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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.

SQL ★★★☆☆
Used occasionally during Ph.D. work and industry internships.

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

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

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 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). 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*

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