

Nathan C Layman, PhD

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Research Interests

My research focuses on using computational science and machine learning to ask ecological and evolutionary questions about outbreak dynamics, host-pathogen co-evolution, and viral transmission. Some of my recent projects include developing predictive models for outbreak forecasting, estimating the efficacy of wildlife disease surveillance using natural language processing-assisted data structuring, and the prediction and mitigation of viral spillover. I am also passionate about open and reproducible science and accurately capturing the uncertainty in models.

Education

- 04/2018 PhD Biology, Washington State University
- 03/2011 BS Biology, University of Washington
- 03/2011 BA Environmental Studies, University of Washington

Expertise

4 years experience with Machine learning, including Generative AI, Natural Language Models, Boosted Regression Trees, and Generalized Additive Models

Mathematical modeling. Development and analysis of a variety of evolutionary mathematical models.

Fieldwork - Design and implementation of multi-year field experiments.

Programming - Proficient in modeling techniques and the analysis of large data sets using R, Python, C++, and Mathematica.

Next generation sequence data analysis - RADseq analysis, reference assembly, GWAS.

Publications

Published

Layman, N.C., Basinski, A.J., Zang, B., Eskew, E.A., Bird, B.H., Ghersi, B.M., Bangura, J., Fichet-Calvet, E., Remien, C.H., Vandi, M., Bah, M., Nuismer, S.L. 2023. *Predicting the fine-scale spatial distribution of zoonotic reservoirs using computer vision*. 2023. Ecology Letters. Ecology Letters, 00: 1-13.

doi.org/10.1111/ele.14307

Nuismer, S.L., **Layman, N.C.**, Redwood, A.J., Chan, B., Bull, J.J. 2021. *Methods for measuring the evolutionary stability of engineered genomes to improve their longevity*. Synthetic Biology, 6(1): 1-10.

doi.org/10.1093/synbio/ysab018

Basinski, A.J., Fichet-Calvet, E., Sjodin, A.R., Varrelman, T.J., Remien, C.H., **Layman, N.C.**, Bird, B.H., Wolking, D.J., Monagin, C., Ghersi, B.M., Barry, P.A., Jarvis, M.A., Gessler, P.E., Nuismer, S.L. 2021. *Bridging the gap: Using reservoir ecology and human sero-surveys to estimate Lassa incidence in West Africa*. PLOS Computational Biology, 17(3): e1008811 [doi:10.1371/journal.pcbi.1008811](https://doi.org/10.1371/journal.pcbi.1008811)

Layman, N.C., Tuschhoff, B.M., Basinski, A.J., Reimen, C.H., Bull, J., Nuismer, S.L. 2021. *Designing transmissible viral vaccines for evolutionary robustness and maximum efficiency*. Vaccine Evolution, 7(1): 1-11. doi:10.1093/ve/veab002

Layman, N.C., Tuschhoff, B.M., Basinski, A., Reimen, C., Bull, J., Nuismer, S. 2020. *Suppressing evolution in genetically engineered systems through repeated supplementation*. Evolutionary Applications. doi:10.1111/eva.13119.

Prior, C.P.*, **Layman, N.C.***, Koski, M.H., Galloway, L.F., Busch, J.W. 2020. *Westward range expansion from middle latitudes explains the Mississippi River discontinuity in a forest herb of eastern North America*. Molecular Ecology, 29: 4473-4486. doi:10.1111/mec.15650

Nuismer, S.L., Remien, C.H., Basinski, A.J., Varrelman, T., **Layman, N.C.**, Rosenke, K., Bird, B., Jarvis, M., Barry, P., Fichet-Calvet, E. 2020. *Bayesian estimation of Lassa virus epidemiological parameters: implications for spillover prevention using wildlife vaccination*. PLOS Neglected Tropical Diseases, 14(9): e0007920. doi:10.1371/journal.pntd.0007920.

Koski, M.H., **Layman, N.C.**, Prior, C.J., Busch, J.W., Galloway, L.F. *Selfing ability and drift load evolve with range expansion*. 2019 Evolution Letters, 3-5: 500-512. doi:10.1002/evl3.136

Layman, N.C., Busch, J.W. 2018. *Bottlenecks and inbreeding depression in autotetraploids*. Evolution, 72-10: 2025-2037. doi:10.1111/evo.13587

Layman, N.C., Fernando, T.R., Herlihy, C.R., Busch, J.W. 2017. *Costs of selfing prevent the spread of a self-compatibility mutation that causes reproductive assurance*. Evolution, 71: 884-897. doi:10.1111/evo.13167

*Shared first authorship

In Prep

Layman, N.C., Cayol, C., Awada, L., Ross, N., Tizzani, P. 2024. *Generative AI-assisted methods for estimating the sensitivity of disease surveillance*. Target: Methods in Ecology and Evolution.

Press

Feb 2017 Harkness, A. *Digest: Prudent self-denial: the advantage of incompatibility in Leavenworthia alabamica*. Evolution. Reviews Layman et al 2017

Grants and selected awards

2017	Rexford Daubenmire Award for Graduate Education - \$30,000
2016	NSF Doctoral Dissertation Improvement Grant (DDIG) - \$20,000
2013-2017	Higinbotham Award - \$12,000
2012-2014	Aase Fellowship - \$4,000

Mentoring

- 2017-2020 Mentored UIIdaho and WSU graduate students in parallel computing as well as coding in R, Python and C++.
- 2018-2019 Mentored UIIdaho undergraduates in modeling, computational biology, coding, and the Gillespie algorithm.
- 2017-2016 Mentored WSU undergraduates in multiplex PCR, microsatellite analysis, RADseq and general lab work

Teaching

- 2013-2018 20-30 hours per week designing, teaching and grading lab sections for the following courses
 - Principles of Organic Evolution
 - Origins in the Natural World
 - Dynamic Systems in the Natural World
 - Introductory Biology

Presentations and invited seminars

- 2019 Spotlight session: *Swamping prevents post-release evolution in genetically modified organisms.*
Evolution 2019, Providence, RI
- 2017 Invited speaker: *The fitness effects of an initial self-compatibility mutation in Leavenworthia alabamica.*
International Botanical Congress 2017, Shenzhen, China
- 2017 Co-author, invited talk: *Population-genetic expectations for trait filtering of self-incompatibility on islands.*
International Botanical Congress 2017, Shenzhen, China
- 2017 Invited speaker: *Inbreeding depression and polyploidy as a genetic island.*
Evolution 2017, Portland, OR
- 2017 Co-author, invited talk: *Population-genetic expectations for trait filtering of self-incompatibility on islands.*
Evolution 2017, Portland, OR
- 2017 Contributed poster: *Why is self-compatibility common on islands?*
Washington State University School of Biological Sciences 2017, Pullman, WA
- 2016 Contributed talk: *Inbreeding depression and the spread of selfing in polyploids.*
EVO-WIBO 2016, Port Townsend, WA
- 2016 Contributed talk: *Inbreeding depression and the spread of selfing in polyploids.*
Washington State University School of Biological Sciences Recruitment Seminar 2016, Pullman, WA
- 2015 Contributed talk: *Inbreeding depression and the spread of selfing in polyploids.*
Botany 2015, Edmonton, AL, CA
- 2014 Contributed poster: *Challenging the Link Between Polyploidy and Self-compatibility.*
Botany 2014, Boise, ID

Other academic activities

Service

- 2017-2020 Reviewed articles for Evolution, The Journal of Evolutionary Biology, The Journal of Heredity, and PLOS
- 2017 Presented introduction to programming workshop series for Washington State University graduate students
- 2016-2017 Washington State University, School of Biological Sciences - Coordinator for the weekly seminar series, Biolunch

Employment history

- 2021-Current Research Scientist, EcoHealth Alliance. *Early disease outbreak forecasting*. New York, NY.
- 2018–2021 Postdoctoral Researcher, University of Idaho. *Modeling the stability of transmissible vaccines*. Developed mathematical models of infectious disease - Moscow ID.
- 2014–2017 Research Assistant, Washington State University. *Challenging the reproductive assurance hypothesis*. Co-designed and implemented large scale field experiment - Moulton AL.
- 2011–2012 Fisheries Technician, Washington Department of Fish and Wildlife. *Maintained, evaluated, and transported fish stocks in central Washington*. - Chelan, WA
- 2011-2012 Botany Technician, United States Forest Service. Supervisor: Brigitte Ranne. *Plant inventory and monitoring in Washington forests*. Supervised a 4 person field crew - Entiat, WA

References

Emma Mendelsohn, Senior Research Scientist, Computational Research Team, EcoHealth Alliance
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Scott Nuismer, Associate Professor, Department of Biological Sciences, University of Idaho
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