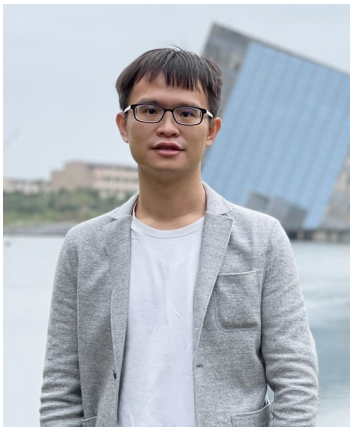
Curriculum Vitae



Name
Chun-Yu Lin

Current Position
Associate Professor
Institute of Bioinformatics and Systems Biology, National Yang Ming Chiao Tung University

Email address
chunyulin@nycu.edu.tw

Education & Professional Experiences (Times New Roman, 11 point)

2023/8 ~	Associate Professor	Institute of Bioinformatics and Systems Biology, National Yang Ming Chiao Tung University
2023/8 ~	Associate Professor (Joint Appointment)	Institute of Data Science and Engineering, National Yang Ming Chiao Tung University
2019/8 ~ 2023/7	Assistant Professor	Institute of Bioinformatics and Systems Biology, National Yang Ming Chiao Tung University
2017/10 ~ 2019/7	JSPS Post-Doctoral Research Fellow	Bioinformatics Center, Institute for Chemical Research, Kyoto University, Japan
2010/9~2014/5	Ph.D.	Institute of Bioinformatics and Systems Biology, National Chiao Tung University
2008/9~2010/7	M.Sc.	Institute of Bioinformatics and Systems Biology, National Chiao Tung University
2004/9~2008/7	B.Sc.	Department of Biotechnology, National Kaohsiung Normal University

Research Interests (Times New Roman, 11 point)
Multi-omics analysis, Network Biology, Bioinformatics, Computational Oncology, and Single-cell Analysis

Selected Publications (※3-5 major papers)

1. Chang, L. Y.[#], Lee, M. Z.[#], Wu, Y.[#], Lee, W. K., Ma, C. L., Chang, J. M., Chen, C. W., Huang, T. C., Lee, C. H., Lee, J. C., Tseng, Y. Y., **Lin, C. Y.*** (2024) Gene set correlation enrichment analysis for interpreting and annotating gene expression profiles, ***Nucleic Acids Research***, 52(3):e17.
2. Chang, L. Y.[#], Hao, T. Y.[#], Wang, W. J.[#], **Lin, C. Y.*** (2024). Inference of single-cell network using mutual information for scRNA-seq data analysis. ***BMC Bioinformatics***, 25: 292
3. Chen, H. H.[#], Hsueh, C. W.[#], Lee, C. H.[#], Hao, T. Y.[#], Tu, T. Y., Chang, L. Y., Lee, J. C., **Lin, C. Y.*** (2023) SWEET: a single-sample network inference method for deciphering individual features in disease, ***Briefings in Bioinformatics***, 24(2):bbad032.
4. **Lin, C. Y.**[#], Lee, C. H.[#], Chuang, Y. H., Lee, J. Y., Chiu, Y. Y., Lee Wu, Y. H., Jong, Y. J., Hwang, J. K., Huang, S. H., Chen, L. C., Wu, C. H., Tu, S. H., Ho, Y. S.*, and Yang, J. M.* (2019) Membrane protein-regulated networks across human cancers, ***Nature Communications***, 10(1):3131.

5. **Lin, C. Y.** *, Ruan, P. Y. , Li, R. M., Yang, J. M., See, S., Song, J. N., and Akutsu, T.* (2019) Deep Learning with Evolutionary and Genomic Profiles for Identifying Cancer Subtypes, ***Journal of Bioinformatics and Computational Biology***, 17(3), 1940005. *Co-corresponding authors

Lecture Title

Patient-specific network-based interpretable machine learning predicts immune checkpoint inhibitor response in cancer patients

Abstract (500 words maximum)

Immune checkpoint inhibitors (ICIs) have transformed cancer therapy by producing durable responses in a subset of patients. However, overall response rates remain limited, and currently used biomarkers, such as PD-1/PD-L1 expression and tumor microenvironment-related features, often show insufficient predictive accuracy and poor cross-cohort generalizability. Network-based biomarkers have emerged for predicting ICI response, but most are derived from aggregate protein-protein interaction (PPI) networks compiled across diverse cell types and biological states or cohort-level co-expression networks. As a result, these networks may obscure patient-specific variation in pathway activity and tumor-immune biology. Recently, single-sample network (SIN) inference methods offer a way to better capture inter-patient heterogeneity, but predictive frameworks that leverage SINs for ICI response modeling remain scarce.

In this talk, I will present SNIPE (Single-sample Network-based analysis for predicting ImmunotheraPy Efficacy), an interpretable machine-learning framework for predicting ICI response from patient-level transcriptomic data. SNIPE is motivated by our prior work in network medicine for extracting individualized biological information from omics data. In particular, it builds on the concept of sample-specific weighted correlation networks (SWEET), which was developed to infer single-sample networks (SINs) that better capture shared and individual-specific molecular wiring than conventional cohort-level networks. By leveraging this patient-centered network perspective, SNIPE constructs high-confidence single-sample networks (hcSINs) that provide a more robust representation of individual tumor biology. To further improve functional interpretation, SNIPE also incorporates single-sample gene set correlation enrichment analysis (ssGscore), an extension of our Gscore method. Whereas Gscore was originally designed to evaluate the association between differentially expressed genes and curated pathways or gene sets using the dataset-derived co-expression network, ssGscore adapts this idea to the single-sample level, enabling the quantification of personalized pathway activity patterns from each patient's inferred network context. Combined with ssGSEA, this strategy generates personalized ICI-response pathway signatures (PIPSs) for each patient. PIPSs were used to train and compare logistic regression, random forest, SVM, and XGBoost, with an across-study evaluation design to assess cross-cohort generalizability. Finally, SHapley Additive exPlanations (SHAP) was applied to quantify pathway contributions and provide biologically interpretable explanations of model predictions.

Across five independent melanoma cohorts comprising more than 300 ICI-treated patients with matched transcriptomic data and ICI response outcomes, SNIPE outperformed predictors based on aggregate PPI-network features and conventional ICI biomarkers. Importantly, the SNIPE-derived signatures were strongly associated with tumor-immune microenvironment characteristics, including leukocyte fraction and CD8+ T-cell infiltration, supporting their biological plausibility. Overall, SNIPE illustrates how patient-specific network modeling and Gscore-derived pathway interpretation can be integrated into an interpretable AI framework for precision immuno-oncology, with potential extension to additional cancer types and therapeutic settings.