Eric M. Kernfeld

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Collaborative statistician and systems biologist seeking a Boston-area biotech role with opportunities to grow towards new technologies and biological questions.

Programming

Python ★★★★★
Machine learning, pipelining, data visualization, and benchmarking across multiple roles.
PyTorch, numpy, scipy, Seaborn, scikit-learn, pandas, scanpy

R ★★★★★
Experimental design, data visualization, hypothesis testing, survival analysis, and machine learning across many roles.
ggplot2, tidyverse, linear models, seurat, BioConductor

SQL ★★★☆☆
Efficient data retrieval via manually written or automatically constructed queries.

Julia ★★★☆☆
Fast biochemical simulations and related inverse problems.

Data Types

scRNA-seq ★★★★★
Used extensively in most of my research since 2016.

ATAC-seq ★★★★☆
Experience with end-to-end analysis of multiple types of scATAC data.

ChIP-seq ★★★★☆
Used collections of data to screen for technical issues and test hypotheses from other sources.

Hi-C ★★★☆☆
Brief experience with alignment, QC, and background models.

Software Tools

Snakemake ★★★★☆
Used at Day Zero and at UMass for NGS quantification pipelines.

Docker ★★★★☆
Used throughout Ph.D. work.

AWS ★★★☆☆
Used S3 and EC2 throughout Ph.D. work.

Professional Experience

Department of Biomedical Engineering — Johns Hopkins University

Ph.D. Research Assistant — *August 2020 – March 2025*

Evaluated **empirical performance** of diverse algorithms for **statistical error control** in gene regulatory networks (paper) and **prediction** of **perturbed gene expression** (preprint).

Data Science Team — Day Zero Diagnostics

Data Science Ph.D. Intern — *July – September 2022*

Compared **genome assemblies** and **antibiotic resistance predictions** using **short-read and long-read data**. Discovered key contamination events. Built a well-documented **software pipeline** spanning from raw reads to biologically interpretable data displays.

Diabetes Center of Excellence — University of Massachusetts Medical School

Bioinformatician — *September 2016 – August 2020*

Derived insights from **scRNA-seq, ChIP-seq, ATAC-seq, and Hi-C** to advance research on stepwise differentiation from endoderm (paper) to foregut (paper) to thymus (paper). Responsible for **close collaboration with biologists, data storage, quantification, quality control, visualization, statistical modeling, writing, and presenting to varied audiences.**

Division of Medical Genetics — University of Washington

Research Assistant — *January – June 2016*

Analyzed **genetic association data** seeking loci that contribute to Alzheimer's Disease (paper). Performed **data visualization** and **survival analysis** using **R** and **PLINK**.

Department of Statistics — University of Washington

Teaching Assistant — *September 2015 – January 2016*

Lectured, prepared materials, graded, and held office hours for statistics courses.

Data Science Team — MedGenome, Inc.

Statistics Intern — *June – August 2015*

Using **Python**, processed **exome sequencing data** to reduce PCR bias when identifying **copy number variations**. Using **R**, planned **experimental design for TCR sequencing**.

Education

Johns Hopkins University — **Baltimore, MD**
Ph.D. Biomedical Engineering — August 2020 – March 2025

University of Washington — **Seattle, WA**
M.S. Statistics — September 2014 – June 2016

Tufts University — **Medford, MA**
B.S. Mathematics, *Summa Cum Laude* — September 2010 – May 2014