

Yuan Xue

SENIOR BIOINFORMATICS DATA SCIENTIST

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EMPLOYMENT

ClearNote Health

San Mateo, California, USA

Senior Bioinformatics Data Scientist

Jan 2022 – Present

- Developed multi-modal cancer detection models integrating proteomics, 5hmC epigenomics, and low-pass WGS from blood-based liquid biopsy. Built multinomial logistic regression for tumor tissue-of-origin prediction (85.2% accuracy), and implemented tumor fraction estimation pipelines from low-pass WGS to support tumor burden monitoring. Contributed to 2 peer-reviewed publications ([Communications Biology](#), [J.M.D.](#)), 4 conference presentations (CSHL, ESMO, ASHG, AACR), and 2 pending patents.
- Led a cross-functional team of wet-lab scientists and bioinformatics engineers to successfully implement assay control processes for clinical cancer diagnostic tests, spanning assay optimization and computational pipeline developments (Nextflow, AWS, dbt, Snowflake). Developed rigorous process efficiency QC metrics; improved cDNA quantification precision by 4X; reduced measurement variation of blood-based proteomics by 10%. Contributed to a pending patent.
- Led feasibility studies evaluating leading sequencing platforms (Illumina, Ultima, Element Bio, Singular) and optimized sequencer workflow, achieving a 28% cost reduction.

RESEARCH EXPERIENCE

Stanford University - Quake Lab

Stanford, California, USA

Doctoral candidate of Bioengineering

September 2015 – December 2021

- Developed single-cell transcriptomic methods to profile *Toxoplasma gondii* and infected host cells. Discovered novel antigenic variation and its regulatory transcription factor, and assessed evolutionary concordance of *Toxoplasma* asexual life-cycle with *Plasmodium*. Built an interactive browser for community data visualization. Published in [eLife](#).
- Led single-cell profiling of murine macrophage response to persistent *Salmonella typhimurium* infection. Performed functional pathway analysis (GSEA, KEGG, Reactome) linking metabolic and immune pathways to infection response, and identified a novel Ace+ macrophage cell type mediating intracellular bacterial persistence. Published in [Science Advances](#).
- Developed biochemical and genomics assays to profile replication fidelity and kinetics of DNA polymerases across evolutionary origins (psychrophilic, mesophilic, thermophilic). Identified a novel cold-active polymerase from *Psychromonas ingrahamii*. Published in [Journal of Biological Chemistry](#).

EDUCATION

Stanford University

Stanford, California, U.S.A.

Ph.D. and M.S. in Bioengineering

Sept 2015 – Dec 2021

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

Reed College

Portland, Oregon, U.S.A.

B.A. in Biology

Sept 2010 – May 2014

Thesis adviser: Dr. Jay Mellies

PUBLICATIONS

1. **Yuan Xue***, Yuhong Ning*, *et al.*, Wayne Volkmuth, Samuel Levy‡. 5-hydroxymethylcytosine analysis reveals stable epigenetic changes in tumor tissue that enable cancer detection in cell-free DNA. [Communications Biology \(2025\)](#).
2. Shimul Chowdhury, Michael Kesling, Micah Collins, Vanessa Lopez, **Yuan Xue**, Glenn Oliveira, Verena Friedl, Anna Bergamaschi, David Haan, Wayne Volkmuth, Samuel Levy‡. Analytical Validation of an Early Detection Pancreatic Cancer Test Using 5-Hydroxymethylation Signatures. [The Journal of Molecular Diagnostics \(2024\)](#).

3. 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. **Nature Communications (2024)**.
 4. 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](#)
 5. **Yuan Xue**, Ido Braslavsky, Stephen R. Quake. Temperature effect on DNA polymerase fidelity. **Journal of Biological Chemistry (2021)**. [bioRxiv preprint](#)
 6. 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](#)
 7. 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](#)
 8. **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](#)
 9. Alexander Tarashansky, **Yuan Xue**, Pengyang Li, Stephen R. Quake, Bo Wang. Self-assembling Manifolds in Single-cell RNA Sequencing Data. **Elife (2019)**. [bioRxiv preprint](#)
 10. **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](#)
 11. **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)**.
 12. 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

CONFERENCES & PRESENTATIONS

Poster presentation	CSHL Biological Data Science
<i>5-hydroxymethylcytosine analysis reveals stable epigenomic changes in tumor tissue that enable cancer detection in cell-free DNA</i>	2024
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 Toxoplasma interactome</i>	2019
Invited talk	Cell Symposia Single Cells: From Technology to Biology
<i>Building a single-cell atlas of Toxoplasma interactome</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 Toxoplasma interactome</i>	2018

Poster presentation <i>Cool biochemistry measured with a hot tool</i>	Stanford Bioengineering department retreat 2017
Poster presentation <i>Temperature adaptation and polymerase fidelity</i>	Gordon Research Conference: Nucleic Acids 2017
Poster presentation <i>Molecular Mechanism of Zinc Disruption of Enteropathogenic Escherichia coli Pathogenesis</i>	Gordon Research Conference: Microbial Toxins & Pathogenicity 2014

AWARDS & HONORS

Bio-X Travel Award <i>Stanford Bio-X program</i>	2019
Stanford Interdisciplinary Graduate Fellowship <i>Awarded to eleven students to support their doctoral research with an interdisciplinary scope for three years.</i>	2018
Postbaccalaureate Research Fellowship <i>Reed College, Biology Department</i>	2014
Summer Experience Research Award <i>Reed College</i>	2013
Gold Team Medal <i>MIT iGEM Competition</i>	2009

PROFESSIONAL SERVICE

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

SKILLS

Languages: English (native), Cantonese (native), Mandarin (native), Japanese (conversational)

Technology Stack: AWS, Nextflow, Docker, Python, R, SQL, PyTorch, scikit-learn, DBT, Snakemake, Snowflake, Slurm

Bioinformatics: familiar with most NGS analysis tools

Domains: single-cell genomics, cfDNA fragmentomics, epigenomics, cancer diagnostics, statistical modeling, deep learning