

MultiGWAS

Tetraploid tools:

☒ GWASpoly

☒ SHEsis

Diploid tools:

☒ PLINK

☒ TASSEL

Run

Inputs

Outputs

Results

Files

Input/Output:

Output Folder: /home/lg/example

Select...

Input Genotype: example-genotype.tbl

Select...

Input Phenotype: example-phenotype.tbl

Select...

GWAS Parameters:

GWAS Model: Full

Significance Level: 0.05

Correction Method: Bonferroni

Number of Best SNPs: 10

Filtering: TRUE

Quality Control Filters:

Minimum Minor Allele Frequency (MAF) for a SNP to be kept: 0.01

Maximum proportion of missing values for a SNP to be kept: 0.1

Maximum proportion of missing values for a sample to be kept: 0.1

Filters out SNPs with HWE exact test p-value below threshold: 1e-10

Terminal

```
default:
genotypeFile : "example-genotype.tbl"
phenotypeFile : "example-phenotype.tbl"
significanceLevel : 0.05
correctionMethod : "Bonferroni"
gwasModel : "Full"
nBest : 10
filtering : TRUE
MAF : 0.01
MIND : 0.1
GENO : 0.1
HWE : 1e-10
tools : "GWASpoly SHEsis PLINK TASSEL"
```

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