

Jesse Zhang

Stanford University
Electrical Engineering Department
Stanford, CA 94305

jessez@stanford.edu
www.jessemzhang.com
(857) 636-9152

EDUCATION	Stanford University , Stanford, CA Ph.D., Electrical Engineering (anticipated 2019) Research interests: Machine Learning, Statistics, Genomics Advisor: David Tse	<i>09/2014-Present</i>
	Stanford University , Stanford, CA M.S., Electrical Engineering	<i>09/2014-06/2016</i>
	Tufts University , Medford, MA B.S., Electrical Engineering	<i>09/2010-05/2014</i>
	Newton South High School , Newton, MA	<i>09/2006-06/2010</i>
RESEARCH PROJECTS	Spatial mapping of single cells using single-cell RNA-seq <i>Collaboration with R. Chiang, V. Ntranos, M. Snyder, and D. Tse</i> <ul style="list-style-type: none">• Developing computational strategies for estimating 3D spatial orientation of cells using data produced by a novel single-cell RNA-seq approach	
	Deep models for learning in genomics <i>Collaboration with F.Farnia, G.Kamath, and D.Tse</i> <ul style="list-style-type: none">• Designing models for sequence-level prediction of genomic features• Developing theory for initializing weights in unsupervised deep networks	
	Single-cell RNA-seq clustering using transcript compatibility counts <i>Collaboration with V. Ntranos, G. Kamath, L. Pachter, and D. Tse</i> <ul style="list-style-type: none">• Developed and implemented novel concept of clustering cells from single-cell RNA-seq datasets based on transcript compatibility counts• Published work in Genome Biology's Single Cell Omics Special Issue	
	Single-cell RNA-seq analysis using deep autoencoders and rPCA <i>Collaboration with B. Wang, J. Zhu, and S. Batzoglou</i> <ul style="list-style-type: none">• Developed method for cleaning single-cell RNA-seq data by implementing a modified version of rPCA. Augmented the rPCA objective with a gene-similarity matrix estimated using a deep autoencoder	

WORK EXPERIENCE	Cellular Research , Menlo Park, CA	06/2016-09/2016
	<i>Bioinformatics Intern</i>	
	<ul style="list-style-type: none"> • Worked on ResolveTM system as part of an interdisciplinary team of biologists, engineers, and bioinformaticians • Designed a Python library for automated analysis of high-dimensional single-cell RNA-seq data (clustering and feature selection) 	
	Stanford MIIL , Stanford, CA	09/2014-12/2014
	<i>EE PhD rotation student</i>	
	<ul style="list-style-type: none"> • Simulated small animal CZT PET system with variable aperture using GATE software • Created MATLAB algorithms for testing normalization methods on simulated data 	
	MC10, Inc. , Cambridge, MA	05/2014-08/2014
	<i>R&D Intern</i>	
	<ul style="list-style-type: none"> • Implemented machine learning and signal processing MATLAB algorithms to facilitate real-time and offline accelerometer data analysis • Collaboratively optimized hardware-software interface 	
	MIT Lincoln Laboratory , Lexington, MA	06/2013-05/2014
	<i>Electrical Engineering Intern/Co-op for Group 33</i>	
	<ul style="list-style-type: none"> • Developed MATLAB algorithms to intelligently extract trace from ionogram images • Created graphical user interface in MATLAB to facilitate ionogram image processing 	
	Tufts Biomedical Engineering Department , Medford, MA	09/2011-08/2012
	<i>Researcher</i> under supervision of David Kaplan, Ph.D.	
	<ul style="list-style-type: none"> • Designed and constructed gold circuits on silk scaffolds using soldering, gold sputter coating, and AutoCAD to control and detect neuronal signals • Processed and analyzed neuronal signals using MATLAB and pCLAMP software 	
	Dana Farber Cancer Institute , Boston, MA	05/2011-08/2011
	<i>Researcher</i> under supervision of Myles Brown, M.D.	
	<ul style="list-style-type: none"> • Conducted experiments to define role of lysine-specific demethylase 1 in human hormone dependent and independent prostate cancer • Performed computational analysis of results using MS Excel, python and cistrome.org 	
TEACHING EXPERIENCE	EE 372: Data Science for HT Sequencing , Stanford, CA	03/2016-06/2016
	<i>Teaching Assistant</i>	
	<ul style="list-style-type: none"> • Worked with academic advisor and fellow group member to design the first course in the Stanford electrical engineering department on computational problems in genomics • Prepared lecture notes, led recitation sections, designed and updated a course website 	
	Stanford Athletic Academic Resource Center , Stanford, CA	03/2016-06/2016
	<i>Tutor</i>	
	<ul style="list-style-type: none"> • Tutored probabilistic systems analysis for three Stanford undergraduate athletes 	

Tufts Academic Resource Center, Medford, MA

08/2012-05/2014

Head Tutor

- Tutored introductory physics, introductory chemistry, calculus III, differential equations, and linear algebra
- Held large-scale review sessions, weekly office hours, 1-on-1 sessions

PAPERS

Ntranos, V.*, Kamath, G. M.*, **Zhang, J. M.***, Pachter, L., & David, N. T. (2016). Fast and accurate single-cell RNA-Seq analysis by clustering of transcript-compatibility counts. *Genome biology*, 17(1), 1. (*equal contributors)

Cai, C., He, H. H., Gao, S., Chen, S., Yu, Z., Gao, Y., Chen, S., Chen, M.W., **Zhang, J.**, Ahmed, M., Wang, Y., Metzger, E., Schüle, R., Liu, X. S., Brown, M., & Balk, S. P. (2014). Lysine-specific demethylase 1 has dual functions as a major regulator of androgen receptor transcriptional activity. *Cell reports*, 9(5), 1618-1627.

HONORS AND AWARDS

National Science Foundation Graduate Fellowship
Honorable mention

03/2016

Tufts University

Summa Cum Laude

05/2014

The Amos Emerson Dolbear Scholarship (\$1355.25)

04/2014

The Class of 1898 Prize (\$1983.91)

04/2014

Tau Beta Pi

11/2012

Eta Kappa Nu

10/2012

Howard Sample Prize Scholarship in Physics (\$566.33)

04/2012

Chinese Consolidated Benevolent Association of New England

CCBA Scholarship (\$2500.00)

12/2010

Junior Achievement of Northern New England

Stephen G. Sullivan Scholarship (\$1000.00)

06/2010

SKILLS

Languages: Python, R, MATLAB, C++, Bash

Packages: Jupyter, TensorFlow, CVX, NumPy, SciPy, scikit-learn, Git, \LaTeX , Hadoop