POLYGENIC
RISK SCORE

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01
Main Logic

- Minor effects of multiple SNPs are aggregated into one score
- To explain the risk of an individual having the subject trait
- Calculation of an individual-level score by summation of weighted SNP effect sizes of risk alleles

- To take linkage disequilibrium into account
- To overcome overfitting

02

Why implement PRS instead of directly summing up GWAS effect sizes?

03
Implementation

- Exclusion of family members
- P-value thresholding to exclude variants that have high uncertainty
- Pruning to select 1 representative variant from each haplotype block