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Eric M. Kernfeld

Collaborative statistician and computational 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.

Perturb-seq
★★★★★
Used extensively in much of my research since 2018.

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.

Professional Experience

Diabetes Center of Excellence — **University of Massachusetts Medical School**
Bioinformatician — *September 2016 – August 2020*

Embedded in Rene Maehr's Laboratory for Stem Cell Biology and Applied Developmental Immunology, I supported and drove NGS-heavy projects to characterize production of thymic epithelium from pluripotent stem cells, as well as the corresponding embryonic process. We used scRNA-seq, Perturb-seq, ChIP-seq, ATAC-seq, and chromatin looping assays at various stages from endoderm (paper) to foregut (paper) to thymus (paper). I collaborated closely with stem cell biologist colleagues, and I drove projects all the way from base-calling through quality control, alignment, quantification, visualization, statistical analysis, interpretation, and in some cases construction of a publishable narrative.

Academic Experience

Department of Biomedical Engineering — **Johns Hopkins University**
Ph.D. Research Assistant — *August 2020 – March 2025*

Supervised by Patrick Cahan and Alexis Battle, I built and evaluated diverse causal models of transcription. On the statistical side, we developed empirical checks of false discovery rate control on incomplete data, arguing that specific human, mouse, and *E. coli* datasets will never allow for error control in causal network inference. I collaborated with biologists to write this finding for a cell biology audience (paper). On the machine learning side, we established a benchmarking suite to evaluate counterfactual predictions. We included biologically and technologically diverse perturbation transcriptomics data. We demonstrated that a simple, previously-overlooked baseline typically outperformed diverse predictive methods (preprint), setting a new bar for gene regulatory networks and virtual cell models.

Division of Medical Genetics — **University of Washington**
Research Assistant — *January – June 2016*

I contributed to analysis of age-at-onset of Alzheimer's Disease by accounting for known genetic effects (paper). I performed data visualization and survival analysis using R and PLINK.

Department of Statistics — **University of Washington**
Teaching Assistant — *September 2014 – January 2016*

I lectured, prepared materials, graded, and held office hours for undergrad statistics courses.

Industry Internships

Data Science Team — **Day Zero Diagnostics**
Data Science Ph.D. Intern — *July – September 2022*

I compared genome assemblies and antibiotic resistance predictions using short-read and long-read data, discovering key contamination events. I built a well-documented software pipeline spanning from raw Nanopore reads to biologically interpretable data displays.

Data Science Team — **MedGenome, Inc.**
Statistics Intern — *June – August 2015*

Using Python, I processed exome sequencing data to reduce PCR bias when identifying copy number variations. Using R, I planned experimental design for TCR sequencing.

Nanopore
★★☆☆☆
Brief experience with microbial genome assembly.

Software Tools

Snakemake
★★★★☆
Used at Day Zero and at UMass for NGS quantification pipelines.

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

Git
★★★★☆
Used since 2014 as an individual with some team-project version control experience.

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

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

Selected Publications **(†: equal contribution)**

Kernfeld E., Yang Y., Weinstock J., Battle A., & Cahan P. (2023). A systematic comparison of computational methods for expression forecasting. bioRxiv, 2023-07.

Kernfeld E., Keener R., Cahan P., & Battle A. (2024). Transcriptome data are insufficient to control false discoveries in regulatory network inference. Cell Systems, 15(8), 709-724.

Kernfeld E.†, Genga R.†, Parsi K., Parsons T., Ziller M., & Maehr R. Single-Cell RNA-Sequencing-Based CRISPRi Screening Resolves Molecular Drivers of Early Human Endoderm Development. Cell Rep. 2019 Apr 16;27(3):708-718.e10.

Kernfeld E.†, Genga R.†, Neherin K., Magaletta M., Xu P., & Maehr R. (2018). A single-cell transcriptomic atlas of thymus organogenesis resolves cell types and developmental maturation. Immunity, 48(6), 1258-1270.

Kernfeld E.†, Magaletta M.†, Lobo M.†, Aliee H., Huey J., Parsons T., et al. Integration of single-cell transcriptomes and chromatin landscapes reveals regulatory programs driving pharyngeal organ development. Nat Commun. 2022 Jan 24;13(1):457.

Kearns N., Lobo M., Genga R., Abramowitz R., Parsi K., Min J, **Kernfeld E**. et al. Generation and molecular characterization of human pluripotent stem cell-derived pharyngeal foregut endoderm. Dev Cell. 2023 Sep 25;58(18):1801-1818.e15.

Blue E., Yu C., Thornton T., Chapman N., **Kernfeld E.**, Jiang N., et al. Variants regulating ZBTB4 are associated with age-at-onset of Alzheimer's disease. Genes Brain Behav. 2018 Jul;17(6):e12429.

Fischer D.†, Fiedler A.†, **Kernfeld E.**, Genga R., Bastidas-Ponce A., Bakhti M., et al. Inferring population dynamics from single-cell RNA-sequencing time series data. Nat Biotechnol. 2019 Apr 1;37(4):461–8.