIOL580, EEPB Graduate Seminar, WUSTL	*2021*
Instructor, BIOL4220, Practical Bioinformatics, WUSTL	*2020*
Invited Lecturer, BIOL1425, Phylogenetic Biology, Brown University, RI	*2016*
Invited Lecturer, IB87, Bioinformatics, UC Berkeley, CA	*2014*
Invited Lecturer, EEB101, Macroevolution, UC Davis, CA	*2013*

Teaching Assistance

Teaching Assistant, IB200A, Principles of Phylogenetics, UC Berkeley, CA	*2012*
Teaching Assistant, IB164, Human Genetics and Genomics, UC Berkeley, CA	*2011*

Mentoring & Advising

Postdoctoral (WUSTL)

Ammon Thompson *National Geospatial-Intelligence Agency*. Viral phylodynamics.	*2021–Present*
Mariana Braga, *Evolution & Ecology*. Host-parasite co-evolution.	*2019—Present*

Graduate, rotation (WUSTL)

Sarah Swiston, *Evolution & Ecology*. Statistical phylogenetics.	*2021*
Justin Baldwin, *Evolution & Ecology*. Bird macroevolution.	*2020*
Aryeh Miller, *Evolution & Ecology*. Reptile macroevolution.	*2020*

Undergraduate (WUSTL)

Ernie Ramos, *Mathematics*. Modeling biome shifts in the Hawaiian silverswords.	*2021-Present*
Walker Sexton, *Biology*. Fossilization biases in space.	*2021-Present*

Undergraduate (UC Berkeley)

Bryan Wang, *Pure Mathematics*. Partition distances.	*2013—2015*
Jaya Narasimhan, *Computer Science*. Comparative transcriptome evolution.	*2012—2014*

Professional Experience

Server administrator, *Varsity Technologies*, San Francisco, CA	*2005—2008*

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

Outreach

Instructor, Stay-at-Home RevBayes Workshop (virtual)	*2021*
Instructor, Stay-at-Home RevBayes Workshop (virtual)	*2020*
Instructor, Molecular Evolution Workshop, Woods Hole, MA	*2018—2019*
Instructor, Bodega Phylogenetics Workshop, UC Davis, CA	*2014–2015, 2019*
Instructor, RevBayes Workshop, Yale University, New Haven, CT	*2019*
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*
Instructor, RevBayes Workshop, UC Berkeley, CA	*2015*
Instructor, Applied Phylogenetics Workshop, NESCent, NC	*2014*
Guest Lecturer, Berkeley High School Science Outreach	*2014, 2015*
Guest Lecturer, Bay Area Scientists in Schools	*2014*
Tutor, 826 Valencia volunteer for English Language Learners	*2009—2010*

Professional Societies

Society of Systematic Biologists	*2012–Present*
Society for the Study of Evolution	*2017–Present*
Geological Society of America	*2017–Present*
International Biogeography Society	*2020–Present*
Society for Advancement of Chicanos/Hispanics and Native Americans in Science	*2021–Present*

Advisors

John P. Huelsenbeck (UC Berkeley)	PhD advisor
Tracy A. Heath (Iowa State University)	Postdoctoral advisor
Michael J. Donoghue (Yale University)	Postdoctoral advisor