Jared G. Galloway

Bioinformatician & ML Scientist

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Summary

I am a bioinformatician and ML scientist with nine years of experience building research software for biological datasets, often in the form of NGS data. I write Python packages, and use workflow managers such as Nextflow or Snakemake to build reproducible pipelines which can be executed in various computing environments like SLURM HPC clusters. I develop models in PyTorch and JAX, from transformers to sparse statistical models. I have co-authored more than 20 publications with 1,800+ citations.

Skills

Bioinformatics & Genomics: NGS data analysis, Phylogenetics, Genomic surveillance, Deep mutational scanning, PhIP-Seq
Machine Learning: JAX, PyTorch, TensorFlow/Keras, Scikit-learn, Transformers, Recurrent neural networks
Modeling & Statistics: Regularized / sparse regression, Global epistasis models, Bayesian statistics, Linear algebra
Languages: Python, R, C/C++, Bash, SQL (coursework), Java, JavaScript
Data: Pandas, Polars, NumPy, Xarray, SciPy, BioPython
Visualization: Matplotlib, Plotnine, Altair
Tools & Infrastructure: Git, GitHub Actions, Docker, Apptainer, Conda/Mamba, Snakemake, Nextflow, SLURM HPC, AWS S3

Experience

Bioinformatics Specialist, Howard Hughes Medical Institute — Jan 2024 – Aug 2026
- Conceptualized and implemented transformer-based deep amino acid selection models (DASM) of viral protein evolution in PyTorch.
- Designed and built multidms, a JAX package that jointly fits multiple deep mutational scanning datasets, now used in the Bloom lab's primary analysis pipelines.
- Built a containerized Nextflow pipeline that ran 50K+ HPC jobs to produce the primary data for a study published in *Cell*.

Bioinformatics Analyst II, Fred Hutchinson Cancer Center — Jan 2021 – Jan 2024
- Designed an algorithm that estimates fitness over time for every codon mutation across a phylogeny of 13M+ viral genomes.
- Deployed public Nextstrain genomic surveillance views of antibody escape for SARS-CoV-2, influenza, and Lassa virus.
- Mentored interns, graduate students, and postdocs in computational methods.

Research Associate, Fred Hutchinson Cancer Center — Mar 2020 – Dec 2020
- Built phippery, a PhIP-Seq analysis suite (Nextflow pipeline from raw sequencing reads to results, Python API for normalization and enrichment statistics, Streamlit app) used in six collaborative publications.
- Co-developed torchdms, a PyTorch package for neural-network global epistasis models.
- Led cross-lab team meetings.

Graduate Teaching Fellow, University of Oregon — Aug 2019 – Mar 2020
- Taught graduate-level Python/Bash scripting and algorithmic thinking.

Scientific Programmer, University of Oregon — Jun 2018 – Jun 2019
- Trained and evaluated recurrent neural networks on simulated genomes to estimate recombination rates (ReLERNN).

Undergraduate Research Assistant, University of Oregon — Jun 2017 – Jun 2018
- Implemented tree-sequence recording in the SLiM population genetics simulator, then benchmarked its speed and memory use for an honors thesis.

Selected Publications

23 publications, 1,800+ citations, h-index 17 (Google Scholar)

- DeWitt, Vora, Araki, **Galloway**, et al. (2026). Replaying germinal center evolution on a quantified affinity landscape. *Cell*.
- **Galloway**, et al. (2023). phippery: a software suite for PhIP-Seq data analysis. *Bioinformatics*.
- Haddox, **Galloway**, et al. (2023). Jointly modeling deep mutational scans identifies shifted mutational effects among SARS-CoV-2 spike homologs. *bioRxiv*.
- Garrett, **Galloway**, et al. (2022). Comprehensive characterization of the antibody responses to SARS-CoV-2 Spike protein finds additional vaccine-induced epitopes beyond those for mild infection. *eLife*.
- Stoddard, **Galloway**, et al. (2021). Epitope profiling reveals binding signatures of SARS-CoV-2 immune response in natural infection and cross-reactivity with endemic human CoVs. *Cell Reports*.
- Adrion, **Galloway**, et al. (2020). Predicting the Landscape of Recombination Using Deep Learning. *Molecular Biology and Evolution*.

Education

Master of Science, Biology, University of Oregon — 2020
Bachelor of Science, Computer & Information Science, University of Oregon — 2018