

# Yung-Han (Tina) Chang

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## EDUCATION

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### The University of Texas MD Anderson Cancer Center

Houston, TX

*Ph.D., Quantitative Science, Biostatistics and Bioinformatics track*

*May 2028*

- Selected Courses: Bayesian Statistics, Statistical Genetics, Clinical Trial Design
- Quantitative Science Program Travel Award (USD 750)

### University of California, Los Angeles

Los Angeles, CA

*M.S., Biostatistics*

*Jun. 2024*

### National Taiwan University

Taipei, Taiwan

*B.S., Agronomy, Biostatistics and Bioinformatics track*

*Jun. 2020*

## EXPERIENCE

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### Graduate Student Researcher

Aug. 2024 - Present

*MD Anderson Cancer Center, Department of Biostatistics*

*Houston, TX*

- Conducting a Bayesian mediation analysis with a Weibull AFT model and mixture priors to identify significant genetic causal mediation pathways in time-to-event outcomes.
- Applied an empirical Bayes two-group framework for replication analysis in three lung cancer Genome-Wide Association Studies (GWAS), identifying 44% more functionally important SNPs.
- Applied multivariate predictive modeling to conduct isoform-level transcriptome-wide association studies (TWAS) for pan-cancer genetic risk, identifying 164% more significant associations compared to traditional methods. [\[Link\]](#)

### Graduate Student Researcher

Sep. 2022 - Jun. 2024

*UCLA, Department of Computational Medicine*

*Los Angeles, CA*

- Examined factors underlying the limited portability of gene expression imputation across ancestries.

### Data Scientist

Sep. 2021 - Sep. 2022

*National Taiwan University Hospital*

*Taipei, Taiwan*

- Conducted a GWAS of headache in the Taiwan Biobank, identifying genetic factors contributing to disease risk. [\[Link\]](#)
- Performed a nationwide retrospective cohort study of 20,022 sepsis patients, demonstrating that sepsis is an independent risk factor for in-hospital cardiac arrest. [\[Link\]](#)
- Assisted in predictive modeling and external validation of *FluDeep*, a deep learning system combining chest X-rays with clinical data to assess influenza mortality risk. [\[Link\]](#)

### Data Specialist Intern

Oct. 2017 - Aug. 2018

*IQVIA*

*Taipei, Taiwan*

- Collaborated with analysts to generate data visualizations and prepare client-facing marketing reports, providing actionable insights for pharmaceutical stakeholders.
- Conducted quality control assessments on pharmaceutical sales and marketing data for international pharmaceutical companies in Asia.

## SKILLS

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- **Programming & Computing:** R, Python, SAS, Bash, MySQL, Linux, High Performance Computing
- **Analysis Methods:** GWAS, TWAS, Colocalization, QTL analysis, Rare Variant Analysis, Gene-set Enrichment Analysis, Meta-analysis, Polygenic Score Construction, Machine Learning
- **Version Control:** Git/GitHub

## PUBLICATIONS

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- **Yung-Han Chang**, Sean T Bresnahan, S Taylor Head, Tabitha A Harrison, Yao Yu, Chad D Huff, Bogdan Pasaniuc, Sara Lindström, Arjun Bhattacharya. [Isoform-level analyses of 6 cancers uncover extensive genetic risk mechanisms undetected at the gene-level.](#) *British Journal of Cancer*, 2025. *Emerging Leaders in Cancer Special Edition.*
- Meng-Han Tsai, Sung-Chu Ko, Amy Huaishuan Huang, Lorenzo Porta, Cecilia Ferretti, Clarissa Longhi, Wan-Ting Hsu, **Yung-Han Chang**, Jo-Ching Hsiung, Chin-Hua Su, Filippo Galbiati, Chien-Chang Lee. [Predicting mortality in hospitalized influenza patients: integration of deep learning-based chest X-ray severity score \(FluDeep-XR\) and clinical variables.](#) *Journal of the American Medical Informatics Association*, 2024
- Ye Liu, Chia-Hung Yo, Jiun-Ruey Hu, Wan-Ting Hsu, Jo-Ching Hsiung, **Yung-Han Chang**, Shyr-Chyr Chen, Chien-Chang Lee. [Sepsis increases the risk of in-hospital cardiac arrest: a population-based analysis.](#) *Intern Emerg Med* 19, 353–363 (2024)
- Wan-Ting Hsu, Yu-Ting Lee, Jasmine Tan, **Yung-Han Chang**, Frank Qian, Kuei-Yu Liu, Jo-Ching Hsiung, Chia-Hung Yo, Sung-Chun Tang, Xia Jiang, Chien-Chang Lee. [Genome–phenome wide association study of broadly defined headache.](#) *Brain Communications*, Volume 5, Issue 3, 2023
- Chien-Chang Lee, Meng-tse Gabriel Lee, I-Hsuan Huang, Jasmine Tan, Zachary R McCaw, Ke-Ying Su, Tzu-Chun Hsu, Ruby YJ Huang, Po-Hsiu Kuo, Shyr-Chyr Chen, **National Taiwan University Hospital, Health Data Science Research Group.** [Genome-wide association study of primary dysmenorrhea in the Taiwan Biobank validates associations near the NGF and IL1 gene loci.](#) *J Hum Genet* 67, 449–458 (2022)

## PRESENTATIONS

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### Formal Statistical Replication Analysis in Lung Cancer Genome-Wide Association Studies

- Poster presentation at the International Genetic Epidemiology Society (IGES) Annual Meeting, Cologne, Germany, Aug. 2025.
- Poster presentation at the American Society for Human Genetics (ASHG) Annual Meeting, Boston, MA, Oct. 2025.

### Isoform-level analyses of 6 cancers uncover extensive genetic risk mechanisms undetected at the gene-level.

- Oral presentation in the Trainee Works in Progress Session, Houston, TX, Jul. 2025.
- Poster presentation at the ASHG Annual Meeting, Denver, CO, Nov. 2024.

### Portability of TWAS Gene Expression Across Ancestries.

- Poster presentation at the IGES Annual Meeting, Nashville, TN, Nov. 2023.
- Poster presentation at the ASHG Annual Meeting, Washington DC, Nov. 2023.