

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 advisers: Stephen Quake, John Boothroyd

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

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

Poster & Conference

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