Jesse Zhang

Stanford University
Electrical Engineering Department
Stanford, CA 94305

jessez@stanford.edu
stanford.edu/~jessez
(857) 636-9152

EDUCATION

Stanford University, Stanford, CA — *09/2014-Present*
Ph.D., Electrical Engineering (anticipated 2019)
Research interests: Machine Learning, Statistics, Genomics
Advisor: David Tse

Stanford University, Stanford, CA — *09/2014-06/2016*
M.S., Electrical Engineering

Tufts University, Medford, MA — *09/2010-05/2014*
B.S., Electrical Engineering

Newton South High School, Newton, MA — *09/2006-06/2010*

WORK EXPERIENCE

Grail, Menlo Park, CA
Computational Biology Contractor — *12/2017-08/2018*
Computational Biology Intern — *08/2017-12/2017*
- Building classifiers and other machine learning tools using Python and R for analysis of cancer genomics data

Cellular Research, Menlo Park, CA
Bioinformatics Intern — *06/2016-09/2016*
- 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)

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 Co-op for Group 33 — *09/2013-05/2014*
Electrical Engineering Intern for Group 33 — *06/2013-08/2013*
- 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
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
Researcher 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
Teaching Assistant   *01/2018-03/2018*
Teaching Assistant   *03/2016-06/2016*
- 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, wrote questions for problem sets, designed and updated a course website: `data-science-sequencing.github.io`

Stanford Athletic Academic Resource Center, Stanford, CA
Tutor   *03/2016-06/2016*
- Tutored probabilistic systems analysis for three Stanford undergraduate athletes

Tufts Academic Resource Center, Medford, MA
Head Tutor   *08/2013-05/2014*
Resident Head Tutor   *08/2012-05/2013*
- 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

Farnia, F.*, **Zhang, J. M.*,** & Tse, D. N. (2018). Generalizable Adversarial Training via Spectral Normalization. In *International Conference on Learning Representations 7.* (*equal contributors)

Zhang, J. M., Kamath, G. M., & Tse, D. N. (2018). Towards a post-clustering test for differential expression. In *Research in Computational Molecular Biology 23.*

Feizi, S., Javadi, H., **Zhang, J.**, & Tse, D. N. (2017). Porcupine Neural Networks: (Almost) All Local Optima are Global. In *Advances in Neural Information Processing Systems 32.*

Zhang, J. M., Fan, J., Fan, H. C., Rosenfeld, D., & Tse, D. N. (2018). An Interpretable Framework for Clustering Single-Cell RNA-Seq Datasets. *BMC Bioinformatics*, 19(1), 93.

Ntranos, V.*, Kamath, G. M.*, **Zhang, J. M.*,** Pachter, L., & Tse, D. N. (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.

INVITED TALKS	Tufts University electrical engineering seminar	*04/2018*
	Becton Dickinson seminar	*06/2016*

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