

EAGLE Home Read Genotypes Read Phenotypes Read Z matrix (if needed) Read Map (optional) Analyse More -

GENOTYPIC DATA

🔍 Hover here for details

Step 1: Choose file type

vcf
 PLINK
 Text/ASCII

Assign marker genotypes to snp genotypes AA, AB, BB, and missing

Step 2: Specify available memory in Gbytes

Step 3: Select marker file

or enter file name (including full path)

Step 4: Upload file

Getting number of individuals and snp from file ...
 Beginning creation of reformatted file ...
 Reading marker data ...

First 5 lines and 12 columns of the marker text file.

```

1 1 1 1 1 1 1 1 1 1 1 1
2 2 2 2 2 2 2 2 2 2 2 2
1 1 1 1 1 1 1 1 1 1 1 1
2 2 2 2 2 2 2 2 2 2 2 2
0 0 0 0 0 0 0 0 0 0 0 0
        
```

Taking transpose of marker data and writing untransposed and transposed

Summary of Marker File

```

File type:          text
Reformatted ASCII file name: /var/folders/zc/ds_yy_s17jd05d_s3sqsm2c000
Number of individuals: 800
Number of loci:     70484
File size (gigabytes): 0.1691616
Available memory (gigabytes): 8
        
```

Writing of marker data to disc is complete ...

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GENOME-WIDE ANALYSIS

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Step 1: Choose trait

Step 2: Choose fixed effects

Sex Batch Weight.Average
 Sex+Batch+Weight.Average

Step 3: Specify number of cpu

Step 4: Specify lambda value (controls the false positive rate)

Set manually
 Set automatically (via permutation)

Specify desired false positive rate.

Specify number of replicates.

Step 5: Perform genome-wide analysis

Number of cores being used for calculation is .. 4

Calculating variance components for null model
 Calculating extBIC for null model
 Calculating matrices that will be used in alternate model.
 Analysing 100 permutations.

Multiple-Locus Association Mapping
Version 1.2

Iteration 1: Searching for most significant marker-trait association.

Number of cores being used for calculation is .. 4
 Significant marker-trait association found.

New results after iteration 1 are

SNP	Chrm	Map Pos	Col Number
Null Model			

Iteration 2: Searching for most significant marker-trait association.

Significant marker-trait association found.

New results after iteration 2 are

SNP	Chrm	Map Pos	Col Number
Null Model			
M12008C5	5	124991768	22264

Iteration 3: Searching for most significant marker-trait association.

Significant marker-trait association found.

New results after iteration 3 are

SNP	Chrm	Map Pos	Col Number
Null Model			
M12008C5	5	124991768	22264
M1530C6	6	17541026	23521

Iteration 4: Searching for most significant marker-trait association.

Significant marker-trait association found.