

# Shang-Yang (Sam) Chen

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Computational Biologist || Data Scientist

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## SUMMARY OF QUALIFICATIONS

- ❖ Ph.D. trained in biomedical informatics with extensive expertise in single-cell omics and high-throughput data analysis
- ❖ Skilled in developing innovative solutions to biological problems in industry settings, including custom pipelines and web-based applications.
- ❖ Highly collaborative, organized, and detail-oriented team player

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

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

**Framework/Packages:** Seurat, scVerse, git, Pandas, Tidyverse, DESeq2, ggplot2, Matplotlib, Scikit-Learn, pyTorch, Django

## EDUCATION

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

## EXPERIENCE

### **DYNO THERAPEUTICS**

**SCIENTIST II, COMPUTATIONAL SCIENCE | FEBRUARY 2024 - AUGUST 2024**

**SCIENTIST I, COMPUTATIONAL SCIENCE | JUNE 2022 – JANUARY 2024**

- ❖ Designed, developed, and implemented a Python-based module that automated the processing and interpretation of large-scale single-cell nuclei RNA sequencing (snRNA-seq) datasets, enabling efficient analysis of over 500,000 nuclei and streamlining downstream biological insights .
- ❖ Led the analysis of snRNA-seq datasets to support the validation of AI-designed gene therapy vector candidates, driving critical advancements in therapeutic development efforts.
- ❖ Partnered with bench biologists, software engineers, and legal teams to develop deliverables for patent applications and external presentations, ensuring scientific accuracy and strategic alignment.

**GENENTECH, ONCOLOGY INFORMATICS | OCTOBER 2021 – APRIL 2022**

### **Bioinformatics intern**

- ❖ Developed an R package, Epiregulon, to infer transcription factor activity by integrating scRNA-seq and scATAC-seq data, enabling accelerated discovery of therapeutics targeting transcriptional regulators.
- ❖ Designed and implemented a benchmarking framework to evaluate Epiregulon against reference databases of TF-target gene interactions, ensuring performance validation.
- ❖ Conducted analysis and interpretation of scATAC-seq datasets to elucidate transcriptional mechanisms in breast cancer subtypes.

**NORTHWESTERN UNIVERSITY | AUGUST 2016 - MAY 2022**

### **Graduate Researcher**

- ❖ Synthesized multi-omics insights to explore macrophage heterogeneity across different organs, advancing our understanding of innate immunity.
- ❖ Developed and implemented custom pipelines for the interpretation of single-cell RNA-seq and CITE-seq data, facilitating high-resolution analysis of cellular heterogeneity.

- ❖ Designed and deployed MAGNET (Macrophage Annotation Gene Network Enrichment Tool), a web application offering enhanced functional enrichment analyses with 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

## **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<sup>−</sup> 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