

# Speaker Bio

**Dr. Jia-Ying Su** is a Postdoctoral Scholar at the Institute of Statistical Science, Academia Sinica, in Taipei, Taiwan. She received her Ph.D. in Biomedical Informatics from National Yang Ming Chiao Tung University in 2025, following an M.S. in Epidemiology and Preventive Medicine from National Taiwan University (2018) and a B.S. in Public Health from China Medical University (2015).

Her research centers on computational biology and statistical modeling of genetic variants linked to human diseases. Dr. Su has made notable strides in elucidating RNA splicing processes, the impact of untranslated region (UTR) mutations on translation, and the factors influencing RNA stability. She has also developed novel computational tools to predict splicing disruptions caused by mutations, including SpliceAPP—an interactive web server designed to support the broader research community.

Her work has been published in journals such as Nature Structural & Molecular Biology, eLife, and BMC Genomics. As a first author or co-lead contributor on several publications, she has shown expertise in advanced genomic profiling techniques, multiplexed functional assays, and high-dimensional mediation analysis.

Beyond her primary research, Dr. Su investigates gene expression variability in cancer, genetic susceptibility to hepatitis virus infection, and immunometabolic factors influencing infection outcomes in critically ill patients. Her contributions have been acknowledged through awards like the Academia Sinica Research Performance Fellowship (2023) and the Institute of Statistical Science Poster Competition Award (2019).