

PowerGWAS/QT Help Topics

PowerGWAS/QT is a statistical program developed for medical investigators to estimate statistical power of detecting SNPs association with quantitative trait (QT) in genome-wide association studies (GWAS).

Power Detection based on ANOVA/F-Test is the default method. It can answer following question: "if the SNP explains x% of the variation (Heritability), with sample size n, what is the statistical power of my study".

Note: The variation explained by a single SNP is usually less than 10%.

Above power calculation is based on the assumptions that the SNP is the causative genetic variant. If you know or would like to make assumptions on the LD between the SNP and the causative variant, you can input a LD number that is less than 1.0. The program will tell you what is the actual sample size needed to reach the result power.

Power Detection based on t-test: when pilot studies have been conducted and prior information is available, or you are comfortable to make assumptions on allele / genotype frequencies, phenotype means and the genetic model, then you are allowed to estimate power based on a t-test.

Note: This function is not available yet.