

# Jesse M. Zhang

10 Comstock Circle, Apt 334, Stanford, CA 94305  
[jessez@stanford.edu](mailto:jessez@stanford.edu) | 857-636-9152 | [jessemzhang.com](http://jessemzhang.com)

**Research Interests:** Machine Learning, Optimization, Genomics, and Statistics

## Education

<b>PhD</b>	<b>Stanford University</b> , Electrical Engineering Research advisor: David Tse	09/2014-Present
<b>MS</b>	<b>Stanford University</b> , Electrical Engineering GPA: 4.02/4.00	09/2014-06/2016
<b>BS</b>	<b>Tufts University</b> , Electrical Engineering GPA: 3.96/4.00	09/2010-05/2014

## Ongoing Research

### Deep-learning models for supervised and unsupervised learning in genomics

*Working with F. Farnia, G. Kamath, and D. Tse*

Over recent years, a plethora of powerful deep learning tools have achieved state-of-the-art performance in several fields. This project involves applying these models for sequence-level prediction of genomic features, such as epigenetic markers, and developing theory for improving unsupervised learning for datasets such as single-cell RNA-seq datasets.

### Single-cell RNA-seq clustering using transcript compatibility counts

*Working with V. Ntranos, G. Kamath, L. Pachter, and D. Tse*

As single-cell RNA-Seq experiments involve more cells and overall greater numbers of reads, the need for a universal and fast method of analysis becomes more apparent. This project focuses on the novel concept of clustering cells based on transcript compatibility counts, or the number of reads that align to a certain set of overlapping transcripts, rather than gene abundances, which is computationally expensive to obtain due to the read alignment step.

- Published May 2016 in Genome Biology's Single Cell Omics Special Issue

### Single-cell RNA-seq analysis using deep autoencoders, rPCA, and gene similarity networks

*Working with B. Wang, J. Zhu, and S. Batzoglou*

Single-cell RNA-Seq experiments suffer from technical noise in addition to variation caused by culture conditions and biological effects. This project attempts to clean the #cells-by-#genes design matrix by solving a modified rPCA objective. The objective is augmented with a Laplacian regularization term, ensuring that the solution conforms to a gene similarity network obtained using a deep autoencoder to nonlinearly map each gene to a low-dimensional space.

## Professional/research experience

### Cellular Research

06/2016-09/2016

#### *Bioinformatics Intern*

- Worked on the Resolve™ 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 Molecular Imaging Instrumentation Laboratory, Stanford, CA

09/2014-12/2014

#### *EE PhD rotation student*

- 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

#### *R&D Intern*

05/2014-08/2014

- 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

#### *Electrical Engineering Intern/Co-op for Group 33*

06/2013-05/2014

- Developed MATLAB algorithms to intelligently extract trace from HF ionogram images
- Created graphical user interface in MATLAB to facilitate ionogram image processing

### Tufts Biomedical Engineering Department, Medford, MA

#### *Researcher under supervision of David Kaplan, Ph.D.*

09/2011-08/2012

- 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

#### *Intern under supervision of Myles Brown, M.D.*

05/2011-08/2011

- 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 High-Throughput Sequencing, Stanford, CA

03/2016-06/2016

#### *Teaching Assistant*

- 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

*Tutor*

- 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

## **Honors and Awards**

### **Tufts University**

Summa Cum Laude

05/2014

- Given to graduates of the Tufts School of Engineering with a GPA of at least 3.8

The Amos Emerson Dolbear Scholarship (\$1355.25)

04/2014

- One of two seniors chosen
- Given to seniors who have shown promise in the field of ECE

The Class of 1898 Prize (\$1983.91)

04/2014

- Awarded to one undergraduate from the school of engineering
- Given to students who, having completed at least two years at Tufts, have best demonstrated high scholarly ability and a wide range of intellectual competence

Tau Beta Pi

11/2012

- Inducted into the national engineering honor society

Eta Kappa Nu

10/2012

- Inducted into the international electrical and computer engineering honor society

Howard Sample Prize Scholarship in Physics (\$566.33)

04/2012

- One of six undergraduates chosen
- Given for outstanding performance in the introductory physics courses

### **Chinese Consolidated Benevolent Association of New England**

CCBA Scholarship (\$2500.00)

12/2010

- One of five freshmen from the class of 2014 chosen
- Given to applicants who demonstrate academic achievement, a history of commitment to their community, leadership potential, and financial need. Applicants must have a permanent home address in MA and be of Chinese descent.

### **Junior Achievement of Northern New England**

Stephen G. Sullivan Scholarship (\$1000.00)

06/2010

- One of three Junior Achievement participants chosen

## Publications

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.

## Skills

<b>Software</b>	MATLAB, C++, Python, Bash, R, Git, LaTeX, Hadoop, SQL, Photoshop TensorFlow, scikit-learn, NetworkX
<b>Laboratory</b>	Soldering, western blot, ChIP-Seq, cell culture, PCR, qPCR, SDS-PAGE
<b>Genomics</b>	SAMtools, bedtools, UCSC Genome Browser, Tuxedo Suite, eXpress, kallisto, Trinity, BLAT

## Activities

Tau Beta Pi	Joined 11/2012
Eta Kappa Nu	Joined 10/2012
IEEE	Joined 08/2012
Tufts Asian American Center	08/2011-05/2012
Compass Fellowship	09/2010-05/2011