

Alexander Ferrena

 FerrenaAlexander

 alexander-ferrena

 Ferrena A

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 ferrenaalexander.github.io

EDUCATION

- Albert Einstein College of Medicine** – Ph.D., Clinical Investigation Aug 2019 – Present (expected graduation May 2024)
- Designed and applied analysis methods for single-cell transcriptomics data from cancer and embryonic development.
 - Authored 10 publications including 4 first author publications with Dr. Deyou Zheng and Dr. Bang Hoang.
 - 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 prestigious and competitive fellowship called the “Ph.D. in Clinical Investigation” (PCI), focused on formal biostatistics training and translational research, fully funding Ph.D. research for three years.
- Columbia University** – M.A., Biotechnology (GPA, 3.6) 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).
 - Served as teaching assistant for “Intro to Genomic Information and Technology” course.
 - Received a [Student Spotlight](#) distinction for academic and research excellence.
- New York University** – B.A., Biology (GPA, 3.3) 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*.

EXPERIENCE

- 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 sequencing data from transgenic mouse models of cancer with Dr. Tuomas Tammela, including single-cell RNA-seq and CITE-seq. Performed analysis of clinical data from patient cohorts with sequencing data including TCGA.
- Bioinformatics Intern** – New York University June 2016 – Sep 2017
- Studied differential expression of in-vitro cultures under distinct metabolic conditions with Dr. David Gresham.

LEADERSHIP

- Founder and President** – Einstein Montefiore Omics Club Jan 2021– Present
- 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 (8 years), Bash and other Unix Shells (8 years), Python (4 years)
- 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 (PyTorch, GANs, pix2pix), model validation and interpretation.