


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Eric M. Kernfeld

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

Ph.D. Research Assistant

Johns Hopkins University

August 2020 – March 2025

Evaluated diverse algorithms for **statistical error control** in gene regulatory networks ([paper](#)) and for **prediction of perturbation transcriptomics**, including **foundation models** and **graph neural networks** ([preprint](#)).

Data Science Team

Data Science Ph.D. Intern

Day Zero Diagnostics

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

Bioinformatician

University of Massachusetts Medical School

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

Research Assistant

University of Washington

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

Teaching Assistant

University of Washington

September 2014 – January 2016

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

Data Science Team

Statistics Intern

MedGenome, Inc.

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

Ph.D. Biomedical Engineering

Baltimore, MD

August 2020 – March 2025

University of Washington

M.S. Statistics

Seattle, WA

September 2014 – June 2016

Tufts University

B.S. Mathematics, *Summa Cum Laude*

Medford, MA

September 2010 – May 2014