


 [ekernf01.github.io](https://github.com/ekernf01)  
 [eric.kern13@gmail.com](mailto:eric.kern13@gmail.com)  
 (814) 777-4464  
 1120 N Eden St  
Baltimore, MD 21213

## 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

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

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

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

# Eric M. Kernfeld

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

## Professional Experience

**Department of Biomedical Engineering**  
*Ph.D. Research Assistant*

**Johns Hopkins University**  
*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**  
*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 carefully crafted displays of key results.

**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 **data storage, initial processing, 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 2015 – January 2016*

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

**Data Science Team**  
*Statistics Intern*

**MedGenome, Inc.**  
*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**  
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