

# Ruoxin Li

 [Linkedin Profile](#)  [Project Portfolio](#)  [GitHub](#)  [uskli@ucdavis.edu](mailto:uskli@ucdavis.edu)  +1 (530)761-8896

## EDUCATION

<b>University of California</b> <i>Ph.D. Student in Graduate Group of Biostatistics(Quon Lab)</i>	<b>Davis, CA, USA</b> <i>2017 – Present</i>
<b>University of California</b> <i>M.Sc. in Statistics</i>	<b>Davis, CA, USA</b> <i>2015 - 2017</i>
<b>Nankai University School of Economics</b> <i>B.A. in International Economics and Trade</i>	<b>Tianjin, P.R.China</b> <i>2011- 2015</i>

## EXPERIENCE

<b>University of California, Davis</b> <i>Research Assistant</i>	<b>2017 – 2023 spring(Expected)</b> <i>Davis, CA</i>
---	---

- Designed and implemented a multitask learning framework for single-cell RNA-seq data which can learn the shift of gene-coexpression network; Analyzed the change of gene regulation pattern on multiple single cell applications such as fetal liver development and neuronal iPSC differentiation
- Developed a recurrent neuron network based auto-regressive generative model for graph generation
- Developed a dimensionality reduction tool scBFA for identifying cell types in both single-cell RNA-seq data and single-cell ATAC seq data. Conducted simulation analysis to reason why scBFA can mitigate the noise in single-cell RNA-seq data with high dropout rate and dispersion estimate. Successfully benchmarked scBFA against existing dimensionality reduction tools on multiple single cell applications such as cell type identification, marker gene enrichment, trajectory inference. Built and submitted scBFA package to *Bioconductor*

<b>University of California, Davis</b> <i>Research Assistant</i>	<b>2015 – 2017</b> <i>Davis, CA</i>
---	--

- Developed a hierarchical bayesian model to predict drug response from tumor cell lines, exploited shared information among similar drugs and learning nonlinear features from kernels

### *Data Analyst*

- Developed a web application tool using R-shiny for educational analytics (such as interactive visualizations of student GPA, admission information, etc.) to aid the decision-making of department deans

## SKILLS

**Programming Languages:** Python, Shell, R, R-Shiny

**Deep Learning/Machine Learning Frameworks:** PyTorch, Sci-Kit Learn, Tensorflow2.

**Techniques and Tools:** high performance computing (HPC), environment management system (e.g. Conda,Pip), version control system (e.g. Git), general sequencing data processing and bioinformatics analysis, single-cell data analysis

**Languages:** Mandarin Chinese (native proficiency) and English (full professional proficiency).

## PUBLICATIONS

Y Choi,Li R, Quon G. Interpretable deep generative models for genomics.2021 Sep 9; biorxiv(preprint);

Li R, Quon G. scBFA: modeling detection patterns to mitigate technical noise in large-scale single-cell genomics data. *Genome Biol.* 2019 Sep 9;20(1):193.

## PRESENTATIONS

Li R, Quon G. Measuring global shifts of gene co-expression patterns in single cell transcriptomes, presented at: **Chan Zuckerberg Initiative (CZI) liver meeting.** June 2021, Virtual

Li R, Quon G. Measuring global shifts of gene co-expression patterns in single cell transcriptomes, Poster presented at: **Cold Spring Harbor meeting on the Biology of Genomes**, May 2021, Virtual