Shang-Yang Chen

Computational Biologist || Data Scientist

sychen9584@gmail.com || (+1) 631.561.7672 || Watertown, MA || LinkedIn || GitHub

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, 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.

Bioinformatics Internship   October 2021 – April 2022
Genentech, Oncology Informatics
- ❖ 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.

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 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.
- ❖ 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− 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. (*Submitted*)

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:

Programming Languages: Python, R, Bash, Java, SQL
Frameworks/Packages: Seurat, Scanpy, Pandas, Tidyverse, ggplot2, Seaborn, Scikit-Learn, pyTorch, Django
Courses: Advanced bioinformatics, Statistical Methods for Bioinformatics, Advanced immunology, Genetics

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