







Jonah E. Einson

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About Me

I am a technically minded research scientist, with a background in statistical genetics and functional genomics. With experience in both academic and industry settings, I have applied my skills to address diverse sets of scientific questions. I currently develop tools to simplify the utilization of genetic evidence in early drug discovery programs.

Social Network

-  [Linkedin Link](#)
-  [Twitter Link](#)
-  [Github Project Page Link](#)

Skills

- Stats
- Genomics
- Bioinformatics
- NGS
- DNA/RNA
- ML/AI
- Molecular Biology
- Linux
- macOS
- </> Coding
 - ✦ Bash, R, and Python
 - ✦ Version control with git
 - ✦ SQL
- 🍃 Genomics
 - ✦ RNA-seq and NGS Processing Pipelines
 - ✦ FASTQ, BAM, VCF and GTF file formats
 - ✦ QTL analysis, Coloc, SuSiE
 - ✦ GWAS harmonization
- 📦 Computational Infrastructure
 - ✦ LSF and Slurm
 - ✦ Nextflow in Google Cloud
 - ✦ AWS Athena

Professional Experience

- 2023 – Present **Senior Scientist II, Genetic Data Sciences** Genscience, New York NY
 - First employee at a small biotech startup, focused on bringing genetics expertise to drug development decisions.
 - Successfully prototyped a genetic evidence integration web app, through close collaborative work with a cross-functional team.
 - Drove early decisions about phenotype and genotype classification strategies, which streamlined future data ingestion tasks.
 - Rebuilt legacy R code into a modern ETL pipeline.

Education

- 2017 – 2022 **Ph.D. Biomedical Informatics** Columbia University, New York NY

Thesis research in the Department of Systems Biology, with advanced coursework in data science and extensive TA experience.
Doctoral Thesis: Common and rare genetic effects on the transcriptome and their contribution to human traits. Defended 8/30/2022
- 2013 – 2017 **Dual B.S. Biochemistry & Statistics** University of Massachusetts, Amherst MA

Top-tier undergraduate program focused on research, with a unique addition of advanced training in statistics.
Commonwealth Honors College Thesis: The Environmental Microbiomes of an Industrial Food Fermentation Facility

Scientific Experience

- 2018 – 2022 **Doctoral Research** Columbia University Irving Medical Center
 - Advised by Dr. Tuuli Lappalainen at the New York Genome Center and the Department of Systems Biology
 - Analyzed of thousands of whole genome sequencing samples from GTEx, TOPMed, and the SSC
 - Optimized a statistical method for detecting evidence of genetic modifiers of rare variant penetrance
 - Utilized AlphaFold to study protein structure perturbation related to splicing QTLs and trait risk
 - Presented at the American Society for Human Genetics annual meeting, Biology of Genomes, and the Gordon Research Conference in Genetics and Genomics
 - Co-authored 2 papers published in *Science*
- 2014 – 2017 **Undergraduate Research** University of Massachusetts Amherst
 - Advised by Dr. David Sela in the Department of Food Science
 - Gained early experience generating and analyzing Illumina sequencing data from microbial 16S analyses
 - Published my first independent project, studying microbial communities in an industrial food processing environment

Publications

Authorship on 6 scientific papers. Refer here for full list.