

Kuan-Hung (Peter) Yeh

707-727-5012 | k1yeh@ucsd.edu | [Linkedin](#) | [Github Website](#)

Biostatistician and Real-World Data Scientist with 4+ years of expertise in statistical modeling and machine learning using claims and EHR datasets. Passionate about leveraging real-world evidence to support clinical decision-making and transform diagnostics and treatment through data-driven innovation.

Languages & Toolkits: R (Markdown, Shiny), Python, SAS, SQL, Git/GitHub

Research Topics: Real-World Evidence (RWE), Causal Inference, Survival Analysis, Clinical Trials

Education

University of California, San Diego

Ph.D in Biomedical Informatics (Overall GPA: 4.0/4.0)

San Diego, CA

Sep. 2023 – Present

University of California, Los Angeles

Master of Science in Biostatistics (Overall GPA: 3.93/4.0)

Los Angeles, CA

Jun. 2023

National Taiwan University

Bachelor of Science in Public Health, Biostatistics Track (Overall GPA: 3.75/4.0)

Taipei, Taiwan

Jun. 2020

Experience

Graduate Researcher

Department of Biomedical Informatics, UCSD Health

Jan. 2024 – Present

La Jolla, CA

- Collaborated with multiple clinical teams to design and conduct research studies, communicating scientific findings effectively and proactively solving problems to inform treatment safety and efficacy.
- Generated real-world evidence in Gastroenterology using Optum claims datasets, enhancing treatment strategy evaluation through advanced survival analysis, multiple imputation, and propensity score methods.

Biostatistician Intern

Foundation Medicine, Inc.

Jun. 2022 – Sep. 2022

Boston, MA

- Developed new criteria using simulation for diagnostic assay precision studies, boosting statistical power by 90%.
- Contributed to the development of statistical software tools, including R function and Shiny app [Demo].
- Conducted statistical analyses (e.g., sample size, power, precision) to ensure quality assurance for new reagent design in FoundationOne Liquid CDx.

Graduate Consultant

Department of Computational Medicine & Medicine Statistics, UCLA

May. 2022 – Jun. 2023

Los Angeles, CA

- Performed mediation analyses and data visualizations for a three-arm randomized controlled trial
- Developed a survival data simulation pipeline to estimate how genetic architecture impacts in survival modeling and polygenic risk score stratification.

Undergraduate Researcher

Biostatistics & Bioinformatics Core lab, NTU

Jun. 2019 – Feb. 2020

Taipei, Taiwan

- Developed the first Asian colon cancer prognostic model using Taiwan Cancer Registry and US-based SEER data.
- Provided a robust overall survival/risk prediction to facilitate clinical shared decision-making [Web].

Selected Publications

- Haynesworth, A., **Yeh, K. H.**, Lee, H. H., Kirkpatrick, M., Boland, B. S., Syal, G., Xu, R., & Singh, S. (2025). Long-Term Outcomes of an Infliximab-First Versus Vedolizumab-First Treatment Strategy in Biologic-Naïve Patients With Ulcerative Colitis. *Alimentary pharmacology & therapeutics*, 61(4), 693–701. <https://doi.org/10.1111/apt.18441>
- Chan, H. C., Huang, C. C., Huang, C. C., Chattopadhyay, A., **Yeh, K. H.**, Lee, W. C., Chiang, C. J., Lee, H. Y., Cheng, S. H., & Lu, T. P. (2022). Predicting Colon Cancer-Specific Survival for the Asian Population Using National Cancer Registry Data from Taiwan. *Annals of surgical oncology*, 29(2), 853–863. <https://doi.org/10.1245/s10434-021-10646-2>
- **Yeh, K. H.**, Lin, C.H., Hsiao, T.H. and Lu, T.P., 2020, December. Genome-wide association study (GWAS) on metabolic syndrome in subjects with abdominal obesity in a Taiwanese population. In 2020 IEEE International Conference on Bioinformatics and Biomedicine (BIBM) (pp. 1403-1407). IEEE.