

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

2015 – 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

2010 – 2014

Portland, OR, USA

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

published on eLife

- > 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

published on eLife

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

Temperature effect on DNA polymerase fidelity

2015 – 2020

Submitted

- > Biochemically characterized error rate and activity of DNA polymerase of psychrophilic, mesophilic, and thermophilic origins.

Publications

1. **Yuan Xue**, Ido Braslavsky, Stephen R. Quake. Temperature effect on DNA polymerase fidelity. **submitted (2020)**. [bioRxiv preprint](#)
 2. 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)**. [bioRxiv preprint](#)
 3. 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*. **mBio (2020)**. [article](#), [bioRxiv preprint](#)
 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](#)
 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](#)
- *equal contributions

Teaching Experience

Teaching Assistant

Microfluidic Device Laboratory (BioE301D)

2018

Stanford University

Teaching Assistant

Introduction to Bioengineering (BioE80)

2017

Stanford University

Teaching Assistant

Microbiology

2014

Reed College

Academic tutor

Biology, Chemistry

2011 – 2014

Reed College

Poster & Conference

Building a single-cell atlas of *Toxoplasma interactome*

Invited talk

2019

National University of Singapore

Building a single-cell atlas of *Toxoplasma interactome*

Invited talk

2019

Cell Symposia Single Cells: From Technology to Biology

Single-cell co-transcriptomic measurement resolves parasitic life cycle and host interactions

Poster presentation

Stanford Bioengineering department retreat

Building a single-cell atlas of *Toxoplasma interactome*

2018

Invited talk

Stanford Microbiology & Immunology department retreat

Cool biochemistry measured with a hot tool

2017

Poster presentation

Stanford Bioengineering department retreat

Temperature adaptation and polymerase fidelity

2017

Poster presentation

Gordon Research Conference (GRC): Nucleic Acids

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 backend, Apache2

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

Experimental Smart-seq2, 10X single-cell, molecular biology techniques (e.g. cloning, expression), HPLC protein purification, 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.