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## 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.

## Eric M. Kernfeld

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

## Professional Experience

<b>Diabetes Center of Excellence</b> <i>Bioinformatician</i>	<b>University of Massachusetts Medical School</b> <i>September 2016 – August 2020</i>
Derived insights from <b>scRNA-seq</b> , <b>ChIP-seq</b> , <b>ATAC-seq</b> , and <b>Hi-C</b> to advance research on stepwise differentiation from endoderm ( <a href="#">paper</a> ) to foregut ( <a href="#">paper</a> ) to thymus ( <a href="#">paper</a> ). Responsible for <b>close collaboration with biologists</b> and <b>driving projects from base-calling all the way through published papers and external talks</b> .	

## Academic Experience

<b>Department of Biomedical Engineering</b> <i>Ph.D. Research Assistant</i>	<b>Johns Hopkins University</b> <i>August 2020 – March 2025</i>
Evaluated diverse algorithms for <b>statistical error control</b> in gene regulatory networks ( <a href="#">paper</a> ) and for <b>prediction of perturbation transcriptomics</b> , including <b>foundation models</b> and <b>graph neural networks</b> ( <a href="#">preprint</a> ).	

<b>Division of Medical Genetics</b> <i>Research Assistant</i>	<b>University of Washington</b> <i>January – June 2016</i>
Analyzed <b>genetic association data</b> seeking loci that contribute to Alzheimer's Disease ( <a href="#">paper</a> ). Performed <b>data visualization</b> and <b>survival analysis</b> using <b>R</b> and <b>PLINK</b> .	

<b>Department of Statistics</b> <i>Teaching Assistant</i>	<b>University of Washington</b> <i>September 2014 – January 2016</i>
Lectured, prepared materials, graded, and held office hours for statistics courses.	

## Industry Internships

<b>Data Science Team</b> <i>Data Science Ph.D. Intern</i>	<b>Day Zero Diagnostics</b> <i>July – September 2022</i>
Compared <b>genome assemblies</b> and <b>antibiotic resistance predictions</b> using <b>short-read and long-read data</b> . Discovered key contamination events. Built a well-documented <b>software pipeline</b> spanning from raw reads to biologically interpretable data displays.	

<b>Data Science Team</b> <i>Statistics Intern</i>	<b>MedGenome, Inc.</b> <i>June – August 2015</i>
Using <b>Python</b> , processed <b>exome sequencing data</b> to reduce PCR bias when identifying <b>copy number variations</b> . Using <b>R</b> , planned <b>experimental design for TCR sequencing</b> .	

## Education

<b>Johns Hopkins University</b> Ph.D. Biomedical Engineering	<b>Baltimore, MD</b> August 2020 – March 2025
<b>University of Washington</b> M.S. Statistics	<b>Seattle, WA</b> September 2014 – June 2016
<b>Tufts University</b> B.S. Mathematics, <i>Summa Cum Laude</i>	<b>Medford, MA</b> September 2010 – May 2014