

Jesse M. Zhang

10 Comstock Circle, Apt 334, Stanford, CA 94305

☎ (857) 636-9152 | ✉ jessez@stanford.edu | 🏠 jessezmzhang.com | 📱 jessezmzhang | 🌐 jessezmzhang

Education

Stanford University

Stanford, CA

MS/PHD IN ELECTRICAL ENGINEERING (**RESEARCH ADVISOR: DAVID TSE, GPA: 4.02/4.30**)

Sep. 2014 - Present

Selected Courses: Mining Massive Data Sets, Information Theory and Statistics, Artificial Intelligence, Applied Statistics, Statistical Inference, Algorithms, Convex Optimization, PGMs, Machine Learning, Statistical Signal Processing, Linear Dynamical Systems

Tufts University

Medford, MA

B.S. IN ELECTRICAL ENGINEERING (**GPA: 3.96/4.00**)

Sep. 2010 - May 2014

Selected Courses: Digital Signal Processing, Digital Image Processing, Feedback Control Systems, Data Structures, Communications

Experience

Stanford Molecular Imaging Instrumentation Laboratory

Stanford, CA

EE PHD ROTATION STUDENT

Sep. 2014 - Dec. 2014

- 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

May 2014 - Aug. 2014

- Implemented machine learning and signal processing algorithms using MATLAB and Python for accelerometer data analysis.
- Collaboratively optimized hardware-software interface.

MIT Lincoln Laboratory

Lexington, MA

EE INTERN/CO-OP

Jun. 2013 - May 2014

- Developed MATLAB algorithms for intelligently extracting traces from HF ionogram images.
- Created graphical user interface in MATLAB to facilitate ionogram image processing.

Tufts Department of Biomedical Engineering, Kaplan Group

Medford, MA

RESEARCHER

Sep. 2011 - Aug. 2012

- Designed and constructed gold circuits on silk scaffolds to control and detect neuronal signals.

Tufts Academic Resource Center

Medford, MA

HEAD TUTOR

Aug. 2012 - May 2014

- Tutored and led group study sessions for physics, chemistry, calculus III, differential equations, and linear algebra.

Publications

Fast and accurate single-cell RNA-Seq analysis by clustering of transcript-compatibility counts

COLLABORATION WITH V. NTRANOS, G. KAMATH, L. PACTHER, AND D. TSE

Submitted Jan. 2016 to *Genome Biology*

- Developed novel concept for clustering cells in single-cell RNA-Seq datasets without quantification of genes.
- Analyzed two recent single-cell datasets using iPython, bash scripts, and a variety of existing quantification tools (see GitHub)

Lysine-specific demethylase 1 has dual functions as a major regulator of AR transcriptional activity

COLLABORATION WITH C. GAI, H. H. HE, M. BROWN, S. P. BALK, X. S. LIU ET AL.

Published Dec. 2014 in *Cell Reports*

- Conducted experiments to define role of LSD1 in prostate cancer as an intern in the Brown group at the Dana Farber Cancer Institute.

Skills

Software MATLAB, iPython, CVX, scikit-learn, Keras, Bash, R, Git, LaTeX, C++, Hadoop, SQL, Photoshop

Genomics Tools SAMtools, bedtools, UCSC Genome Browser, Tuxedo Suite, eXpress, Trinity, BLAT

Honors & Awards

Summa Cum Laude, Tau Beta Pi, Eta Kappa Nu, Amos Emerson Dolbear Scholarship, Class of 1898 Prize, CCBA Scholarship, Howard Sample Prize Scholarship in Physics, JA Stephen G. Sullivan Scholarship