

Polygenic risk construction for type 2 diabetes using the Taiwan  
Biobank and public summary statistics for East Asian  
individuals

Ren-Hua Chung

Division of Biostatistics and Bioinformatics, Institute of Population  
Health Sciences, National Health Research Institutes

**Abstract**

Type 2 diabetes (T2D) is a complex disease caused by multiple genes, environments and their interactions. Several large-scale genome-wide association studies have been performed for T2D for different populations such as European, African American, and East Asian individuals. Due to the recent development of polygenic risk score (PRS) construction method that considers trans-ethnic effects of genetic variants (i.e., PRS-CSx), we aimed to apply PRS-CSx to the Taiwan Biobank data and public summary statistics to calculate the PRS for East Asian individuals. Different scenarios were used to calculate the PRS, including adjusting and without adjusting for BMI in the association tests, and sex-combined and sex-specific effect size estimations. The PRS calculated under different scenarios were evaluated using a separate validation dataset from the Taiwan Biobank. We evaluated the performance of the PRS using different metrics, such as area under the curve, variation of T2D explained by the PRS, and odds ratio per standard deviation change of the PRS for T2D. The PRS with the best performance was selected and a final test dataset also from the Taiwan Biobank was used to validate the results.