Michael James Landis

michael.landis@wustl.edu
landislab.org
Last updated: May 09, 2023

Education

2015	Ph.D. Integrative Biology
	Designated Emphasis in Computational & Genomic Biology
	University of California, Berkeley, CA
2005	B.S. Computer Science
	California State University, Long Beach, CA

Employment

2019—	Assistant Professor
	Department of Biology
	Department of Computer Science & Engineering (courtesy appointment)
	Washington University, St. Louis, MO

Research experience

2016—2019	Postdoctoral fellow, Yale University, New Haven, CT
2016	Postdoctoral researcher, Iowa State University, Ames, IA
2010—2015	Graduate researcher, University of California, Berkeley, CA
2009—2010	Bioinformatician, Children's Hospital of Oakland, Oakland, CA

Research Interests

I research relationships between evolutionary processes and patterns through a combination of biological, computational, and statistical approaches. My current interests include statistical phylogenetics, historical biogeography, the evolution of ecological interactions, phenotypic evolution, pathogen host-switching, stochastic processes, model design, Bayesian inference, and deep learning. My work typically involves the development of new probabilistic models and inference methods to test evolutionary hypotheses in biological and simulated datasets.

Fellowships & Awards

2019	Yale Donnelley Postdoctoral Environmental Fellowship (resumed)
2017—2018	NSF Postdoctoral Research Fellowship
2016	Yale Donnelley Postdoctoral Environmental Fellowship
2016	Ernst Mayr Award (Society of Systematic Biologists)
2015	UC Berkeley Integrative Biology Summer Research Award
2012, 2015	UC Berkeley Computational Biology Travel Award
2013	National Evolutionary Synthesis Center Graduate Student Fellowship
2012	Google Summer of Code Student Fellowship

External grants

2021—2024	NSF-DEB 2040347: "Modeling the Origin and Evolution of Hawaiian Plants"
	Awarded $1.12M to PIs Landis (Lead), Zapata, Wagner, Rønsted ($547k to WUSTL)

Internal grants

2022	WUSTL ITF: "The Human-Wildlife Interface: Disease Dynamics and Pandemic Prevention"
	Awarded $116k to PIs Milich (co-Lead), Landis (co-Lead), Wang

Submitted external grants

2023   NSF BII: "Institute for Vector-Borne System Dynamics: Integrating across Biological Scales to Understand Pathogen Transmission" Requested $15M to PIs Losos (Lead), Adalsteinsson, Boon, Brisson, Bente, Deem, Flowers, Landis. ($11M to WUSTL)

2022   NSF EEID & NIH FIC: "Phylogenetic modeling of viral transmission dynamics at the human wildlife interface in Uganda" Requested $3M to PIs Milich (Lead), Landis, Wang ($3M to WUSTL)

2023   NSF DEB: "Diversity, function, biogeography, and phylogeny of the freshwater riverine microbiome in North America: mapping the known and unknown." Requested $2M to PIs Ling (Lead), Landis, Knouft ($1.4M to WUSTL).

Manuscripts – Under Review   ‡: group postdoc co-author

2023   1.   **‡A Thompson**, B Liebeskind, EJ Scully EJ, **Landis MJ**. 2023. Deep learning approaches to viral phylogeography are fast and as robust as likelihood methods to model misspecification. bioRxiv 2023.02.08.527714.

Manuscripts – Accepted   ‡: group postdoc co-author

2023   1.   Kawahara AY, Storer C, Carvalho APS, Plotkin DM, Condamine F, **‡Braga MP**, ..., **Landis MJ**, ..., Lohman DJ (88 authors). Evolution and diversification dynamics of butterflies. Accepted. Nature Ecology & Evolution.

Manuscripts – Published   ‡: group postdoc co-author; *: shared first author; §: shared corresp. author

2023   1.   Quintero IM, **Landis MJ**, Jetz W, Mórlòn H. 2023. The build-up of the present-day tropical diversity of tetrapods. Accepted. Proceedings of the National Academy of Sciences. 120:e2220672120.

            2.   Nielsen SV, Vaughn A, Leppälä, **Landis MJ,** Mailund T, Nielsen R. 2023. Bayesian inference of admixture graphs on Native American and Arctic populations. PLoS Genetics 19:e1010410.

2022   3.   Dismukes W, **‡Braga MP**, Hembry DH, Heath TA, **Landis MJ**. Cophylogenetic methods to untangle the evolutionary history of ecological interactions. Annual Reviews of Ecology, Evolution, and Systematics. 53:275–298.

            4.   Donoghue MJ, Eaton DAR, Maya-Lastra CA, **Landis MJ**, Sweeney PJ, Olson, ME, Cacho NI, Moeglin MK, Gardner JR, Heaphy NM, Castorena M, Segovia Rivas A, Clement WL, Edwards EJ. 2022. Replication radiation of a plant clade along a cloud forest archipelago. Nature Ecology & Evolution. doi:10.1038/s41559-022-01823-x.

            5.   Barido-Sottani J, Justison JA, Borges R, Brown JM, Dismukes W, do Rosario Petrucci B, Fabreti Guimarães L, Höhna S, **Landis MJ**, Lewis PO, May MR, Mendes FK, Pett W, Redelings BD, Tribble CM, Wright AM, Zenil-Ferguson R, Heath TA. 2022. Lessons learned from organizing and teaching virtual phylogenetics workshops. Bulletin of the Society of Systematic Biologists doi:10.18061/bssb.v1i2.

            6.   Wendt EW, Malabarba LR, **‡Braga MP**, Boeger WA, **Landis MJ**, Carvalho TP. Phylogeny, species delimitation, and ecological and morphological diversity of Characithecium (Monogenoidea: Dactylogyridae). 2022. Parasitology 149: 700–716.

            7.   **Landis MJ**, Quintero I, Muñoz MM, Zapata F, Donoghue MJ. Phylogenetic inference of where species spread or split across barriers. 2022. Proceedings of the National Academy of Sciences 119: e2116948119.

            8.   Tribble CM, Freyman WA, Lim JY, **Landis MJ**, Barido-Sottani J, Kopperud BT, Höhna S, May MR. 2022. RevGadgets: an R Package for visualizing Bayesian phylogenetic analyses from RevBayes. Methods in Ecology and Evolution 13: 314–323.

2021   9. Höhna S, **Landis MJ**, and Huelsenbeck JP. 2021. Parallel power posterior analyses for fast computation of Bayes factors in phylogenetics. PeerJ: 9:e12438.

10. ‡**Braga MP**, Janz N, Nylin S, Ronquist F, and **Landis MJ**. 2021. Phylogenetic reconstruction of ancestral ecological networks through time for pierid butterflies and their host plants. Ecology Letters 24: 2134-–2145.

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

12. **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.

2020   13. ‡**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.
        Awarded Best Paper in Systematic Biology in 2020.

14. 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.

15. 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.

16. Quintero I and **Landis MJ**. 2020. Interdependent phenotypic and biogeographic evolution driven by biotic interactions. Systematic Biology 69: 739–755.

2018   17. **Landis MJ**, Freyman WA, and Baldwin BG. 2018. Retracing the Hawaiian silversword radiation despite phylogenetic, biogeographic, and paleogeographic uncertainty. Evolution 72: 2343–2359.

18. 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.

2017   19. **Landis MJ** and Schraiber JG. 2017. Pulsed evolution shaped modern vertebrate body sizes. Proceedings of the National Academy of Sciences 114: 13224–13229.

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

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

2016   22. 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.

2015   23. Schraiber JG and **Landis MJ**. 2015. Sensitivity of quantitative traits to mutational effects and number of loci. Theoretical Population Biology 102:85–93.

2014   24. 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.

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

2013   26. **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.

27. ***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.

Perspectives – Published

2023   1. Upham NS, **Landis MJ**. 2023. Genomics expands the mammalverse. Science. 380: 358-359.

Book Chapters – Published

2020   2. 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.

Research Software

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, trait evolution under the coalescent   github.com/Schraiber/quant_trait_coalescent

Presentations – Invited   *: graduate student invited

2023   Standalone Meeting for the Society of Systematic Biologists, UNAM, Mexico City
2022   Meeting of Systematics, Biogeography, and Evolution (virtual)
        *Melinda Denton Endowed Seminar on Plant Systematics, University of Washington
        *Ecology and Evolution Seminar, University of Minnesota, Minneapolis (virtual)
        Biodiversity Research Center Seminar, University of British Columbia, Vancouver (virtual)
2021   European Society of Evoutionary Biologists, Satellite Meeting (virtual)
        Biology Seminar, University of Nebraska, Lincoln (virtual)
        Statistics Seminar, Washington University in St. Louis (virtual)
2020   Biology Seminar, University of Missouri, St. Louis (virtual)
        Living Earth Collaborative Seminar, Washington University in St. Louis (virtual)
2019   St. Louis Ecology, Evolution & Conservation Seminar, Lewis & Clark Community College
        Biological Sciences Seminar, Auburn University
2018   Plant Biology Seminar, University of Georgia
        Evolution & Systematics Seminar, University of Connecticut
        Phyloseminar, an online society-sponsored seminar (http://phyloseminar.org/)
        Department of Biology Seminar, University of Oregon
        Department of Biology Seminar, Washington University in St. Louis
2017   Symposium on Computational Paleobiology, Geological Society of America, Seattle
        Systematics Seminar, Swedish Museum of Natural History
2016   Computational Genomics Seminar, Temple University
2015   Symposium on Parametric Biogeography, Evolution Conference in Guaruja, Brazil
2013   Phylogenetics & Evolutionary Biology Seminar, North Carolina State University
        Workshop on Mathematics for an Evolving Biodiversity, University of Montréal
        Center for Population Genomics Seminar, UC Davis

Presentations – Contributed

2022   International Biogeography Society Conference (virtual)
2022   Evolution Conference (virtual)
2021   Evolution Conference (virtual)
2020   Midcontinent Paleobotanical Colloquium (virtual)
2019   Evolution Conference in Providence

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

Professional Reviews

Journals	American Journal of Botany, Annals of Botany, 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, Proceedings of the National Academy of Sciences USA, Systematic Biology, Trends in Ecology & Evolution, Zoological Journal of the Linnean Society
Grants	NSF reviewer, SSB Ernst Mayr applications, SSB graduate award grants

University Service

2019—	EEPB Steering Committee
2019—	EEPB Admissions Committee

Departmental Service

2023—	Biology Faculty Excellence Task Force
2022—2023	Hiring Committee for Genetics & Genomics Faculty
2022	Hiring Committee for Urban Biology & Environmental Justice Faculty
2019—	Spector & Quatrano Awards Committee
2019—	WUSTL Biology Curriculum Committee
2012—2013	Co-chair, Integrative Biology Graduate Student Assembly, UC Berkeley

Society Service

2023—	Organizer for SSB Mentoring Program
2023	Co-creator of new SSB Mentoring Program
2022—	Associate Editor for Systematic Biology
2021—	Legacy Committee member for Society for Systematic Biologists (society history, etc.)
2021—	Faculty mentor for WUSTL Chapter within the Society for Advancement of Chicanos/Hispanics and Native Americans in Science
2021, 2022	One-off ERC mentor for Evolution meeting
2019—2022	Council member for Society for Systematic Biologists
2018—2022	Editorial board member for Systematic Biology
2019	Symposium organizer for Society of Systematic Biologists on The Bright Side of Phylogenetics

Teaching & Courses

2020—2022	Instructor, BIOL4220, Practical Bioinformatics, WUSTL
2022	Invited Lecturer, EEB103, Statistical Phylogenetics & Speciation, UC Davis
2021	Instructor, BIOL580, EEPB Graduate Seminar, WUSTL
2016	Invited Lecturer, BIOL1425, Phylogenetic Biology, Brown University
2014	Invited Lecturer, IB87, Bioinformatics, UC Berkeley
2013	Invited Lecturer, EEB101, Macroevolution, UC Davis

Teaching Assistance

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

Research Lab Mentoring & Advising
WUSTL Postdoctoral Scholar
2023—   Albert Soewongsono, Mathematical Phylogenetics
2021—   Fábio Mendes, Computational Phylogenetics
2019—2021   Mariana Braga, Evolution & Ecology

ORISE Postdoctoral Scholar (academic mentor)
2021—   Ammon Thompson, Statistical Epidemiology

WUSTL PhD Student (advised)
2021—   Sarah Swiston, EEPB
2022—   Sean McHugh, EEPB

WUSTL Undergraduate
2023—   Jonathan Liu, Biology & Mathematics
2022—2023   Yu (Sunny) Zichen, Mathematics & Computer Science
2021—2023   Walker Sexton, Biology
2021—2023   Mihir Shah, Biomedical Engineering
2021   Ernie Ramos, Mathematics

UC Berkeley Undergraduate
2013—2015   Bryan Wang, Mathematics
2012—2014   Jaya Narasimhan, Computer Science

PhD Program Mentoring & Advising
WUSTL PhD Student (rotation)
2023—   Clinton Jules, Computer Science
2022   Preston Pennington, EEPB
2021   Sean McHugh, EEPB
2020   Sarah Swiston, EEPB
2020   Justin Baldwin, EEPB
2020   Aryeh Miller, EEPB

WUSTL dissertation committee member
2023—   Yeganeh Sekhavati, Anthropology
2022—   Justin Baldwin, EEPB
2022—   Aryeh Miller, EEPB
2022—   Changxu Fan, Immunology
2022—   Jenna Lin, BBSB
2021—   Brock Mashburn, EEPB
2021—   Jhan Salazar, EEPB
2020—   Wen-Hsi Kuo, EEPB
2020—2022   Erika Schumacher, EEPB (graduated)
2020   Qi Wang, Statistics

Outreach

2021	Instructor, Stay-at-Home RevBayes Workshop (virtual)
2020	Instructor, Stay-at-Home RevBayes Workshop (virtual)
2018—2019	Instructor, Molecular Evolution Workshop, Woods Hole
2019	Instructor, Bodega Phylogenetics Workshop, UC Davis
2019	Instructor, RevBayes Workshop, Yale University, New Haven
2017	Instructor, Fossil tip-dating with RevBayes, GSA Meeting, Seattle
2017	Instructor, Biogeography with RevBayes, SSB Meeting, Baton Rouge
2017	Instructor, Introduction to RevBayes, Yale, New Haven
2014—2016	Teaching Assistant, Molecular Evolution Workshop, Woods Hole
2015	Instructor, RevBayes Workshop, UC Berkeley
2014, 2015	Instructor, Bodega Phylogenetics Workshop, UC Davis
2014	Instructor, Applied Phylogenetics Workshop, NESCent
2014, 2015	Guest Lecturer, Berkeley High School Science Outreach
2014	Guest Lecturer, Bay Area Scientists in Schools
2009—2010	Tutor, 826 Valencia volunteer for English Language Learners

Professional Societies

2009—	Society of Systematic Biologists
2012—	Society for the Study of Evolution
2018—	International Biogeography Society
2021—	Society for Advancement of Chicanos/Hispanics and Native Americans in Science
2017—2020	Geological Society of America

Professional Experience

2005—2008	IT Consultant, Varsity Technologies, San Francisco, CA

Advisors

PhD	John P. Huelsenbeck
	Department of Integrative Biology
	UC Berkeley
Postdoctoral	Tracy A. Heath
	Department of Ecology, Evolution, and Organismal Biology
	Iowa State University
Postdoctoral	Michael J. Donoghue
	Department of Ecology and Evolutionary Biology
	Yale University