

# Yuan Xue (Soso)

Single-cell data science, biochemistry, machine learning, 🐼  
Bioengineering Ph.D. Candidate @ Quake lab, Stanford

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## Background statement

I have over a decade long experience in life sciences research. I have expertise in most modern experimental and analytical methods for high-throughput measurement, data processing, and systematic analysis. I also have research experience in protein chemistry, infectious microbiology, and cellular biology.

## Education

### Stanford University

Ph.D. Bioengineering. Thesis adviser: Stephen Quake

2017 - now

Stanford, CA, USA

### Stanford University

M.S. Bioengineering

2015 - 2017

Stanford, CA, USA

### UT Southwestern Medical Center

Biophysics (enrolled in Ph.D. program)

2014 - 2015

Dallas, TX, USA

### Reed College

B.A. Biology. Thesis adviser: Jay Mellies

2010 - 2014

Portland, OR, USA

### La Salle Catholic College Preparatory

2007 - 2010

Portland, OR, USA

### Diocesan Boys' School

2003 - 2007

Hong Kong, PRC

## Awards & Honors

### Stanford Bio-X Travel Award

2019

### Stanford Bio-X SIGF Fellow

2018

- > One of 11 students awarded with a three-year fellowship to conduct interdisciplinary research on the topics of parasitology and single-cell bioinformatics co-advised by professors John Boothroyd and Stephen Quake

### Reed College Larry Ruben Postbac. Research Fellow

2014

### Reed College Summer Experience Awardee

2013

### Reed College Independent Research Awardee

2012

### iGEM Competition Team Gold Medalist

2009

## Projects

### Life-cycle of *Toxoplasma gondii* and co-transcriptomic analysis of host infection

2018-now

- > Produced the first single-cell atlas of *Toxoplasma*. Built an [interactive visualization website](#) with Apache2, Flask, Bokeh. Comparative analysis to *Plasmodium berghei* revealed concerted genetic program to life-cycle.

### A novel single-cell analysis algorithm: self-assembling manifolds (SAM)

2017-2019

- > Single-cell sequencing reveals novel germ cell population in a parasitic flatworm, *Schistosoma mansoni*.

### Temperature effect on DNA polymerase fidelity

2015-2018

- > Characterized error rate of DNA polymerase adapted to a wide range of temperature. Found their polymerase fidelity is differentially sensitive to changes in reaction temperature. Manuscript currently in preparation.

## Publications

1. Pengyang Li, Dania Nanes Sarfati\*, **Yuan Xue**\*, Xi Yu, Alexander Tarashansky, Stephen R. Quake, John Boothroyd. Single-cell analysis of *Schistosoma mansoni* reveals a conserved genetic program controlling germline stem cell fate. Submitted (**2020**).  
\*equal contribution
2. Suchita Rastogi, **Yuan Xue**, Stephen R. Quake\*, John Boothroyd\*. Differential Impacts on Host Transcription by ROP and GRA Effectors from the Intracellular Parasite *Toxoplasma gondii*. Submitted. Accepted on **mBio (2020)**. [bioRxiv preprint](#)  
\*equal contribution
3. **Yuan Xue**, Stephen R. Quake. Temperature effect on DNA polymerase fidelity. In preparation (2019).
4. **Yuan Xue**, Terence Theisen, Suchi Rastogi, Abel Ferrel, Stephen R. Quake\*, John Boothroyd\*. A single-parasite transcriptional atlas of *Toxoplasma gondii* reveals novel control of antigen expression. **eLife (2020)**. [article](#), [bioRxiv preprint](#)  
\*equal contribution
5. Alexander Tarashansky, **Yuan Xue**, Pengyang Li, Stephen R. Quake, Bo Wang. Self-assembling Manifolds in Single-cell RNA Sequencing Data. **Elife (2019)**. [article](#), [bioRxiv preprint](#)
6. **The Tabula Muris Consortium**, Stephen R. Quake, Tony Wyss-Coray, Spyros Darmanis. Single-cell transcriptomics of 20 mouse organs creates a Tabula Muris. **Nature (2018)**. [article](#), [bioRxiv preprint](#)
7. **Yuan Xue**, Jossef Osborn, Anand Panchal, Jay L. Mellies. The RpoE stress response pathway mediates reduction of enteropathogenic *Escherichia coli* virulence by zinc. **Applied and Environmental Microbiology (2015)**. [spotlight research article](#)
8. Jing Zhou, Shi-Hao Tan, Valerie Nicolas, Chantal Bauvy, Nai-Di Yang, Jianbin Zhang, **Yuan Xue**, Patrice Codogno, Han-Ming Shen. Activation of lysosomal function in the course of autophagy via mTORC1 suppression and autophagosome-lysosome fusion. **Cell Research (2013)**. [article](#)

## Teaching Experience

<b>TA in microfluidic device laboratory (BioE301D) @ Stanford University</b>	2018
<b>TA in introduction to bioengineering (BioE80) @ Stanford University</b>	2017
<b>TA in microbiology @ Reed College</b>	2014
<b>Academic tutor in cellular biology and chemistry @ Reed College</b>	2011-2014

## Poster & Conference

<b>Building a single-cell atlas of <i>Toxoplasma</i> interactome</b>	2019
<i>Invited speaker at National University of Singapore</i>	<i>Yuan Xue et al.</i>
<b>Building a single-cell atlas of <i>Toxoplasma</i> interactome</b>	2019
<i>Invited speaker at Cell Symposia Single Cells: From Technology to Biology</i>	<i>Yuan Xue et al.</i>
<b>Single-cell co-transcriptomic measurement resolves parasitic life cycle and host interactions</b>	2018
<i>Poster presenter @ Stanford Bioengineering department retreat</i>	<i>Yuan Xue et al.</i>
<b>Building a single-cell atlas of the <i>Toxoplasma</i> interactome</b>	2018
<i>Invited speaker @ Stanford Microbiology &amp; Immunology department retreat</i>	<i>Yuan Xue et al.</i>

## Cool biochemistry measured with a hot tool

Poster presenter @ Stanford Bioengineering department retreat

2017

Yuan Xue, Stephen R. Quake

## Temperature adaptation and polymerase fidelity

Poster presenter @ Gordon Research Conference (GRC): Nucleic Acids

2017

Yuan Xue, Stephen R. Quake

### Skills

**Languages** English, Cantonese, Mandarin, Japanese, Python, R, C++, Bash,  $\text{\LaTeX}$

**Visualization** matplotlib, plotly, seaborn, bokeh, networkX, graphviz, graph-tool

**Machine learning** numpy, pandas, sklearn, scikit-learn, tensorflow, keras

**Workflows** snakemake, cloud computing (e.g. AWS, Slurm)

**Web development** Flask-REST api, Apache2

**Bioinformatics** STAR RNA aligner, htseq-count, salmon, velocity, samtools, cell ranger, scanpy

**Experimental** Smart-seq2, 10X 5' feature barcoding, molecular cloning, HPLC protein purification, gel-based assay, FACS, tissue culturing, fluorescence imaging, viral transfection, high-throughput liquid-handling

### Maintained packages

**singleCell\_snake** A snakemake pipeline for local/Slurm submission of single cell data alignment and transcript counting

**DensityPlot** A python package for generating density plot commonly seen in FACS analysis

**bag\_of\_velocity** A Slurm submission script for parallel submission of RNA velocity alignment

**nheatmap** A multi-level heatmap plotting tool with the option to perform hierarchical clustering.