

# 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

- ❖ 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.

**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***

- ❖ Synthesized multi-omics insights to explore macrophage heterogeneity across different organs, advancing our understanding of innate immunity.
- ❖ Conducted comprehensive analysis of RNA-seq and ATAC-seq datasets to investigate the roles of transcriptional and epigenomic dynamics in rheumatoid arthritis and aging.
- ❖ 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.
- ❖ Awarded the American Heart Association (AHA) predoctoral fellowship in recognition of research excellence.

## **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)

**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. Chlebowsky, 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