Jesse M. Zhang

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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, AI, Applied Statistics, Statistical Inference, Algorithms, Convex Optimization, Probabilistic Graphical Models, Machine Learning, Statistical Signal Processing, Linear Dynamical Systems

Tufts University *Medford, MA*

BS in Electrical Engineering (**GPA:** 3.96/4.00) *Sep. 2010 - May 2014*

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

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.
- Built and presented an algorithm that was selected to become the core feature of the company's first application on the market.

MIT Lincoln Laboratory *Lexington, MA*

EE Intern/Co-op *Jun. 2013 - May 2014*

- Developed MATLAB algorithms for denoising and automatically extracting traces from high-frequency 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. Pachter, and D. Tse *Submitted Jan. 2016 to **Genome Biology***

- Developed novel concept with Ntranos and Kamath for clustering cells in single-cell RNA-Seq datasets without quantification of genes.
- Analyzed two recent single-cell datasets using iPython, Bash, 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 and performed computational analyses to define role of LSD1 in prostate cancer.
- Contributions were made as an intern in the Brown group at the Dana Farber Cancer Institute between May 2010 and Aug. 2010.

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