AT data

Three files: .ped, .map, and .pheno files.

**Genotype.ped**

1307 rows, each row starts with FID IID, and other 4 fields (listed below); it’s then followed by SNPs (ACGTs). Total field (column) is 6+2\*N (N is the number of SNPs), two fields represent one allele (diploid plant).

The fist 6 fileds are:

1. Family ID ('FID')
2. Within-family ID ('IID'; cannot be '0')
3. Within-family ID of father ('0' if father isn't in dataset)
4. Within-family ID of mother ('0' if mother isn't in dataset)
5. Sex code ('1' = male, '2' = female, '0' = unknown)
6. Phenotype value ('1' = control, '2' = case, '-9'/'0'/non-numeric = missing data if case/control)

e.g. 9381 9381 0 0 0 0 T T …

9380 9380 0 0 0 0 C C …

9378 9378 0 0 0 0 T T …

……

General introduction of .ped file can be found at

<https://easygwas.ethz.ch/faq/view/15/>

**phenotypes.pheno**

1307 (+1) rows, (with header), and 109 fields (columns)

ALL fields in the 1st row (header):

FID IID Emco5 At1 After\_Vern\_Growth Secondary\_Dormancy Germ\_in\_dark DSDS50 Seed\_bank\_133-91 Storage\_7\_days Storage\_28\_days Storage\_56\_days At1\_CFU2 As As\_CFU2 Bs Bs\_CFU2 At2 At2\_CFU2 As2 As2\_CFU2 Emwa1 Trichome\_avg\_C Trichome\_avg\_JA Aphid\_number Bacterial\_titer LD LDV SD SDV FT10 FT16 Emoy\* FT22 0W 2W 4W 8W FLC FRI 8W\_GH\_FT 8W\_GH\_LN 0W\_GH\_FT Hiks1 0W\_GH\_LN FT\_Field FT\_GH LN10 LN16 LN22 Li7 B11 Na23 Mg25 Noco2 P31 S34 K39 Ca43 Mn55 Fe56 Co59 Ni60 Cu65 Zn66 <i>avrPphB</i> As75 Se82 Mo98 Cd114 Seed\_Dormancy FT\_Diameter\_Field FT\_Duration\_GH LC\_Duration\_GH LFS\_GH MT\_GH <i>avrRpm1</i> RP\_GH FW DW LES YEL LY Silique\_16 Silique\_22 Germ\_10 Germ\_16 <i>avrRpt2</i> Germ\_22 Width\_10 Width\_16 Width\_22 Chlorosis\_10 Chlorosis\_16 Chlorosis\_22 Anthocyanin\_10 Anthocyanin\_16 Anthocyanin\_22 <i>avrB</i> Leaf\_serr\_10 Leaf\_serr\_16 Leaf\_serr\_22 Leaf\_roll\_10 Leaf\_roll\_16 Leaf\_roll\_22 Rosette\_Erect\_22 Hypocotyl\_length Seedling\_Growth Vern\_Growth

e.g. FID IID Emco5 At1 …

9381 9381 nan nan …

9380 9380 nan nan …

9378 9378 nan nan …

…

General introduction of .pheno file can be found at

<https://easygwas.ethz.ch/faq/view/16/>

**Genotype.map**

214 051 rows, each represent a SNP; 4 fields (columns) each row. Columns are: Chromosome code, SNP(Variant) identifier, Position in morgans or centimorgans (optional; also safe to use dummy value of '0'), Base-pair coordinate

e.g. Chr1 Chr1\_657 0 657

Chr1 Chr1\_3102 0 3102

Chr1 Chr1\_4648 0 4648

Chr1 Chr1\_4880 0 4880

…