Alexander Ferrena

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EXPERIENCE

Senior Bioinformatics Programmer – NYU Langone Health, Cardiovascular Research Center Aug 2024 – Present

- Staff scientist bioinformatician working in an internal departmental consulting team providing highly collaborative applied bioinformatics analysis for over a dozen labs in diverse indications and data modalities.
- Specialized in application and development of single-cell and spatial transcriptomic methods in immunology.
- Made extensive, daily use of R and Unix shell, and moderate use of Python, for data analysis and method development.

Bioinformatics Consultant – Singulomics Corporation Aug 2022 – Mar 2024

- Developed and maintained an automated R pipeline package for 10X Visium spatial transcriptomics data analysis.

Computational Biology Research Assistant – Memorial Sloan Kettering Cancer Center May 2018 – June 2020

- Analyzed single-cell transcriptomics, CITEseq, and clinical data, as part of a team project now published in Nature.

EDUCATION

Albert Einstein College of Medicine – Ph.D., Cancer Bioinformatics Aug 2019 – May 2024

- Authored 10 bioinformatics-focused papers (4 first-author), related to cancer, immunology and development.
- Developed a pipeline package for scRNA-seq integration and replicate-aware cross-group comparison.
- Led research summarized in thesis titled *Molecular and Clinical Implications of Skp2 inhibition in Osteosarcoma*, including basic research with sequencing of novel transgenic mouse models of cancer, and clinical research with sequencing data from cancer patients from large cohort studies including TCGA, NCI TARGET, and others.
- Applied for and received a highly competitive “Ph.D. in Clinical Investigation” (PCI) fellowship focused on formal biostatistics training and clinical research with translational focus, fully funding Ph.D. research for three years.

Columbia University – M.A., Biotechnology Sep 2017 – May 2019

- Completed a thesis titled *The Impact of Aging on Lung Adenocarcinoma* including original analysis of single-cell transcriptomics and CITE-seq to study lung tumors under mentorship of Dr. Tuomas Tammela (MSKCC).
- Received a Student Spotlight distinction for academic and research excellence.

New York University – B.A., Biology Sep 2012 – May 2016

- Pursued a STEM-heavy courseload including molecular biology, chemistry, and physics.
- Interned in Dr. Stephen Small’s embryonic development research lab, awarded best poster in group at undergraduate research conference for poster titled *Identification and Characterization of Orthodenticle-Dependent Enhancers*.

LEADERSHIP

Founder and President – Einstein Montefiore Omics Club Jan 2021– May 2024

- Founded this club for omics education and networking. Organized goal-oriented teams. Ran an Intro to Omics Workshop series of 7 sessions attended by >150 people. Designed code vignettes for teaching bioinformatics.

TECHNICAL SKILLS

Data Modalities Experience

- High-throughput sequencing analysis, single-cell RNA-sequencing, spatial transcriptomics, single-nuclei RNA-seq, bulk RNA-seq, multi-omics (scRNA+ATAC, CITE-seq), clinical and pre-clinical data, survival data.

Programming and Computing

- Languages: R and Unix Shells (extensive since 2016), Python (moderate use since 2020)
- Bioinformatics software: R (Seurat, EdgeR, FGSEA, InferCNV), Bash (STAR, velocyto), Python (scVelo, Cellrank, Scanpy)
- Cloud computing: HPC usage (SLURM, Sun Grid Engine > 7 years), AWS

Statistics and Machine Learning

- Statistics: Regression, generalized linear models, multivariate statistics, PCA, survival analysis, Cox regression
- Machine Learning: pre-processing, data cleaning and formatting, automation, K-fold cross-validation, classification (Louvain and K-means clustering), deep learning (LLM tool development), model validation and interpretation.