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PERSONAL STATEMENT

I am an Engineer with a background in Computer & Information Science and a focus on research in the Biological Sciences. I have nine years of hands-on experience conducting various flavors of methods development, implementation, and analysis in an academic research environment. In practice, my work has consisted primarily of creating machine learning-based software tools that allow researchers to analyze and interpret complex biological datasets. My research often involves using cutting-edge statistical methods to filter artifacts, normalize/encode data, fit models, and visualize data so that results are scientifically sound and practically useful. I finished my position with the Matsen Lab at Fred Hutch in August 2026. I am currently taking some time to work on personal projects and professional development. I take pride in clearly communicating my work and enjoy the discussions that follow.

EDUCATION

- **Master of Science · Biology** **University of Oregon**
Knight Campus · Bioinformatics and Genomics *Eugene, OR · June, 2019 → December, 2020*
- **Bachelor of Science · Computer & Information Science** **University of Oregon**
Arts & Sciences · Departmental Honors · Minor in Product Design *Eugene, OR · August, 2013 → July, 2018*

TECHNICAL SKILLS

- **Languages:** Python (preferred), R, C/C++, Bash, Java, JavaScript
- **ML & Data Science:** JAX, TensorFlow/Keras, PyTorch, Scikit-learn, Pandas, Polars, NumPy, Xarray, SciPy, BioPython
- **Visualization:** Matplotlib, Plotnine (grammar of graphics), Altair (interactive visualization)
- **Tools & Infrastructure:** Git, GitHub Actions, Travis CI, Quay, Docker, Apptainer (formerly Singularity), Conda/Mamba, Snakemake, Nextflow, SLURM HPC, AWS S3, GNU make, CMake, SCons, zsh/bash, Vim, tmux, VSCode, L^AT_EX, HTML, Markdown
- **Mathematics:** Advanced & Bayesian Statistics, Linear Algebra, Discrete Math, Calculus
- **Operating Systems:** Linux (Ubuntu preferred), macOS, Windows

EXPERIENCE

- **Bioinformatics Specialist** **Howard Hughes Medical Institute**
Public Health Sciences Division · Matsen Lab *Bozeman, MT (Remote) · January, 2024 → August, 2026*
 - **Jointly modeling deep mutational scanning (DMS) datasets:** Developed a novel approach for jointly modeling multiple distinct DMS experimental datasets. The method was validated *in-silico* (using simulated data) as well as *in-vitro* (testing mutations in the lab, directly). I implemented a functional API into a JAX-based python package, [multidms](#) [1], which is now used in a primary analysis pipeline across multiple labs.
 - **Bioinformatics for studying affinity maturation in germinal centers:** Working with wet lab researchers to meet their needs, I created an efficient Nextflow pipeline that leveraged high-performance computing clusters and software containerization to perform over 50K independent data-processing steps and produce more than 140 feature-rich phylogenetic trees. This work provided the primary data and analysis for a large, collaborative study across multiple groups, since published in *Cell* [14].
 - **Administrative data management:** Executed best-practice management and storage of sensitive data in various computational environments including HPC file systems and AWS S3 buckets. Additionally, I was responsible for scrubbing sensitive data from repository histories before publication.
 - **Visualization/Communication of results:** Visualized data for researchers and produced final figures for publication to communicate patterns in data clearly. Regularly presented results and background of my research projects to a range of audiences including lab meetings, collaborative meetings, and team meetings.
- **Bioinformatics Analyst II** **Fred Hutchinson Cancer Center**
Public Health Sciences Division · Matsen Lab *Bozeman, MT (Remote) · January, 2021 → January, 2024*
 - **Algorithmic design for mutational fitness estimation:** As requested by researchers, I conceptualized and implemented an algorithmic approach into a custom Snakemake pipeline for estimating mutational fitness trajectories (through time) for every possible codon-mutation that may have occurred within a phylogeny (evolutionary history) of more than 13 million empirical viral genomes.
 - **Genomic surveillance of viral escape:** Built and deployed custom, public Nextstrain pages for viruses such as [SARS-CoV-2](#), Influenza, Lassa, and others — each of which provide estimates of viral escape to antibodies of interest. This work has provided analysis tools for various studies and informed the potential effectiveness of these antibodies as therapeutics.
 - **Colleague consultation:** Provided various degrees of help and guidance to undergraduate interns, graduate students, postdocs, and other faculty with computational tasks surrounding active research projects and employee onboarding. These tasks include but are not limited to algorithmic implementation, command line interface, HPC clusters, workflow management, machine learning, version control, compute environments, and build systems.

○ Research Associate

Paid Internship · Computational Biology · Matsen Lab

Fred Hutchinson Cancer Center

Seattle, WA · March, 2020 → December, 2020

- **PhIP-Seq software and analysis:** Developed a suite of software tools, [phipperry](#), for analysis of raw Phage ImmunoPrecipitation Sequencing (PhIP-Seq) data that consisted of a python package for modeling and computing enrichment statistics, an interactive application for visualizing results of the processed data, and an end-to-end (raw data → results) Nextflow pipeline for encapsulating the standard analysis workflows in a portable and reproducible manner. In addition, it will inform us of best practices and future experiments carried out in the wet lab. Multiple collaborative publications have used this software to process data and produce results [3, 4, 5, 18, 20, 22].
- **Neural Networks for global epistasis modeling:** Worked with a graduate student to implement a global epistasis modeling software package, [torchdms](#), using the PyTorch library.
- **Team Organization:** Set up and led team meetings to brainstorm, set short-term goals, and present results across multiple labs and studies for various team members.

○ Graduate Teaching Fellow

BIO 410/510 · Biology Department · UO Graduate School

University of Oregon

Eugene, OR · August, 2019 → March, 2020

- **Teaching:** Led discussions, taught lessons, and proctored exams for four classroom hours each week for a graduate-level class focused on Python/Bash scripting, Unix file formatting/parsing, and other algorithmic thinking activities.
- **Assignment Design:** Constructed Docker containers and a Jupyter Notebook auto-grade pipeline for students to have a unified environment for Python programming. Hosted office hours and graded ≈ 100 assignments/exams per week with feedback.

○ Scientific Programmer

Institute of Ecology and Evolution · Ralph & Kern Co-Lab

University of Oregon

Eugene, OR · June, 2018 → June, 2019

- **Software Engineering:** Leveraged software engineering best practices such as architecture design, version control, and continuous integration for various open-source software projects, including [tskit](#), [stdpopsim](#), and [ReLERNN](#).
- **Experimentation and model development:** Evaluated the application of simulated data for training recurrent deep learning models (RNNs) to predict recombination rate estimates across the consensus genome of empirical populations. This work provided the analysis pipeline in the resulting publication [6].
- **Analysis of population demography inference tools:** Constructed a snakemake pipeline for published analysis outlining a comparison of population demography inference tools [23].

○ Undergraduate Research Assistant

Institute of Ecology and Evolution · Ralph & Kern Co-Lab

University of Oregon

Eugene, OR · June, 2017 → June, 2018

- **Algorithmic implementation of tree sequence recording:** Implemented tree sequence recording algorithm into widely used population genetic simulation software, [SLiM](#), and contributed to the writing in the resulting publication [8].
- **Algorithmic benchmarking:** Utilized cluster resources, visualization tools, and more to compare large-scale simulations and benchmark performance across various metrics, including memory allocation and user runtime. This work was written up and formally presented in my [undergraduate honors thesis](#) and used to inform ongoing studies.
- **Simulation studies of rapid evolution:** Developed and analyzed large-scale, realistic evolutionary simulation models to study migration patterns involved in the rapid evolution of stickleback fish on the Alaskan coast. I then led the publication of this study [7].

○ Discrete Math Course Grader

Mathematics Department

University of Oregon

Eugene, OR · June, 2016 → June, 2017

- **Grading:** Graded and constructed feedback for ≈ 100 weekly assignments focused on proofs, set theory, and combinatorics.

HIGHLIGHTED SOFTWARE PROJECTS

○ multidms



Using Google's JAX library, this open-source Python package provides the utilities for jointly modeling multiple distinct Deep Mutational Scanning datasets. The interface includes a number of tools that help to easily prepare and encode data, initialize and fit models, perform out-of-sample prediction, and interactively visualize the resulting parameter values of interest. This software adds to the growing list of tools for modeling DMS data and has been used to produce results for multiple studies.

○ phipperry



The phipperry software suite provides tools for analyzing data from phage display methods that use immunoprecipitation and deep sequencing to capture antibody binding to peptides, often referred to as "PhIP-Seq" experiments. This software has three main components that can be used separately or in conjunction: (i) a Nextflow pipeline, phip-flow, to process raw sequencing data into a compact, multidimensional dataset format, allowing for end-to-end reproducible workflow automation. (ii) a Python API, phipperry, which provides interfaces for tasks such as count normalization, enrichment calculation, multidimensional scaling, modeling for significant enrichment of peptides, and finally, (iii) a Streamlit application, phip-viz, as an interactive interface for visualizing the data as a heatmap in a flexible manner.

○ ReLERNN



ReLERNN is a Python-based CLI tool for *Re*combination-*L*andscape *E*stimation using *R*ecurrent *N*eural *N*etworks. This software implements a deep learning method for estimating a genome-wide recombination map that is accurate even with small numbers of pooled or individually sequenced genomes. Rather than use summaries of linkage disequilibrium as its input, ReLERNN takes columns from a genotype alignment, which are then modeled as a sequence across the genome using a recurrent neural network.

- [1] H. K. Haddox, J. G. Galloway, B. Dadonaite, J. D. Bloom, F. A. Matsen, and W. S. DeWitt. Jointly modeling deep mutational scans identifies shifted mutational effects among sars-cov-2 spike homologs. *bioRxiv*, Aug. 2023. <http://dx.doi.org/10.1101/2023.07.31.551037>.
- [2] J. G. Galloway, K. Sung, S. S. Minot, M. E. Garrett, C. I. Stoddard, A. C. Willcox, Z. A. Yaffe, R. Yucha, J. Overbaugh, and F. A. Matsen. phipperry: a software suite for phip-seq data analysis. *Bioinformatics*, 39(10), Sept. 2023. <http://dx.doi.org/10.1093/bioinformatics/btad583>.
- [3] M. E. Garrett, J. G. Galloway, C. Wolf, J. K. Logue, N. Franko, H. Y. Chu, F. A. Matsen, and J. M. Overbaugh. Comprehensive characterization of the antibody responses to SARS-CoV-2 spike protein finds additional vaccine-induced epitopes beyond those for mild infection. *eLife*, 11, jan 2022. <https://doi.org/10.7554%2Felife.73490>.
- [4] C. I. Stoddard, J. Galloway, H. Y. Chu, M. M. Shipley, K. Sung, H. L. Itell, C. R. Wolf, J. K. Logue, A. Magedson, M. E. Garrett, K. H. Crawford, U. Laserson, F. A. Matsen, and J. Overbaugh. Epitope profiling reveals binding signatures of SARS-CoV-2 immune response in natural infection and cross-reactivity with endemic human CoVs. *Cell Reports*, 35(8):109164, may 2021. <https://doi.org/10.1016%2Fj.celrep.2021.109164>.
- [5] M. E. Garrett, J. Galloway, H. Y. Chu, H. L. Itell, C. I. Stoddard, C. R. Wolf, J. K. Logue, D. McDonald, H. Weight, F. A. Matsen, and J. Overbaugh. High-resolution profiling of pathways of escape for SARS-CoV-2 spike-binding antibodies. *Cell*, 184(11):2927–2938.e11, may 2021. <https://doi.org/10.1016%2Fj.cell.2021.04.045>.
- [6] J. R. Adrion, J. G. Galloway, and A. D. Kern. Predicting the landscape of recombination using deep learning. *Molecular Biology and Evolution*, 37(6):1790–1808, feb 2020. <https://doi.org/10.1093%2Fmolbev%2Fmsaa038>.
- [7] J. Galloway, W. A. Cresko, and P. Ralph. A few stickleback suffice for the transport of alleles to new lakes. *G3 Genes|Genomes|Genetics*, 10(2):505–514, feb 2020. <https://doi.org/10.1534%2Fg3.119.400564>.
- [8] B. C. Haller, J. Galloway, J. Kelleher, P. W. Messer, and P. L. Ralph. Tree-sequence recording in SLiM opens new horizons for forward-time simulation of whole genomes. *Molecular Ecology Resources*, 19(2):552–566, feb 2019. <https://doi.org/10.1111%2F1755-0998.12968>.

SUPPORTING AUTHOR PUBLICATIONS

- [9] C. R. Carr, K. H. Crawford, M. Murphy, J. G. Galloway, H. K. Haddox, F. A. I. Matsen, K. G. Andersen, N. P. King, and J. D. Bloom. Deep mutational scanning reveals functional constraints and antibody-escape potential of lassa virus glycoprotein complex. *Immunity*, 2024. <https://doi.org/10.1016/j.immuni.2024.06.013>.
- [10] F. C. Welsh, R. T. Eguia, J. M. Lee, H. K. Haddox, J. Galloway, N. V. V. Chau, A. N. Loes, J. Huddleston, T. C. Yu, M. Q. Le, N. T. Nhat, N. T. L. Thanh, A. L. Greninger, H. Y. Chu, J. A. Englund, T. Bedford, F. A. Matsen, M. F. Boni, and J. D. Bloom. Age-dependent heterogeneity in the antigenic effects of mutations to influenza hemagglutinin. *Cell Host & Microbe*, 32(8):1397–1411, Aug. 2024. <https://doi.org/10.1016/j.chom.2024.06.015>.
- [11] G. E. Boyle, K. A. Sitko, J. G. Galloway, H. K. Haddox, A. H. Bianchi, A. Dixon, M. K. Wheelock, A. J. Vandi, Z. R. Wang, R. E. S. Thomson, et al. Deep mutational scanning of cyp2c19 in human cells reveals a substrate specificity-abundance tradeoff. *Genetics*, 228(3):iyae156, 2024.
- [12] H. K. Haddox, G. Angehrn, L. Sesta, C. Jennings-Shaffer, S. D. Temple, J. G. Galloway, A. S. Hinrichs, W. S. DeWitt, J. D. Bloom, F. A. Matsen IV, et al. The mutation rate of sars-cov-2 is highly variable between sites and is influenced by sequence context, genomic region, and rna structure. *Nucleic Acids Research*, 53(11):gkaf503, 2025.
- [13] H. K. Haddox, O. Abdel Aziz, J. G. Galloway, J. Kent, C. R. Cooper, C. Jennings-Shaffer, W. Dumm, S. D. Temple, J. D. Bloom, and F. A. Matsen IV. Clonal interference and changing selective pressures shape the escape of sars-cov-2 from hundreds of antibodies. *Virus Evolution*, 12(1):veaf104, 2026.
- [14] W. S. DeWitt, A. A. Vora, T. Araki, J. G. Galloway, T. Alkutkar, J. Bortolatto, T. B. R. Castro, W. Dumm, C. Jennings-Shaffer, T. Jia, et al. Replaying germinal center evolution on a quantified affinity landscape. *Cell*, 189(16):4980–4996, 2026.
- [15] D. K. Ralph, A. G. Bakis, J. G. Galloway, A. A. Vora, T. Araki, G. D. Victora, Y. S. Song, W. S. DeWitt, and F. A. Matsen. Inference of germinal center evolutionary dynamics via simulation-based deep learning. *eLife*, 14:RP108880, 2026.
- [16] A. G. Bakis, A. A. Vora, T. Araki, T. Jia, J. G. Galloway, C. Jennings-Shaffer, G. D. Victora, Y. S. Song, W. S. DeWitt, F. A. Matsen IV, et al. Bayesian inference of antibody evolutionary dynamics using multitype branching processes. *arXiv preprint arXiv:2508.09519*, 2025.

- [17] H. K. Haddox, A. S. Hinrichs, C. Jennings-Shaffer, K. Johnson, C. T. Benton, J. G. Galloway, J. D. Bloom, and F. A. Matsen IV. Phylogenetically estimated neutral rates and fitness effects of mutations to influenza proteins. *bioRxiv*, 2026.
- [18] C. I. Stoddard, K. Sung, Z. A. Yaffe, H. Weight, G. Beaudoin-Bussi eres, J. Galloway, S. Gantt, J. Adhiambo, E. R. Begnel, E. Ojee, J. Slyker, D. Wamalwa, J. Kinuthia, A. Finzi, F. A. Matsen, D. A. Lehman, and J. Overbaugh. Elevated binding and functional antibody responses to sars-cov-2 in infants versus mothers. *Nature Communications*, 14(1), Aug. 2023. <http://dx.doi.org/10.1101/2023.10.06.561250>.
- [19] M. Fourment, C. J. Swanepoel, J. G. Galloway, X. Ji, K. Gangavarapu, M. A. Suchard, and F. A. M. IV. Automatic differentiation is no panacea for phylogenetic gradient computation. *Genome Biology and Evolution*, 15(6), jun 2023. <https://doi.org/10.1093%2Fgbe%2Fevad099>.
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- [23] J. R. Adrion, C. B. Cole, N. Dukler, J. G. Galloway, A. L. Gladstein, G. Gower, C. C. Kyriazis, A. P. Ragsdale, G. Tsambos, F. Baumdicker, J. Carlson, R. A. Cartwright, A. Durvasula, I. Gronau, B. Y. Kim, P. McKenzie, P. W. Messer, E. Noskova, D. O.-D. Vecchyo, F. Racimo, T. J. Struck, S. Gravel, R. N. Gutenkunst, K. E. Lohmueller, P. L. Ralph, D. R. Schrider, A. Siepel, J. Kelleher, and A. D. Kern. A community-maintained standard library of population genetic models. *eLife*, 9, jun 2020. <https://doi.org/10.7554%2Felife.54967>.

PROFESSIONAL REFERENCES

Available upon request.

ACHIEVEMENTS

- **Graduate Thesis Project:** Machine learning for identifying synapses.
- **Undergraduate Honors Thesis Project:** Speeding up the Tortoise: a case study in the optimization of forward-moving evolutionary simulations. The manuscript can be found on the [University Arxiv](#).
- **Game Development:** Developed a 3D infinite flyer game, [Squirrel suiter](#) for Windows and Android, available on Google Play.
- **Community Service:** Built trail for [Montana Conservation Corps](#) and acquired 300+ hours community service.