# Make pheno: How does it work

In LDAK, --make-pheno follows the heritability models.

Example commands:

${dir\_LDAK} \

  --make-phenos ${dir\_RA}/data/makepheno/Trait\_1 \

  --bfile ${dir\_data}/geno \

  --weights ${dir\_RA}/data/geno\_weighting\_thin.thin \

  --power -0.25 \

  --her 0.9 \

  --num-phenos 5 \

  --num-causals 50000 \

  --extract ${dir\_RA}/data/snps\_1\_to\_12\_geno.txt

Required options:

--bfile: the genotype files, with .bed/.bim/.fam

--weights: the predictor weightings, serves as in the following equation.

(1)

--power: to specify how the predictors are scaled, as in the above equation.

--her: to specify the heritability for the simulated phenotype, serving as .

--number-phenos: the number of phenotypes to generate at once.

--num-causals: to specify the number of SNP predictors contributing to the phenotype.

--extract: a file with a list of SNP ID, and removes all **unlisted** variants from the current analysis. In this analysis, the SNPs in the first half chromosomes are genetically related to the phenotype, and the second half are non-genetically related.

A screenshot of a computer

Description automatically generated

Fig. 1 Example of a phenotype file

As shown in Fig. 1, a phenotype file contains FID, IID and Phenotype values. For a simulated phenotype, the values are standardized.

(2)

When X and Y are standardized, we assume that