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Eric M. Kernfeld

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

Programming

Python ★★★★★
Used heavily during Ph.D. work and during industry internships. *PyTorch, numpy, scipy, Seaborn, scikit-learn, pandas, scanpy*

R ★★★★★
Used heavily during Ph.D. work, at UMass, and at UW. *ggplot2, tidyverse, linear models, seurat, BioConductor*

Julia ★★★☆☆
Used occasionally during Ph.D. work and at UW.

C++ ★★★☆☆
Used in project-based undergrad courses.

Data Types

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

ATAC-seq ★★★★☆
Conducted end-to-end analysis of multiple types of scATAC data at UMass.

ChIP-seq ★★★★☆
Familiar with many technical aspects, but limited experience with raw reads and new data.

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

Software Tools

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

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

Snakemake ★★★★☆
Used heavily at Day Zero and at UMass.

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 carefully crafted displays of key results.

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 **data storage, initial processing, 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](#)). Gained experience in **data visualization, survival analysis, 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*

Contributed to cancer immunotherapy projects. Formulated and tested hypotheses and processed **exome sequencing data**. Produced predictive software in **R and Python**.

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