This additional tool (predict\_v2) predicts the genetic value for some test data set based on estimated genetic effects from a training set. You can wrap everything, for example, in a script. I have prepared a shell script with varying gamma for you though I have never applied it on my own. Please, modify it the way you want. Also, you likely need some different gamma for epistatic effects.

Input for predict\_v2 is actually predict.par, but in the shell script predict\_0.par is modified; it contains the dummy codes.

&input

genofile="Data/XTest.txt", … Genotypes in test set

effectfile="output/DummyOut.eff", … effect estimates, output from fbayesWG

colgebv=3, … column with genetic effects in file above

skiplines=1, … skip one header line

solveDom=.false., … as usual

solveEpi=.false., … as usual

simfile="none.txt", … NA, I used this in a simulation study and plotted simulated effects vs. estimated effects

tbvfile="Data/yTest.txt", … true breeding values or observed phenotypes for later calculation of correlation with predicted genetic values, only 1 column vector!

outfile="output/gebv\_DummyOut.txt", … output file for predicted genetic values (columns for additive part, additive+dominant part, add+dom+epi part)

plotfile="none.R", … NA, some file with R-code for plotting simulated vs. estimated effects

plot=.false., … if false, simfile and plotfile are neglected

reparamMethod=2, … as usual

standardise=.true., … experimental, leave at true

maf=0.01 … as usual

/