

Abstract

Ischemic stroke susceptibility is significantly influenced by polygenic factors, yet current Polygenic Risk Scores (PRS) are produced from predominantly European Genome-Wide Association Studies (GWAS). Using European ancestry genetic weights to non-European cohorts often reduces prediction accuracy. Southeast Asia, specifically Indonesia, remains very underrepresented in genomic consortia, leaving a huge gap in determining the most effective models for risk stratification. To address this, the study develops a standardized bioinformatics cross-ancestry PRS pipeline and evaluates its computational feasibility through a matched pilot study in an Indonesian cohort

Keywords: *Ischemic Stroke, Polygenic Risk Score, Ancestry Adjustment, Bioinformatics pipeline, Precision Medicine, Indonesian population*