Jideofor Ezike

Permanent Address:
Los Angeles, CA

Email: jezike3@gmail.com
Cell: 914.258.4751
https://jideoforezike.com

OBJECTIVE: PhD Candidate in the Computational & Systems Biology PhD Program at the Massachusetts Institute of Technology. Interested in the intersection of machine learning, and high dimensional biological datasets, to better understand disease progression and developmental biology.

EDUCATION

Carnegie Mellon University, Pittsburgh, PA **May 2015**
Bachelor of Science: Chemical Engineering
Double Major: Biomedical Engineering

Massachusetts Institute of Technology*, Cambridge, MA* **Sept 2018-May 2025**
Thesis: *Applications of Native and Engineered Genetic Barcodes in Single-Cell RNA-Sequencing Data to Study Clonal Evolution and Cellular Phenotypic Diversity*
Doctor of Philosophy: Computational & Systems Biology
Advisors: Aviv Regev & Gad Getz

RELEVANT COURSEWORK

6.883: Modeling with machine learning: from algorithms to applications **6.874:** Computational Systems Biology: Deep Learning in the Life Science **6.860:** Statistical Learning Theory and Applications **18.6501:** Fundamentals of Statistics **7.85:** The Hallmarks of Cancer

RESEARCH EXPERIENCE

Regev & Getz Lab at Broad Institute of MIT & Harvard: Graduate Researcher **Nov 2019-Present**
Developing pipelines for studying lineages and tumor evolution in single-cell mutation data:

1. Developed pipeline for denoising somatic mutations from full length scRNA-seq data in the context of cancer. Accounting for inherent false positive and negative noise in scRNA-seq by implementing different heuristic & machine learning approaches for denoising artefactual signal. *(manuscript in prep)*

2. Reconstructed single-cell lineage trees for PC9 clones using heritable CRISPR indels. Implemented GLMs and Fisher's exact tests of neighboring clades to identify genes and modules that shift and associate with cancer persistence potential. Pharmacological validation experiments demonstrated synergistic effects on lung cancer persister cell survival. Implicated pathways are associated with patient survival and disease progression. *(manuscript in prep)*

3. The dynamics of hematopoiesis over the human lifespan:
Large scRNA-seq study profiling ~60k HSPCs cells ranging from gestation to 77yo across 26 donors. One of lead analysts in study. Quantified lineage fate biases across lifetime as well as identified the genes that drive commitment into these different lineages using graph based lineage tracing methods. (see Nat. Methods paper).

4. Technology development 5' 10x mito-seq Multiple Myeloma (MM) project. Called mitochondrial mutations from novel assay developed in lab to enrich for mitochondrial reads. Identified mitochondrial SNVs in MM patient samples highly associated with CNVs in single cells. Reconstructing lineage trees from mitochondrial SNVs to identify higher resolution subclones in MM patients (n=~20).

Regev Lab at Broad Institute of MIT & Harvard: Graduate Rotation Student **June 2019-Aug 2019**
Applied deep learning methods to analyze single cell data that underwent pooled Crispr-mediated genomic screen (Perturb-seq). Designed and implemented model to predict differential expression of genes using promoter sequences, and guideRNA as feature space to learn.

6.874 Final Project/Gifford Lab Rotation Project: Graduate Rotation Student **Feb 2019-May 2019**
Conducted comparative analysis and benchmarking of multiple deep learning methods that predict spectra/distribution of mutations caused by NHEJ repair of Crispr-mediated double strand breaks

Harvey Lodish Lab at MIT: Research Technician **July 2018-2019**

Analyzed single cell RNA sequencing data of primary early erythroid progenitor cells, the precursors to mature red blood cells. Performed clustering and pseudotime inferencing of the individual cells, a metric for estimating developmental stages of an individual cell. My contribution helped identify that cells in the presence of dexamethasone (glucocorticoid steroid widely used for increasing red blood cell output in vitro and in clinic) lagged behind in earlier stages in development where proliferative potential is greater. This finding also was validated with functional assays with mouse primary cells (see Developmental Cell Paper). Followup work with Hojun Li, MD,PhD involves learning the gene programs involved in the dexamethasone response.

Harvey Lodish Lab at MIT: Research Technician **July 2015-2018**

Objective was to identify long non-coding RNA that play a role in early red blood cell progenitor's self-renewal capacity. Used public raw sequencing data of red blood cell progenitors to perform de novo assembly of transcriptome. Applied comparative genomics as well as protein-coding filtering techniques to remove transcripts likely to form functional protein and/or small peptides. Performed differential expression analysis to identify hundreds of transcripts that are differentially expressed between two early progenitors. Validated differential expression of few interesting candidates with RT-PCR, using RNA extracted from primary human erythroid CD34+ cells

Whitehead Institute for Biomedical Research at MIT: Research Intern **Jun 2014-Aug 2014**

Performed an EMSA phoshomimetic assay that demonstrated when key site (S225) on Heat Shock Factor 1 (HSF1) is mutated to negatively charged aspartate, it loses DNA binding ability, suggesting that phosphorylation is not the switch that activates HSF1. Continuation of research on regulatory activation of HSf1 protein. (see eLife paper).

LEADERSHIP

National Society for Black Engineers (NSBE): Programs Chair **Aug 2013-Aug 2014**

Managed Programs Zone, consisted of five members.
Organize and plan community service events, social events and membership retention events. Member of the Primary Eboard.

Young African Leadership Association: Activities Chair **Aug 2012-Mar 2013**

Planned several events to promote awareness of African cultures and ideals.

WORK EXPERIENCE

Life Technologies: EHS/Organic Production Intern **Jun 2013-Aug 2013**

Performed organic synthesis to identify ideal radical initiator to replace benzoyl peroxide in a product stream. Analyzed both TLC and NMR data to track progression of reactions and ultimately devised first radical initiator free protocol.

SKILLS

Bioinformatics: "Tuxedo" RNA-sequencing tools (sequence alignment & assembly), Bedtools, Variant Calling Methods, GATK, single cell transcriptomics
Programming: Python, MATLAB, Ruby, R
Applications: Pytorch, TensorFlow, Keras, Jupyter Notebook, Pandas, Numpy, Scanpy, Docker
Laboratory: Visible Spectrophotometer, High-Performance Liquid Chromatography, confocal microscopy, bacterial cell culture, tissue culture, DNA transformation, aseptic technique, Bradford Lowry Method, Flourometry, Atomic Absorption, Gravimetric Analysis, Gas Chromatography, NMR, Protein expression, protein purification, SDS PAGE, quickchange mutation, PCR, RT-PCR, DNA cloning, Western Blot, Co-immunoprecipitation
Languages: Conversant in Igbo and Proficient in French

AWARDS

NHGRI F99/K00 Fellow	**April 2023-Present**
Ford Foundation Fellowship Honorable Mention	**March 2020**
NIH NIDDK Fellowship Recipient	**Jan 2016-2018**
Xerox Technical Minority Scholarship	**Aug 2011-May 2015**
Omega Psi Phi Scholarship Pierre Toussaint Scholarship	**Aug 2011-May 2015**

PUBLICATIONS

[1] B. Zhitomirsky*, **J. Ezike*,** E. Hopkins, M.G. Jones, J. Tsuji, N. Haradhvala, Y. Geffen, M. Miller, B.P. Danysh, L. Parida, J.S. Weissman, A. Regev and G. Getz. Single-cell phylogenies for the study of cancer

drug persistence potential. ***(manuscript in prep)***.
[2] J. Ezike, T.H. Coorens, J.Lee, M. Nomura, D. Silverbush, A. Regev, M. Suva, G. Getz. Somatic Mutation Denoising from full-length Single-Cell RNA-Sequencing Reveals known Cancer Associated Mutational Signatures and Clonal Markers. ***(manuscript in prep)***.
[3] H. Li, P. Côté, M. Kuoch, **J. Ezike,** K. Frenis, A. Afanassiev, L. Greenstreet, M. Tanaka-Yano, G. Tarantino, S. Zhang, J. Whangbo, V. Butty, E. Moiso, M. Falchetti, K. Lu, G. Connelly, V. Morris, D. Wang, A. Chen, G. Bianchi, G. Daley, S. Garg, D. Liu, S. Chou, A. Regev, E. Lummertz da Rocha, G. Schiebinger, R. Rowe. The dynamics of hematopoiesis over the human lifespan. Nat Meth. 2024.
[4] A. Noronha et al., AXL and error-prone DNA replication confer drug resistance and offer strategies to treat EGFR-mutant lung cancer. Cancer Discovery, 2022.
[5] H. Li, A. Natarajan, **J. Ezike**, I.M. Barrasa, Y.Le, Z.A. Feder, H. Yang, C. Ma, S. Markoulaki, H.F. Lodish. Rate of Progression through a Continuum of Transit-Amplifying Progenitor Cell States Regulates Blood Cell Production. Developmental Cell, 2019.
[6] X. Gao, H-Y Lee, E. Lummertz da Rocha, C. Zhang, Y-F Lu, D. Li, Y. Feng, **J. Ezike**, R.R. Elmes, I.M.Barrasa, P. Cahan, H. Li, G.Q. Daley, H.F. Lodish. TGF-β Inhibitors Stimulate Red Blood Cell Production by Enhancing Self-Renewal of BFU-E Erythroid Progenitors. Blood, 2016.
[7] X. Zheng, J. Krakowiak, N. Patel, A. Beyzavi, **J. Ezike**, A.S. Khalil, D. Pincus. Dynamic control of Hsf1 during heat shock by a chaperone switch and phosphorylation. eLife, 2016.