

Adjustment

Read inputs

Read
Config
file

Genotype file
Phenotype file
GWAS model
Significance
Correction
N associations
QC filters

Read Input Data

Preprocessing

Clean

Filter

Format

Multi Analysis

Polyploids

GWASpoly

SHEsis

Diploids

Plink

Tassel

Integration

Scan

Summarize

Report

SNPs tables

Shared SNPs

SNPs profiles

Associations

Shared chromosomes