

Post-GWAS Analysis

Introduction of Post-GWAS Analysis

- Genome-wide association study (GWAS) is a method to find variant sequences in the whole genome of humans or plants and animals. The principle of whole-genome association analysis is to use millions of single nucleotide polymorphisms (SNPs) in the genome as molecular genetic markers to conduct control analysis or correlation analysis at the whole-genome level. It is a strategy of discovering gene mutations that affect complex traits through comparison. GWAS analysis methods can discover and identify a large number of genetic variations associated with complex traits.
- Although a large number of SNPs can be identified through GWAS research, the SNP sites that can explain biological functions are very limited. And as more and more SNPs are found in non-coding regions, they affect the expression of specific genes through distal or proximal regulatory mechanisms. People have reason to believe that changes in gene expression regulated by SNPs are an important mechanism that affects traits. Therefore, researchers from the University of Chicago developed a gene-based association analysis software- PrediXcan using machine learning methods. PrediXcan conducts post analysis on the results of GWAS array to establish the correlation between SNP-regulated gene expression and traits.



Fig 1 Analysis Process of Post-GWAS Analysis.

Analysis Content

- Conduct group stratification analysis, analyze and understand the stratification information of materials.
- Perform linkage disequilibrium analysis, the level of linkage disequilibrium can determine the accuracy of the association analysis and the number of selected markers.
- Combining population genotype and phenotype data, use a mixed linear model to perform genome-wide association analysis, and perform gene function annotations on the analyzed sites that are strongly associated with the target trait.
- Use PrediXcan's predict function to estimate the gene expression level regulated by SNP.
- Association analysis of gene expression and target traits.

Application Filed

- Research on susceptibility genes for tumors and complex diseases.

- Disease warning, genetic counseling, early diagnosis, risk assessment and drug selection.
- Research on crop specific traits.

MedAI uses artificial intelligence to provide one-stop service for life science research. Here, we provide post-GWAS array analysis based on PrediXcan according to customers' requirement. If you have any GWAS analysis-related needs, please feel free to contact us, we will provide you with the most professional and considerate service according to your needs. We sincerely look forward to working with you!