

Yuan Xue

BIOINFORMATICS SCIENTIST

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EMPLOYMENT

ClearNote Health

San Mateo, California, USA

Bioinformatics Scientist II

Jan 2022 – Present

- contributes to optimization of molecular assays and development of computational methods for cancer detection based on circulating cfDNA in blood
- orchestrates project timelines, designs experimental plans, analyzes data, evaluates results with statistical methods, and presents findings to internal and external stakeholders
- develops methods and bioinformatics pipelines to quantify cfDNA and genomic CNV based on whole-genome sequencing and 5hmC-enriched sequencing data

EDUCATION

Stanford University

Stanford, California, U.S.A.

Ph.D. in Bioengineering

Sept 2015 – Dec 2021

Thesis advisers: Dr. Stephen Quake, Dr. John Boothroyd

Stanford University

Stanford, California, U.S.A.

M.S. in Bioengineering

Sept 2015 – May 2017

Reed College

Portland, Oregon, U.S.A.

B.A. in Biology

Sept 2010 – May 2014

Thesis adviser: Dr. Jay Mellies

AWARDS & HONORS

Bio-X Travel Award

Stanford Bio-X program

2019

Stanford Interdisciplinary Graduate Fellowship

Awarded to eleven students to support their doctoral research with an interdisciplinary scope for three years.

2018

Postbaccalaureate Research Fellowship

Reed College, Biology Department

2014

Summer Experience Research Award

Reed College

2013

Gold Team Medal

MIT iGEM Competition

2009

SELECTED PUBLICATIONS

1. Yuhong Ning*, **Yuan Xue***, Verena Friedl, David Haan, Anna Bergamaschi, Gulfem Guler, Kyle Hazen, Aaron Scott, Tierney Phillips, Erin McCarthy, Christopher K. Ellison, Roger Malta, Albert Nguyen, Vanessa Lopez, William Gibb, Romola Cavet, Shimul Chowdhury, Wayne Volkmuth, Samuel Levy‡. 5-hydroxymethylcytosine analysis reveals stable epigenetic changes in tumor tissue that enable cancer detection in cell-free DNA. **under review (2024)**.
2. Dania Nanes Sarfati, **Yuan Xue**, Eun Sun Song, Ashley Byrne, Daniel Le, Spyros Darmanis, Stephen R. Quake, Adrien Burlacot, James Sikes‡, Bo Wang‡. Coordinated wound responses in a regenerative animal-algal photosymbiotic metaorganism. **Accepted at Nature Communications (2024)**.
3. Trung Pham‡*, **Yuan Xue***, Susan Brewer, Kenneth E. Bernstein, Stephen R. Quake‡, Denise Monack‡. Single-cell profiling reveals functional diversity of granuloma macrophages during persistent Salmonella infection. **Science Advances (2023)**. [bioRxiv preprint](#)
4. **Yuan Xue**, Ido Braslavsky, Stephen R. Quake. Temperature effect on DNA polymerase fidelity. **Journal of Biological Chemistry (2021)**. [bioRxiv preprint](#)

5. Pengyang Li, Dania Nanes Sarfati*, **Yuan Xue***, Xi Yu, Alexander Tarashansky, Stephen R. Quake, Bo Wang. Single-cell analysis of *Schistosoma mansoni* reveals a conserved genetic program controlling germline stem cell fate. **Nature Communications (2020)**. [bioRxiv preprint](#)
 6. 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)**. [bioRxiv preprint](#)
 7. **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)**. [bioRxiv preprint](#)
 8. Alexander Tarashansky, **Yuan Xue**, Pengyang Li, Stephen R. Quake, Bo Wang. Self-assembling Manifolds in Single-cell RNA Sequencing Data. **Elife (2019)**. [bioRxiv preprint](#)
 9. **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)**. [bioRxiv preprint](#)
 10. **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)**.
 11. 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)**.
- *equal contributions; ‡corresponding authors

PROFESSIONAL SERVICE

Teaching Assistant	Stanford University
<i>Microfluidic Device Laboratory (BioE301D)</i>	2018
Teaching Assistant	Stanford University
<i>Introduction to Bioengineering (BioE80)</i>	2017
Teaching Assistant	Reed College
<i>Microbiology</i>	2014
Academic Tutor	Reed College
<i>Biology, Chemistry</i>	2011 – 2014

CONFERENCES & PRESENTATIONS

Oral presentation	ESMO Congress
<i>5-Hydroxymethylcytosine analysis reveals stable epigenetic changes in tumor tissue that enable cfDNA cancer predictions</i>	2022
Invited talk	National University of Singapore
<i>Building a single-cell atlas of <i>Toxoplasma interactome</i></i>	2019
Invited talk	Cell Symposia Single Cells: From Technology to Biology
<i>Building a single-cell atlas of <i>Toxoplasma interactome</i></i>	2019
Poster presentation	Stanford Bioengineering department retreat
<i>Single-cell co-transcriptomic measurement resolves parasitic life cycle and host interactions</i>	2018
Invited talk	Stanford Microbiology & Immunology department retreat
<i>Building a single-cell atlas of <i>Toxoplasma interactome</i></i>	2018
Poster presentation	Stanford Bioengineering department retreat
<i>Cool biochemistry measured with a hot tool</i>	2017

Poster presentation*Temperature adaptation and polymerase fidelity*

Gordon Research Conference: Nucleic Acids

2017

Poster presentation*Molecular Mechanism of Zinc Disruption of Enteropathogenic Escherichia coli Pathogenesis*

Gordon Research Conference: Microbial Toxins & Pathogenicity

2014

SKILLS

Languages: English, Cantonese, Mandarin, Japanese, Python, R, Bash, \LaTeX **Visualization:** matplotlib, plotly, seaborn, bokeh, networkX, graphviz, graph-tool**Machine Learning:** numpy, pandas, sklearn, scikit-learn, tensorflow, keras, statsmodels**Workflows:** Nextflow, Snakemake, cloud computing (e.g. AWS, slurm), Docker**Web development:** Flask-REST backend, Apache2**Bioinformatics:** STAR, minimap2, htseq-count, bedtools, salmon, velocity, samtools, scanpy, Kraken**PACKAGE CONTRIBUTIONS**

singleCell.snake*A snakemake pipeline for local/Slurm submission of single cell data alignment and transcript counting.***nheatmap***A python package to generate multi-level heatmap with extensive configuration options.***DensityPlot***A python package to generate density scatter plot.***bag_of_velocity***A bash / python script for parallel submission of RNA velocity alignment on Slurm.*