Shang-Yang (Sam) Chen

Computational Biologist || Data Scientist

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SUMMARY OF QUALIFICATIONS

❖ Ph.D. trained in biomedical informatics with extensive expertise in multi-omics integrative analysis.
❖ Skilled in developing innovative solutions to biological problems in industry settings, including custom pipelines and web application development.
❖ Highly collaborative, organized, and detail-oriented team player

Skills: Bioinformatics, Single Cell Omics, Epigenomics, Biostatistics, Data Analytics, Data Visualization, ML/AI, Webapp Development, Version Control, Immunology, Genomics, Cloud Computing

Programming Languages/Platforms: Python, R, Bash, Java, SQL

Framework/Packages: Seurat, Scanpy, git, Pandas, Tidyverse, DESeq2, ggplot2, Matplotlib, Scikit-Learn, pyTorch, Django, AWS, BioPython

EDUCATION

Ph. D. | Biomedical Informatics | Northwestern University | 2016-2022

EXPERIENCE

ROC ARMY | SEPTEMBER 2024 - JANUARY 2025
❖ Mandatory national service

DYNO THERAPEUTICS

SCIENTIST I/II, COMPUTATIONAL SCIENCE | JUNE 2022 - AUGUST 2024
❖ Developed and implemented a Python-based module to automate processing and interpretation of large-scale single-nucleus RNA sequencing (snRNA-seq) data, enabling efficient analysis of over 500,000 nuclei and accelerating biological insights.
❖ Led snRNA-seq data analysis to validate AI-designed gene therapy vector candidates, contributing to key advancements in therapeutic development.
❖ Collaborated with bench biologists, software engineers, and legal teams to deliver patent applications and external presentations, ensuring scientific accuracy and strategic alignment.

GENENTECH, ONCOLOGY INFORMATICS | OCTOBER 2021 – APRIL 2022
Bioinformatics intern
❖ Developed the R package Epiregulon, enabling inference of transcription factor (TF) activity in single cells by constructing gene regulatory networks (GRN). Integrated scATAC-seq and scRNA-seq data with public bulk TF ChIP-seq data to facilitate therapeutic discovery targeting TFs.
❖ Designed and implemented a benchmarking framework to evaluate Epiregulon against reference databases of TF-target gene interactions, ensuring robust performance evaluation.
❖ Analyzed and interpreted scATAC-seq datasets to uncover transcriptional mechanisms in breast cancer subtypes.

NORTHWESTERN UNIVERSITY | AUGUST 2016 - MAY 2022
Graduate Researcher
❖ Synthesized multi-omics insights to investigate macrophage heterogeneity in the joint, advancing understanding of rheumatoid arthritis pathogenesis.
❖ Developed and implemented custom pipelines for single-cell RNA-seq and CITE-seq data analysis, enabling high-resolution characterization of cellular heterogeneity.

- ❖ Designed and deployed MAGNET (Macrophage Annotation Gene Network Enrichment Tool), a web application for enhanced functional enrichment analyses using curated macrophage gene sets.

ACADEMIC FELLOWSHIPS

AMERICAN HEART ASSOCIATION PREDOCTORAL FELLOWSHIP | 2019 – 2021
- ❖ Elucidating the Roles of Resident Cardiac Macrophages in Post-Infarction Reperfusion Injury

SELECT PUBLICATIONS

A. Peer-reviewed Original Investigations

MAGNET: A Web-based Application for Improved Functional Enrichment Analysis of Cell-type-specific Data. SY Chen, G. Gadhvi, D. Winter. PLoS One; January 2023; 18(1):e0272166

Tissue-resident, extravascular Ly6c− monocytes are critical for inflammation in the synovium. A. Montgomery, **SY Chen**, Y. Wang, G. Gadhvi, M. Mayr, C. Cuda, S. Dominguez, H-K M. Makinde, M Gurra, A. Misharin, A. Mandelin, E. Ruderman, A. Thakrar, S. Brar, M. Carbs, K. Aren, M. Akbarpour, A. Filer, S. Nayer, A. Teososio, T. Major, A. Bharat, GR. Budinger, D. Winter, H. Perlman. Cell reports; May 2023; 42 (5)

Critical role of synovial tissue-resident macrophage niche in joint homeostasis and suppression of chronic inflammation. QQ Huang, R. Doyle, **SY Chen**, Q. Sheng, AV Misharin, Q. Mao, D. Winter, RM Pope. Science Advances; January 2021

Epiregulon: Inference of single-cell transcription factor activity to predict drug response and drivers of cell state. T. Włodarczyk , A. Lun, D. Wu, M. Shi , X. Ye, S. Menon, S. Toneyan, K. Seidel, L. Wang, J. Tan, **SY Chen**, T. Keyes, A. Chlebowski, A. Waddell, W. Zhou, Y. Wang, Q. Yuan, Y. Guo, LF Chen, B. Daniel, A. Hafner, M. He, A. Chibly, Y. Liang, Z. Duren, C. Metcalfe , M. Hafner, C. Siebel, MR Corces, R. Yauch, S. Xie, X. Yao. *(In revision)*

Transcriptional profiling of pediatric cholestatic livers identifies three distinct macrophage populations. S. Taylor, SY Chen, G. Gadhvi, L. Feng, K. Gromer, H. Abdala-Valencia, K. Nam, S. Dominguez. A. Montgomery, P. Reyfman, L. Ostilla, J. Wechsler, C. Cuda, R. Green, H. Perlman, D. Winter. PLoS One; January 2021

Maintenance DNA methylation is essential for regulatory T cell development and stability of suppressive function. KA. Helmin, L Morales-Nebreda, MA. Torres Acosta, KR. Anekalla, SY Chen, H Abdala-Valencia, Y Politanska, P Cheresh, M Akbarpour, EM. Steinert, SE. Weinberg, BD. Singer; Journal of Clinical Investigation; September 2020

B. Abstracts

Optimizing Intravitreal Delivery to the Non-Human Primate Retina with Machine Guided AAV Capsid Design. S. Abesteh, I. Brenckle, Z. Cargill, I. Chen, **S. Chen**, D. Deny, J. Fathima, J. Gerold, A. Ghosh, J. Grush, E. Kelsic, H. Kuchwara, J. Kwasnieski, K. Lin, E. Lykken, E. Marrogi, K. Maryak, P. McDonel, H. Levitin, A. Miles, N. Nagabhushana, D. Pignatta, B. Satinsky, B. Saxena, C. Sengel, A. Sheridan, T. Tarbell, M. Thommes, H. Turunen, N. White, S. Wolock. 2024 ASGCT Annual Meeting

Applying Artificial Intelligence to MultiProperty Optimization of AAV Capsids for Neuronal Gene Delivery. M. Deshpande, D. Bloodgood, B. Diaz-Rohrer, K. Looby, S. Hilton, **S. Chen**, S. Sinai, K. Lin, J. Kwasnieski, A. Veres, E. Kelsic
2023 ASGCT Annual Meeting