Jesse M. Zhang

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Education

Stanford University *Stanford, CA*

MS/PhD in Electrical Engineering (**Research advisor:** David Tse, **GPA:** 4.02/4.00) *Sep. 2014 - Jun. 2016/Sep. 2014 - Present*

Selected Courses: Information Theory, Deep Learning for Natural Language Processing, Mining Massive Data Sets, Machine Learning, Artificial Intelligence, Statistical Modeling, Statistical Inference, Algorithms, Convex Optimization, Probabilistic Graphical Models, 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

Projects

Learning the language of the genome using recurrent neural networks *Spring 2016*
- Designed a bidirectional recursive neural network for predicting epigenetic markers given genome sequence (used TensorFlow).

Denoising single-cell RNA-seq datasets using deep autoencoders *Fall 2015*
- Used deep autoencoder to clean and cluster a single-cell dataset for Artificial Intelligence final project (used Keras and scikit-learn).

Prediction of significant price changes in trading cards *Fall 2014*
- Crafted and analyzed a dataset of card prices using SVM and logistic regression for Machine Learning final project (used MATLAB).

Active noise-canceling iPhone application *Fall 2013 - Spring 2014*
- Modeled ambient noise and designed noise cancellation algorithms for senior capstone project (used MATLAB and Xcode).

Experience

Cellular Research *Menlo Park, CA*

Bioinformatics Intern *Jun. 2016 - Sep. 2016*
- Worked on the Resolve™ 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 *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.

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 *Published May 2016 in **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 wet lab experiments and performed computational analyses to define role of LSD1 in prostate cancer.

Skills

Languages Python, R, MATLAB, C++, Bash

Packages Jupyter, TensorFlow, CVX, NumPy, SciPy, scikit-learn, Git, LaTeX, Hadoop