Shang-Yang Chen

Computational Biologist || Data Scientist

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Profile

Computational Biology Ph.D. with extensive expertise in analyzing and developing tools for high-throughput genomic data, with a specialization in single-cell data analysis. Demonstrated expertise in innate immunology, leveraging advanced bioinformatics techniques to uncover biological insights and drive impactful research. Skilled in developing innovative solutions to biological problems, including custom pipelines and web-based applications. Passionate about integrating AI/machine learning approaches to advance data analysis, predictive modeling, and biomedical research outcomes

Education

Northwestern University, Chicago, IL 2016-2022

Ph.D. in Computational Biology GPA: 3.89
DGP Integrated Biomedical Sciences Program - Biomedical Informatics Track
"Characterizing Macrophage Heterogeneity in Tissues Through High-Throughput Transcriptomics Technologies and Algorithms"

Stony Brook University, Stony Brook, NY 2012-2016
Bachelor of Science in Biochemistry, *honors degree* GPA: 3.69
Minor in Information Systems

Research and Work Experiences

Scientist II, Computational Science February 2024 - August 2024
Scientist I, Computational Science June 2022 – January 2024
Dyno Therapeutics

- 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.

Bioinformatics Internship October 2021 – April 2022
Genentech, Oncology Informatics

- 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.

Ph.D. Candidate Summer 2017-May 2022
Deborah Winter, Northwestern University
Characterizing Macrophage Heterogeneity in Tissues Through High-Throughput Transcriptomics Technologies and Algorithms

- 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.

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)

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*)

Synovial Macrophage Heterogeneity Confers Differential Response to Acute and Chronic Inflammatory Arthritis. SY Chen, A. Montgomery, P. Homan, S. Dominguez, C. Cuda, G. Gadhvi, S. Jung, GR Budinger, A. Misharin, M. Mayr, D. Winter, H. Perlman. (*In preparation*)

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; 7(2):eabd0515.

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;16(1):e0244743.

Macrophages drive the inflammatory phase in experimental osteoarthritis
A Montgomery, N Fahy, S Hamilton, B Eckman, L De Almeida, S Ishihara, MG Mayr, SY Chen, G Gadhvi, C Cuda, AM Malfait, Y Bastiaansen-Jenniskens, DR. Winter. BioRxiv; June 2020.

Influenza-induced activation of recruited alveolar macrophages during the early inflammatory phase drives lung injury and lethality.
CM. Koch, KR Anakella, YS Hu, M Ciesielski, G Gadhvi, **SY Chen**, M Turner, Y Cheng, BM Coates, H Abdala-Valencia, PA Reyfman, AV Misharin, GR Budinger, DR Winter, KM Ridge. BioRxiv; June 2020

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

DNA methylation as a regulator of the neonatal CD4+ T cell response to pneumonia
McGrath-Morrow SA, Ndeh R, Helmin KA, **Chen SY**, Anekalla KR, Abdala-Valencia H, Collaco JM, D'Alessio FR, Misharin AV, Singer BD. Journal of Biological Chemistry; July 2018; JBC-RA118

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 Multi Property 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.i 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

Characterizing Heterogeneity of Synovial Macrophages in Rheumatoid Arthritis Patients. SY Chen, Y. Wang, A. Montgomery, S. Dominguez, C. Cuda, G. Gadhvi, H. Perlman, D. Perlman
2020 ACR Convergence 2020

The Dynamics of Macrophage Sub-Populations in the Inflammatory Phase Following Joint Trauma. S. Hamilton, A. Montgomery, N. Fahy, M. Mayr, **SY Chen**, G. Gadhvi, Y. Bastiaansen-Jenniskens, D. Winter
2020 ACR Convergence 2020

Single Cell RNA-sequencing Reveals Distinct Macrophage Subsets in the Joint with Differing Ontogenies During Steady-state and Arthritis
SY Chen, A Montgomery, P Homan, G Gadhvi, D Winter, H Perlman
2019 ACR/ARHP Annual Meeting

A Novel Subclass of Intravascular Non-classical, Tissue Resident Synovial Monocyte Is Critical for Rheumatoid Arthritis Pathogenesis
A Montgomery, **SY Chen**, D Winter, H Perlman
2019 ACR/ARHP Annual Meeting

The Role of Flip in Differentiation and Survival of Synovial Tissue Resident Macrophages
Q Huang, R Doyle, **SY Chen**, A Misharin, D Winter, R Pope
2019 ACR/ARHP Annual Meeting

Tissue Resident Macrophages Establish a Niche That Limits Monocyte to Macrophage Differentiation in Synovial Tissue during Homeostasis
Q Huang, R Doyle, A Misharin, **SY Chen,** D Winter, R Pope
2018 ACR/ARHP Annual Meeting

Presentations

Poster Presentation, Keystone Symposia: Single Cell Biology, Florence (Cancelled) May 2020
- Unmasking the heterogeneity of joint macrophages in health and disease using single-cell RNA-sequencing

Oral Presentation, American College of Rheumatology Annual Meeting, Atlanta November 2019
Poster Presentation, Cell Symposia: Transcriptional Regulation, Chicago October 2019
- Single cell RNA-sequencing reveals ontogenically-distinct macrophage subsets in the joint during steady state and arthritis

Poster Presentation, Lewis Landsberg Research Day, Northwestern University April 2019
- MAGNET: Macrophage Annotation of Gene Network Enrichment Tool

Poster Presentation, Lewis Landsberg Research Day, Northwestern University April 2018
- Transcriptional profiling of synovial macrophages in arthritic mice

Poster Presentation, Computational Research Day, Northwestern University April 2017
- Building a Bisulfite Sequencing Data Analysis Workflow

Poster Presentation, URECA, Stony Brook University April 2016
- Seasonal Variation in Lifespan and Starvation Resistance in *D. melanogaster*

Academic Honors & Fellowships

American Heart Association Predoctoral Fellowship 2019 - 2021
Project: Elucidating the Roles of Resident Cardiac Macrophages in Post-Infarction Reperfusion Injury

OSG User School 2017, University of Wisconsin-Madison July 2017
Workshop on high-performance computing clusters
Selected to represent Northwestern University with full funding support

URECA Summer Research Grant Summer 2015
Project: Comparison of seasonal variation in starvation resistance between *D. melanogaster* and *D. simulans*.

Tsai Hsing School Foundation Fellowship 2012 - 2016
Provided full tuition and living expenses support for undergrad studies at Stony Brook University

Early Career Experiences

Research Rotations 2016 - 2017
Northwestern University

- Conducted *in silico* benchmarking of RNA-seq library preparation protocols and collaborated with the sequencing core to evaluate Lab Information Management Systems (LIMS).
- Developed computational pipelines, including automation scripts for bisulfite sequencing workflows.
- Built an R-based probabilistic model to simulate and infer cell lineage trees from enhancer profiles.

Undergraduate Researcher 2015 - 2016
Stony Brook University
Comparison of seasonal variation in starvation resistance between D. melanogaster and D. simulans.

- Investigated seasonal variation in starvation resistance and sexual polymorphism in *D. melanogaster* and *D. simulans*, leading a project on pupation behavior.

Summer Lab Intern Summer 2013
Taipei Medical University

- Assisted in lab mouse care and performed cell culture, PCR, and gel electrophoresis on human cancer cell lines.

Professional Organizations

Member of the Midwest Taiwanese Biotechnology Association (MTBA) 2019-present

Member of the International Society for Computational Biology (ISCB) 2017-present

Member of the American College of Rheumatology (ACR) 2019-2022

Member of the American Heart Association (AHA) 2017-2022

Skills & Relevant Courses:

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

Certification & Training

DeepLearning.AI Deep Learning Specialization	2024
DeepLearning.AI Machine Learning Specialization	2024
Northwestern Kellogg School of Management	
Management for Scientists and Engineers Certificate	2020
Datacamp Coding Best Practices with Python	2020
Datacamp Tidyverse Fundamentals	2020
National Taiwan University Summer Python Bootcamp	2016