

# Jesse Zhang

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EDUCATION	<b>Stanford University</b> , Stanford, CA Ph.D., Electrical Engineering (anticipated 2019) Research interests: Machine Learning, Statistics, Genomics Advisor: David Tse	<i>09/2014-Present</i>
	<b>Stanford University</b> , Stanford, CA M.S., Electrical Engineering	<i>09/2014-06/2016</i>
	<b>Tufts University</b> , Medford, MA B.S., Electrical Engineering	<i>09/2010-05/2014</i>
	<b>Newton South High School</b> , Newton, MA	<i>09/2006-06/2010</i>
WORK EXPERIENCE	<b>Grail</b> , Menlo Park, CA <i>Computational Biology Contractor</i>	<i>12/2017-08/2018</i>
	<i>Computational Biology Intern</i>	<i>08/2017-12/2017</i>
	<ul style="list-style-type: none"><li>• Building classifiers and other machine learning tools using Python and R for analysis of cancer genomics data</li></ul>	
	<b>Cellular Research</b> , Menlo Park, CA <i>Bioinformatics Intern</i>	<i>06/2016-09/2016</i>
	<ul style="list-style-type: none"><li>• Worked on Resolve<sup>TM</sup> system as part of an interdisciplinary team of biologists, engineers, and bioinformaticians</li><li>• Designed a Python library for automated analysis of high-dimensional single-cell RNA-seq data (clustering and feature selection)</li></ul>	
	<b>MC10, Inc.</b> , Cambridge, MA <i>R&amp;D Intern</i>	<i>05/2014-08/2014</i>
	<ul style="list-style-type: none"><li>• Implemented machine learning and signal processing MATLAB algorithms to facilitate real-time and offline accelerometer data analysis</li><li>• Collaboratively optimized hardware-software interface</li></ul>	
	<b>MIT Lincoln Laboratory</b> , Lexington, MA <i>Electrical Engineering Co-op</i> for Group 33	<i>09/2013-05/2014</i>
	<i>Electrical Engineering Intern</i> for Group 33	<i>06/2013-08/2013</i>
	<ul style="list-style-type: none"><li>• Developed MATLAB algorithms to intelligently extract trace from ionogram images</li><li>• Created graphical user interface in MATLAB to facilitate ionogram image processing</li></ul>	

**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

**EE 372: Data Science for High-Throughput Sequencing**, Stanford, CA

EXPERIENCE

*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](https://github.com/data-science-sequencing)

**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

**Zhang, J. M.**, Kamath, G. M., & David, N. T. (2018). Towards a post-clustering test for differential expression. *bioRxiv*, 463265.

Feizi, S., Javadi, H., **Zhang, J.**, & David, N. T. (2017). Porcupine Neural Networks: (Almost) All Local Optima are Global. In *Advances in Neural Information Processing Systems 32*, 2018.

**Zhang, J. M.**, Fan, J., Fan, H. C., Rosenfeld, D., & David, N. T. (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., & 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.

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

HONORS AND	<b>National Science Foundation Graduate Fellowship</b>	
AWARDS	Honorable mention	03/2016

	<b>Tufts University</b>	
	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

	<b>Chinese Consolidated Benevolent Association of New England</b>	
	CCBA Scholarship (\$2500.00)	12/2010

	<b>Junior Achievement of Northern New England</b>	
	Stephen G. Sullivan Scholarship (\$1000.00)	06/2010

SKILLS	<b>Languages:</b> Python, R, MATLAB, C++, Bash
	<b>Packages:</b> Jupyter, TensorFlow, CVX, NumPy, SciPy, scikit-learn, Git, L <sup>A</sup> T <sub>E</sub> X