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Titel:

Accessible Software for Genotype–Phenotype Analyses

Abstract:

Understanding the relationship between genotype and phenotype remains a central challenge in medical research. In case studies, the comparison with larger reference datasets is useful for verifying candidate genes or variants. While common approaches such as genome-wide association studies or polygenic risk scores usually focus on a single trait, many complex diseases require the integration of multiple factors, including demographic and clinical data. We introduce a flexible tool for genotype–phenotype analyses that allows users to define cohorts based on multiple traits. The tool supports standard analyses such as burden testing through an efficient and intuitive interface, making it especially suitable for exploratory studies and researchers without extensive bioinformatics expertise.