

Manual for iGS

iGS: an Integrated Graphical User Interface Software for Genomic Selection

Version 0.1

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gBLUP

EM-LASSO

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Data format

To simplify the usage of this software, we only support one data format, other common formats (HapMap, vcf and plink ped format) could be easily transformed by using other tools (like blink, R).

Phenotype data

Header must be provided in phenotype data. And the first column will be taken as the individual name. Multiple phenotypes are supported and users could select the certain phenotype for analysis. Missing phenotype was indicated by NA.

Taxa	phe1	phe2	phe3
Ind1	223.75855	88.291641	47.405383
Ind2	240.02525	NA	49.017183
Ind3	NA	97.474841	48.928283
Ind4	228.80225	89.714241	48.544283
Ind5	250.11015	114.00184	NA
Ind6	239.54475	114.08254	NA
Ind7	245.35535	102.22144	48.693983
Ind8	231.31385	107.11114	48.928283

Genotype data

Covariate data