

Shang-Yang (Sam) Chen

Computational Biologist || Data Scientist

sychen9584@gmail.com || (+1) 631.561.7672 || Boston, MA || [LinkedIn](#) || [GitHub](#)

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. 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. Teososo, 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