

Jesse Zhang

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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>
WORK EXPERIENCE	Grail , Menlo Park, CA <i>Computational Biology Intern</i> <ul style="list-style-type: none">• Building classifiers and other machine learning tools using Python and R for analysis of cancerous genomics data	<i>08/2017-Current</i>
	Cellular Research , Menlo Park, CA <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)	<i>06/2016-09/2016</i>
	Stanford MIIL , Stanford, CA <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	<i>09/2014-12/2014</i>
	MC10, Inc. , Cambridge, MA <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	<i>05/2014-08/2014</i>
	MIT Lincoln Laboratory , Lexington, MA <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	<i>06/2013-05/2014</i>

Tufts Biomedical Engineering Department, Medford, MA 09/2011-08/2012
Researcher under supervision of David Kaplan, Ph.D.

- 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
Researcher under supervision of Myles Brown, M.D.

- 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
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

PAPERS Feizi, S., Javadi, H., **Zhang, J. M.**, & David, N. T. (2017). Porcupine Neural Networks: (Almost) All Local Optima are Global. *arXiv preprint arXiv:1710.02196*.

Zhang, J. M., Fan, J., Fan, H. C., Rosenfeld, D., & David, N. T. (2017). An Interpretable Framework for Clustering Single-Cell RNA-Seq Datasets. *bioRxiv*, 191254.

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	<i>03/2016</i>
	Tufts University	
	Summa Cum Laude	<i>05/2014</i>
	The Amos Emerson Dolbear Scholarship (\$1355.25)	<i>04/2014</i>
	The Class of 1898 Prize (\$1983.91)	<i>04/2014</i>
	Tau Beta Pi	<i>11/2012</i>
	Eta Kappa Nu	<i>10/2012</i>
	Howard Sample Prize Scholarship in Physics (\$566.33)	<i>04/2012</i>
	Chinese Consolidated Benevolent Association of New England	
	CCBA Scholarship (\$2500.00)	<i>12/2010</i>
	Junior Achievement of Northern New England	
	Stephen G. Sullivan Scholarship (\$1000.00)	<i>06/2010</i>
SKILLS	Languages: Python, R, MATLAB, C++, Bash	
	Packages: Jupyter, TensorFlow, CVX, NumPy, SciPy, scikit-learn, Git, L ^A T _E X, Hadoop	