- GWAusage -
Comprehensive package for complex trait GWAS implementing data mining

----

Sheng Zhang: Developer
Owen Baker: Developer
William Schwarzmann: Developer
Richard Copin: Writer
Brandon Blobner: Lead
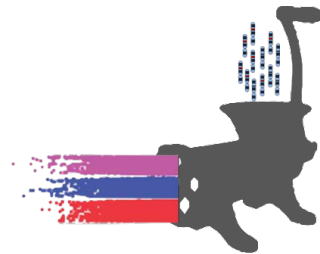
Genome-wide Association Study (GWAS)

- 1492 cases of recurrent acute or chronic pancreatitis

- 869 controls

- 9,838,266 SNPs
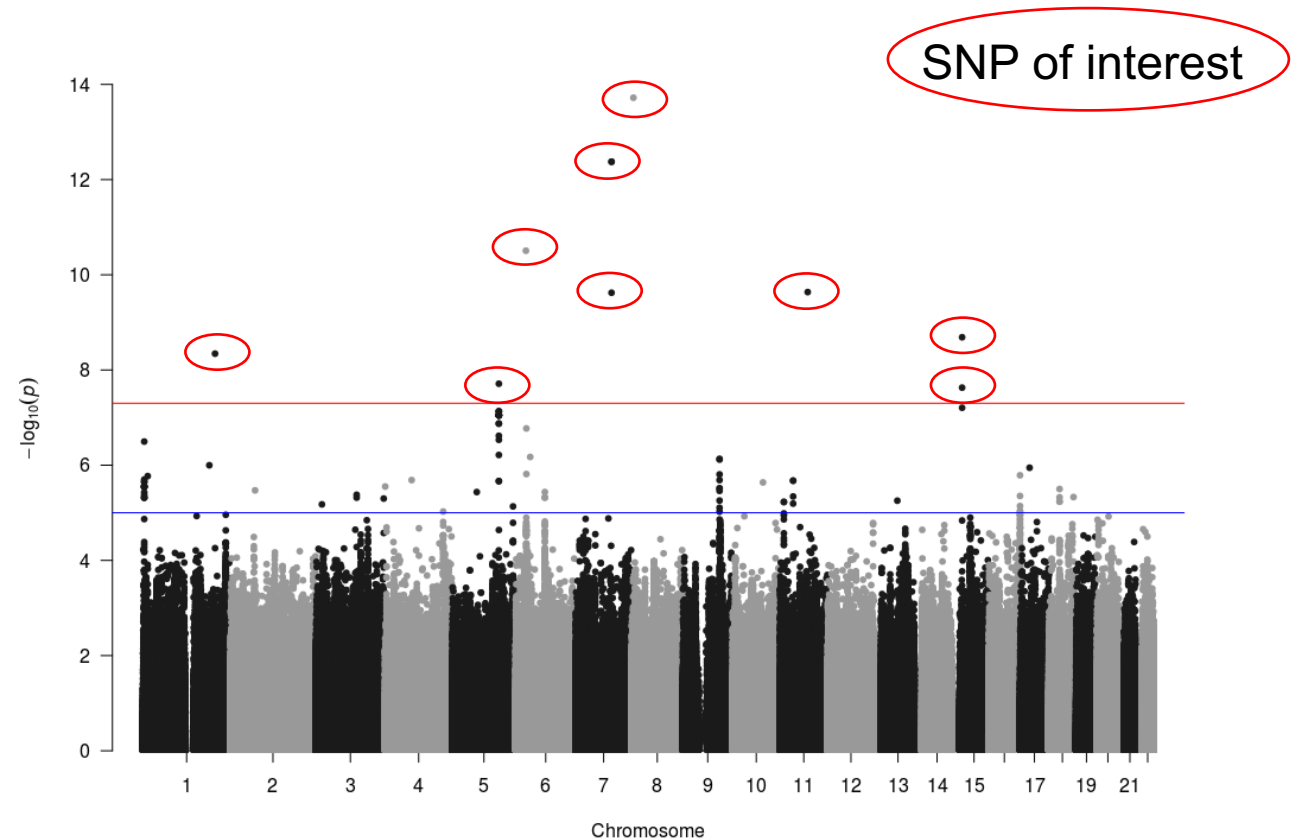
Module 1	Input / Filtering using Plink	• Formatting the genotyping data (from vcf to plink format) • Filtering SNPs and individuals
Module 2	Module generation and stepwise regression R	• Generate the full model from a phenotype and covariant file • Stepwise regression to determine the contributing covariates • GCTA generate a genetic relatedness metrics • Conduct GWAS
Module 3	Results filtering	• Visual representation • Filter the significant loci (determine thresholds) • locusZoom
Module 4	Data mining	• Interrogate public databases to determine the significance of each SNPs in different conditions