Adam N. Spierer

Boston, MA

https://www.AdamSpierer.com   https://www.github.com/adamspierer/   https://www.linkedin.com/in/adamspierer

KEY SKILLS

Coding: Python, R, Bash, Nextflow, Git, Jupyter, Linux, cloud-based high-performance computing, AWS, S3, SLURM
Data Analysis / Visualization Tools: Pandas, Numpy, Scipy, Matplotlib, RDkit, TensorFlow, Tidyverse, ggplot2, RShiny
Data Repositories: CCLE, DepMap, TCGA, GTEx, COSMIC, UniProt, StringDB, ALS Answers
High Dimensional Data: Proteomics, Transcriptomics, Genomics, High-Content Imaging, GWAS, CRISPR screens

EDUCATION

BROWN UNIVERSITY (MS & PHD), PROVIDENCE, RI   2013 – 2020
FOCUS: Quantitative Genetics / Computational Biology
DISSERTATION: Mapping the genetic architecture of fruit fly locomotion [link]
COURSEWORK: Bioinformatics, Statistics, Data Visualization, Computer Science, Machine Learning, Instrumentation, Microscopy, Fiji

- Applied multi-omic methods to find genetic modifiers of *Drosophila* flight ability and variability, looking at individual and epistatic variants, whole genes, gene sub-networks, and modules of co-expressed genes. [*PLoS Genetics*]
- Developed end-to-end video capture/analysis pipeline to rapidly quantify fruit fly climbing kinematics. [Github; JEB]
- Collaborated on a program to calculate whole gene significance in genotype-phenotype mapping. [PEGASUS_flies]
- Contributed to an interdisciplinary fellowship project for non-model organism de novo genome assembly [*O. grillus*] and differential gene expression analysis in amphipods un/infected by a parasitic flatworm [Molecular Ecology].

COLBY COLLEGE (BA), Waterville, ME   2009 – 2013
MAJOR: Biology—Cell and Molecular Biology/Biochemistry [Honors]
COURSEWORK: Molecular Biology, Biochemistry, Genetics, Evolution, Quantitative Chemistry, Wet Lab, Leadership, Communication

WORK EXPERIENCE

SCIENTIST II - COMPUTATIONAL BIOLOGY   2023 – 2025
SCORPION THERAPEUTICS, BOSTON, MA

- Developed a fast, scalable, and automated Intact Mass Spectrometry program for peak labeling and quantification, longitudinal compound QC, and hit classification of covalent compound-protein interactions for cancer drug discovery.
- Led Activity-Based Protein Profiling proteome-wide cysteine ligandability profiling analysis for cancer new target ID.
- Integrated multi-omic publicly available datasets and DepMap for novel target identification and biomarker discovery.
- Created computer applications for wet lab biologists and chemists to increase reproducibility and throughput.

SCIENTIST I - COMPUTATIONAL BIOLOGY   2021 – 2022
FAZE MEDICINES, CAMBRIDGE, MA

- Analyzed high-throughput image-based CRISPR and small molecule screens to identify oncogenic targets, using PCA and dimension reduction algorithms to QC data, apply batch correction, and call hits from composite metrics.
- Utilized linear models for indication selection & target ID with DepMap dependency scores, leading to target validation.
- Identified potentially-phase separating oncofusion targets and indications from DepMap & TCGA.
- Directed CRO development of a modular Nextflow GWAS pipeline using statistical genetics tools like ssimp, coloc, CC-GWAS, and S-PrediXcan to identify ALS/FTD-associated variants from public datasets.

POSTDOCTORAL RESEARCH ASSOCIATE   2020 – 2021
BROWN UNIVERSITY, PROVIDENCE, RI

- Mapped paired-end, pooled RNAseq reads to a reference genome and applied linear models to count tables, testing for complex, multi-factorial genotype x genotype x environment interactions in *Drosophila*. [Journal of Heredity]
- Leveraged a particle detector [GitHub] and random forest model to identify flowering *Hydroanthus* tree range and distribution in the Amazon rainforest from publicly available satellite imagery/remote sensing data.

SELECTED PUBLICATIONS

Spierer AN, et al. 2021. Natural variation in the regulation of neurodevelopmental genes modifies flight performance in *Drosophila*. *PLoS Genetics* [GitHub]
Spierer AN, Zhuo L, Yoon D, Rand, DM. 2021. FreeClimber: Automated quantification of climbing performance in *Drosophila*. *Journal of Experimental Biology*; [GitHub]

For a complete list, please visit my Google Scholar profile [link]