

# 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 (2023)**.
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. **under review (2023)**.
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

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## PROFESSIONAL SERVICE

<b>Teaching Assistant</b> <i>Microfluidic Device Laboratory (BioE301D)</i>	Stanford University 2018
<b>Teaching Assistant</b> <i>Introduction to Bioengineering (BioE80)</i>	Stanford University 2017
<b>Teaching Assistant</b> <i>Microbiology</i>	Reed College 2014
<b>Academic Tutor</b> <i>Biology, Chemistry</i>	Reed College 2011 – 2014
<b>Peer reviewer</b> <i>Frontiers In Pharmacology, Frontiers In Oncology, Frontiers In Immunology, Sensors, BMC Immunology, Autophagy, Applied Sciences, Aging Cell, Journal of Cellular Physiology, International Journal of Molecular Sciences, Journal of Leukocyte Biology, Health Informatics Journal, MDPI Microbiology, MDPI Algorithms</i>	

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## CONFERENCES & PRESENTATIONS

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

**Poster presentation***Cool biochemistry measured with a hot tool*

Stanford Bioengineering department retreat

2017

**Poster presentation***Temperature adaptation and polymerase fidelity*

Gordon Research Conference (GRC): Nucleic Acids

2017

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**SKILLS****Languages:** English, Cantonese, Mandarin, Japanese, Python, R, Bash, L<sup>A</sup>T<sub>E</sub>X**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

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**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.*