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. 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).**

2. **Yuan Xue***, Yuhong Ning*, 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).**

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**

Professional Service

Teaching Assistant — Stanford University
Microfluidic Device Laboratory (BioE301D) — *2018*

Teaching Assistant — Stanford University
Introduction to Bioengineering (BioE80) — *2017*

Teaching Assistant — Reed College
Microbiology — *2014*

Academic Tutor — Reed College
Biology, Chemistry — *2011 – 2014*

Conferences & Presentations

Poster presentation — CSHL Biological Data Science
5-hydroxymethylcytosine analysis reveals stable epigenomic changes in tumor tissue that enable cancer detection in cell-free DNA — *2024*

Oral presentation — ESMO Congress
5-Hydroxymethycytosine analysis reveals stable epigenetic changes in tumor tissue that enable cfDNA cancer predictions — *2022*

Invited talk — National University of Singapore
Building a single-cell atlas of Toxoplasma interactome — *2019*

Invited talk — Cell Symposia Single Cells: From Technology to Biology
Building a single-cell atlas of Toxoplasma interactome — *2019*

Poster presentation Stanford Bioengineering department retreat
Single-cell co-transcriptomic measurement resolves parasitic life cycle and host interactions *2018*

Invited talk Stanford Microbiology & Immunology department retreat
Building a single-cell atlas of Toxoplasma interactome *2018*

Poster presentation Stanford Bioengineering department retreat
Cool biochemistry measured with a hot tool *2017*

Poster presentation Gordon Research Conference: Nucleic Acids
Temperature adaptation and polymerase fidelity *2017*

Poster presentation Gordon Research Conference: Microbial Toxins & Pathogenicity
Molecular Mechanism of Zinc Disruption of Enteropathogenic Escherichia coli Pathogenesis *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, velocyto, 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_velocyto
A bash / python script for parallel submission of RNA velocity alignment on Slurm.