Shang-Yang (Sam) Chen

Computational Biologist || Data Scientist || Boston, MA

sychen9584@gmail.com || Personal Website ||LinkedIn || GitHub || Google Scholar

SUMMARY OF QUALIFICATIONS

- Ph.D. trained computational biologist with deep expertise in multi-omics integrative analysis, including scRNA-seq, scATAC-seq, and bulk NGS data.
- Proven track record of developing scalable, production-grade pipelines and tools for biological discovery in industry settings.
- Experienced in cross-functional collaboration with biologists, engineers, legal, and executive teams; contributed to patent filings and scientific conference presentations.
- Obtained permanent work authorization. No visa sponsorship required.

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, UNIX, Java, SQL

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

- Designed and deployed production-grade Python modules for automated processing, QC, and analysis of snRNA-seq data, scaling internal datasets and enabling efficient handling of > 1.5 million nuclei.
- Served as the primary analysis lead for snRNA-seq data across ocular, brain, and liver organ programs, supporting validation of AI-designed gene therapy vector candidates.
- Performed integrative analysis of bulk tissue NGS data from non-human primates, mice, and in vitro assays, contributing to the design and selection of high-performing AAV variants.
- Collaborated with wet lab biologists to optimize experimental design and troubleshoot data quality; worked with engineers to scale pipelines and with legal/executive teams to prepare IP filings and conference presentations.

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. 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

- Integrated multi-omics data to characterize macrophage heterogeneity across organs, advancing insights into innate immunity.
- Designed and implemented custom pipelines for single-cell RNA-seq and CITE-seq data, enabling high-resolution mapping of cellular diversity.
- Conducted comprehensive analysis of RNA-seq and ATAC-seq datasets to uncover transcriptional and epigenomic mechanisms in rheumatoid arthritis and aging.
- Developed and deployed MAGNET, a web application for enhanced functional enrichment analyses using curated gene sets.
- Awarded the American Heart Association (AHA) predoctoral fellowship in recognition of research excellence in computational immunology.

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)*

B. Industry Conference 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

Non-Human Primate Evaluation of an Engineered AAV Capsid for Retinal Cell Specific and Biofactory-Based Ocular Gene Therapies. H. Turunen, A. Miles, B. Diaz-Rohrer, S. Hilton, **S. Chen**, K. Maryak, S. Sinai, K. Lin, J. Kwasnieski, A. Veres, E. Kelsic
2023 ASGCT Annual Meeting