Chi-Jane Chen

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Education

The University of North Carolina at Chapel Hill, NC, USA Expected Graduation Date: *05/2026*

Ph.D Student of Computer Science

- Overall GPA: 4.0/4.0

The University of North Carolina at Chapel Hill, NC, USA

Master's Degree in Computer Science *08/2021-05/2023*

- Overall GPA: 4.0/4.0

National Taiwan Ocean University, Keelung, Taiwan

B.S. in Computer Science and Engineering *02/2016-06/2018*

- Overall GPA: 4.0/4.0 • Class Ranking: 1/53

National Dong Hwa University, Hualien, Taiwan

Department of Computer Science and Information Engineering *09/2014-01/2016*

- Overall GPA: 4.19/4.5 (3.87/4.0) • Class Ranking: 3/58

Honors and Awards

2021.08	**Scholarship**, UNC Five Years Research Assistantship
2018.06	**Second Prize**, Outstanding Academic Achievement in National Taiwan Ocean University
2018.01	**Excellence Award**, Senior Project Contest in National Taiwan Ocean University
2017.03	**Best Paper Award**, IEEE WAINA-2017
2015.12	**Third Prize Scholarship**, Academic Excellence by National Dong Hwa University
2015.05	**Third Prize Scholarship**, Academic Excellence by National Dong Hwa University

Skills

- Programming: Python, Java, C/C++ • OS: Windows, macOS, Linux
- Tools or Package: MySQL, Git, PyTorch, TensorFlow, SciPy, Scanpy, NumPy, pandas, scikit-learn

Research and Experience

Taiwan Semiconductor Manufacturing Company, Ltd. *2025.07-2025.08*

SUPERVISOR: PING CHIEH WU

Position: Optimal Pattern Correction Tech. Dept III, R&D Summer Internship

GPU Performance Optimization and Workflow Acceleration

- Analyzed OPC and ILT workflows to evaluate computational efficiency across CPU and GPU implementations, and formulated migration and optimization strategies for underperforming functions to accelerate overall runtime performance.
- Conducted GPU performance profiling using NVIDIA Nsight Systems and NVTX, identified critical bottlenecks, and optimized memory transfer patterns to minimize host–device latency and enhance throughput.

CompCy Lab, The University of North Carolina at Chapel Hill *2021.08-Present*

SUPERVISOR: PROF. NATALIE STANLEY

Position: Graduate Research Assistant

My overarching goal is to detect and summarize complex cellular patterns linked to clinical or experimental outcomes assayed through single-cell technologies. I aim to develop advanced AI, machine learning, and large language model (LLM) tools to focuses on automating the analysis of single-cell data.

Segmentation-Free Approaches for Predicting Sample-Level Phenotypes from IMC Data

- Develop segmentation-free approaches for automated diagnostic prediction from spatial signatures using Imaging Mass Cytometry (IMC), focusing on microenvironment analysis.
- Created a segmentation-optimal encoding technique for building diagnostic predictors that accommodate complex cellular morphologies
- Leveraged Large Language Models (LLMs) to generate phenotype-specific cellular microenvironment summaries for enhanced diagnostic insights.

An Advanced Deep-Learning Model Enhancing Per-Sample Feature Representations in Single-Cell Data Through Feature Learning

- Utilizes advanced supervised machine learning techniques, models cells within each patient sample as a discerning subset, and incorporates permutation-invariant architectures for enhanced robustness.
- Computes per-sample feature representations by integrating targeted clinical outcome and supplementary patient covariates.
- Achieved 92% accuracy on CyTOF datasets profiling pregnant women, surpassing the highest baseline by 8% in lung cancer dataset.

Predicting Outcomes in Women with Chlamydia Trachomatis Infection Based on CyTOF Data

- Led predictive bioinformatics analysis of T-cell CyTOF data from multiple Chlamydia-infected women.
- Developed comprehensive three-stage prediction model integrating cell-population discovery, per-sample feature engineering, and clinical outcome prediction using scikit-learn's random forest algorithm.
- Identified crucial frequency and functional responses within specific cell types, achieving a superior prediction accuracy of 93% in forecasting chlamydia follow-up outcomes among coinfected participants, surpassing the baseline by 12%.

Cytocoarsening Graph Reduction for Large Single-Cell Datasets

- Enhances scalability by refining single-cell graph representation across multiple patient samples through integration of phenotypical similarities and clinical/experimental attributes.
- Utilizes NetworkX for graph analysis, supplemented by SciPy and Scanpy for enhanced dataset processing, enabling more efficient graph-based analyses.

Biomedical Informatics Lab, National Taipei University of Technology / National Taiwan Ocean University

2016.02 - 2021.06

SUPERVISOR: PROF. TUN-WEN PAI

Position: Full-time Research Assistant

Integrating Disease Trajectory of Preterm Birth and Whole-exome Sequencing for Facilitating Biomarker Panel Construction

- Developed an efficient testing kit for high-risk preterm birth women in collaboration with biotech companies.

Prevention of high-risk preterm delivery based on disease trajectory and comorbidity from governmental medical records

- Developed a preterm birth detection through preterm disease trajectory pattern analysis. Compared normal pregnancy women with preterm birth women, determined the significant odds ratio of each disease pattern.

Application of the PrefixSpan algorithm for chronic disease analysis and Construction of a metadata schema for medical data in networking applications

- Applied the PrefixSpan algorithm to mine data on patient trajectories for seven specific chronic diseases that have high prevalence rates in Taiwan. Proposed metadata schema for integrating multiple heterogeneous hospitalization records, analyzing the issue of long-term treatment.

Publications

- **Chen, Chi-Jane**, and George, Betsy and Dhawka, Luvna and Evangelista, Baggio and Stanley, Natalie (2026). ”MICRON learns outcome-associated representations of spatial immune microenvironments.” bioRxiv, 2026-04.
- Huang, Jhen-Li, Yang, Cing-Han, **Chen, Chi-Jane**, Chen, Chie-Pein, Pai, Tun-Wen (2025). ”Using historical data and Next-Generation Sequencing technology to investigate biomarkers affecting preterm birth and associated diseases”, PeerJ (under peer review).
- **Chen, Chi-Jane**, Chen, Yuhang , Yun, Sukwon, Chen, Tianlong, Stanley, Natalie (2025). ”Spatial Coordinates as a Cell Language: A Multi-Sentence Framework for Imaging Mass Cytometry Analysis”, Findings of the Association for Computational Linguistics (ACL Findings).
- **Chen, Chi-Jane**, Yi, Haidong, and Stanley, Natalie (2024). ”Conditional Similarity Triplets Enable Covariate-Informed Representations of Single-Cell Data”, *BMC Bioinformatics Journals*.
- Yount, Kacy S., **Chen, Chi-Jane** et al. (2024). ”Unique T cell signatures are associated with reduced Chlamydia trachomatis reinfection in a highly exposed cohort”, *Journal of Clinical Investigation (JCI Insight)*.
- **Chen, Chi-Jane**, Crawford, Emma, and Stanley, Natalie (2023). ”A Graph Coarsening Algorithm for Compressing Representations of Single-Cell Data with Clinical or Experimental Attributes”, *Pacific Symposium on Biocomputing (PSB).* Hawaii.
- Chen, Yit-Jin, **Chen, Chi-Jane** and Chen, Chi-Jim (2018). “Schemes of Data Visualization for Ground Vibration Prediction Induced by Trains”, The 47th International Congress and Exposition on Noise Control Engineering (Inter-Noise 2018), *Institute of Noise Control Engineering.* Chicago.
- Chen, Yit-Jin, Liu, Chih-Hao, Chen, Chi-Jim and **Chen, Chi-Jane** (2018). “Application of Ensemble Learning Algorithm for Ground Vibration Prediction”, *Asian Conference on Engineering and Natural Sciences (ACENS 2018), Higher Education Forum.* Osaka.
- **Chen, Chi-Jane**, Pai, Tun-Wen, Huang, Jhen-Li, Lo, Ying-Tsang, Lin, Shih-Syun and Yeh, Chun-Chao (2017). “Construction of a Metadata Schema for Medical Data in Networking Applications”, *31st International Conference on Advanced Information Networking and Applications Workshops (WAINA), IEEE, 597-600.* Taipei. **(Best paper award)**
- **Chen, Chi-Jane**, Pai, Tun-Wen, Lin, Shih-Syun, Yeh, Chun-Chao, Liu, Min-Hui and Wang, Chao-Hung (2016). “Application of PrefixSpan Algorithms for Disease Pattern Analysis”, *International Computer Symposium (ICS), IEEE, 274-278.* Chiayi.