GW **McElfresh** | Computational Biology PhD

Oregon Health & Science University – Oregon National Primate Research Center

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Professional Summary

Computational biologist with expertise spanning single-cell and spatial transcriptomics, mathematical modeling, machine learning, and structural biology. I build analytical frameworks that turn high-dimensional biological data into actionable insights—from co-developing a widely-used rhesus macaque immune reference atlas to authoring open-source tools adopted across the single-cell sequencing community. Equally comfortable designing a stochastic model, deploying an HPC pipeline at scale, or collaborating with wet-lab immunologists to answer disease-relevant questions. Seeking to apply multiscale analytical expertise to challenging problems at the intersection of biology, data science, and translational research.

Education

University of Kansas **Lawrence, KS**
PhD, Computational Biology *2015–2020*
Dissertation: *Multiscale analyses of cellular signaling and regulation in response to multiple stress conditions*
Advisor: J. Christian Ray, PhD

Drury University **Springfield, MO**
B.S., Mathematics & Physics *2011–2015*
Graduated with honors

Research Experience

Oregon National Primate Research Center / OHSU **Portland, OR**
Computational Biologist 3 *Dec 2024–Present*

- Co-developed the **Rhesus Immune Reference Atlas (RIRA)**—the first immune-focused, multi-tissue single-cell atlas for rhesus macaques—integrating data across >15 tissues and providing a community-standard reference for reconciling transcriptional profiles with established immune lineages (*Cell Genomics*, 2025)
- Designed and deployed end-to-end scRNA-seq pipelines for studies of HIV/SIV, Tuberculosis, and Yellow Fever, enabling discovery of correlates of protection in NHP vaccine models
- Authored and maintain open-source R packages hosted on GitHub: **cellhashR** (scRNA-seq cell-hashing demultiplexing, widely adopted across the single-cell community) and **tcrClustR** (TCR repertoire clustering and analysis)
- Developed a supplemental alignment pipeline capturing allele-specific MHC-I regulation and other immune signals systematically missed by dominant scRNA-seq workflows
- Collaborated across multiple labs to translate high-dimensional data into biological hypotheses and manuscript-ready analyses

Oregon National Primate Research Center / OHSU **Portland, OR**
Computational Biologist 2 *Nov 2020–Dec 2024*
Promoted to Computational Biologist 3, January 2025

University of Kansas, Ray Lab **Lawrence, KS**
Graduate Researcher *2015–2020*

- Characterized overlapping transcriptomic stress responses (stimulons) in *E. coli* using bulk RNA-seq, identifying shared gene programs across divergent stressors—co-first author on two resulting manuscripts
- Built stochastic and agent-based models of bacterial cell-cycle dynamics to reconstruct inheritance of stress signals across generations
- Developed and benchmarked template-based protein–protein docking approaches in collaboration with the Vakser Lab (KU), contributing to structural modeling best-practice guidelines

University of Missouri, Zou Lab   **Columbia, MO**
Undergraduate Researcher   *Summer 2014*
Developed multi-target molecular docking methods for protein kinase inhibitor selectivity studies; presented at the University of Missouri Summer Undergraduate Research Symposium

Drury University, Deligkaris Lab   **Springfield, MO**
Undergraduate Researcher   *2013–2015*
Derived and implemented a vibrational entropy correction for DNA–small molecule docking in AutoDock, improving binding free energy predictions; published as first author in *Computational Biology and Chemistry* (2018)

Technical Skills

Transcriptomics: Bulk RNA-seq, scRNA-seq (10X Genomics), spatial transcriptomics (NanoString GeoMx/CosMx); DESeq2, edgeR, kallisto/sleuth, Seurat, Scanpy, STAR

Machine Learning: PCA, UMAP, t-SNE; classification, clustering; CNNs, autoencoders, deep neural networks (TensorFlow, PyTorch); Bayesian & frequentist inference

Mathematical Modeling: Stochastic biochemical models (Gillespie, CME), agent-based models, dynamical systems, graph theory, network analysis

Structural Biology: Protein–protein docking (template-based & *ab initio*), small molecule docking (AutoDock, Vina), molecular dynamics, protein design (PyRosetta)

Programming: Python (expert: pandas, numpy, scipy, scikit-learn, TensorFlow, PyTorch), R (advanced: Bioconductor), MATLAB, Mathematica, C++, bash, Perl, SQL, FORTRAN

Infrastructure: Git/GitHub/BitBucket, Docker, Singularity/Apptainer, SLURM/PBS HPC

Data Formats: LaTeX, Markdown, YAML, XML, SBML, HTML/CSS, Parquet, JSON, SQL

Lab Skills: RNA-seq library preparation (Illumina), bacterial molecular genetics, microbiology culture & quantification, aseptic technique

Selected Publications

✝: Co-first / first authorship

2025: Mahyari E, Boggy GJ, **McElfresh GW**, et al. Enhanced interpretation of immune cell phenotype and function through a rhesus macaque single-cell atlas. *Cell Genomics*, 5(5).

2025: Bimber BN, Sunshine J, **McElfresh GW**, et al. Viral escape mutations do not account for non-protection from SIVmac239 challenge in RhCMV/SIV vaccinated rhesus macaques. *Frontiers in Immunology*, 15: 1444621.

2023: Wang H, **McElfresh GW**✝, et al. Signatures of antibiotic tolerance and persistence in response to divergent stresses. *bioRxiv* 2023.02.05.527212.

2022: Boggy GJ, **McElfresh GW**, et al. BFF and cellhashR: analysis tools for accurate demultiplexing of cell hashing data. *Bioinformatics*, 38(10), 2791–2801. doi:10.1093/bioinformatics/btac213

2020: Chakravarty D, **McElfresh GW**, et al. How to choose templates for modeling of protein complexes. *Proteins*, 88(9), 1070–1081. doi:10.1002/prot.25875

2018: **McElfresh GW**✝, Deligkaris C. A vibrational entropy term for DNA docking with AutoDock. *Computational Biology and Chemistry*, 73, 9–14. doi:10.1016/j.compbiolchem.2018.03.027

2018: **McElfresh GW**✝, Ray JCJ. Intergenerational Cellular Signal Transfer and Erasure. In: *The Interplay of Thermodynamics and Computation in Natural and Artificial Systems*.

Full list: Google Scholar | ORCID 0000-0002-1948-7571

Selected Presentations

2022: **McElfresh GW** et al. Integration of Spatial and Single Cell Transcriptomics Identifies Novel Pathologically Relevant Markers in SIV- and *M. tuberculosis*-infected Rhesus Macaques. *Nonhuman Primate Models for AIDS*.

2021: **McElfresh GW** et al. Single Cell Transcriptomic Profiling of Early Tuberculosis Infection and Granuloma Formation in Rhesus Macaque. *Nonhuman Primate Models for AIDS*.

2019: **McElfresh GW**, Drawert B, Ray JCJ. Discrete timescales of effects that stress signals have on the cell cycle. *q-bio Conference*.

2018: **McElfresh GW**, Drawert B, Ray JCJ. Reconstructing the Role of Inheritance in Stress Signaling. *Modeling of Protein Interactions*.

2014: **McElfresh GW**, Deligkaris C. Inclusion of Empirical Entropic Contributions to Binding Free Energy of Ligand-DNA Systems During Docking. *ACS Midwest Regional Meeting*.

Teaching Experience

University of Kansas   **Lawrence, KS**
Lab Teaching Assistant — Bioinformatics   *F2018, F2019, S2020*
Led hands-on computational labs covering sequence alignment, phylogenetics, and transcriptomic analysis pipelines

University of Kansas   **Lawrence, KS**
Discussion Leader & Primary Grader — Genetics   *Summer 2017*

University of Kansas   **Lawrence, KS**
Lab Teaching Assistant — Intro Cellular & Molecular Biology   *F2016, F2017*

University of Kansas   **Lawrence, KS**
Lab Teaching Assistant — Intro Organismal Biology   *S2016*

University of Kansas   **Lawrence, KS**
Lab Teaching Assistant — Intro Principles of Biology   *F2015*

Awards & Honors

2019: Graduate Research Award, University of Kansas

2015: Outstanding Physics Student Researcher, Drury University

Service

Reviewing: Peer reviewer, *Nature Communications*

Open Source: Contributor and maintainer, cellhashR, RIRA, CellMembrane, and other open-source tools