```r
1.    ##Genomic prediction example using rrBLUP and BLR packages###

2.    setwd('/home/williams/Desktop/gwas_examples')

3.    library(rrBLUP)

4.    ## Import phenotypes. Heritability of this trait is only 0.33
5.    pheno <- read.csv('pheno.csv')

6.    ##Import marker data
7.    maizeMrks <- read.csv('maizeMrks.csv', row.names=1)


8.    ## Let's split the dataset into a set for estimating marker
      effects and choosing markers and a set for validation. 200 in
      training pop and 102 in validation pop
9.    phenoEst <- pheno[1:200, ]
10.   phenoValid <- pheno[201:302, ]
11.   mrksEst <- as.matrix(maizeMrks[1:200, ])
12.   mrksValid <- as.matrix(maizeMrks[201:302, ])


13.   ##Estimate marker effects using rrBLUP package and make
      predictions in validation population
14.   mrkEffs <- mixed.solve(y=phenoEst$Yield, Z=mrksEst)$u
15.   gebvVec1 <- mrksValid%*%mrkEffs
16.   (predAb1 <- cor(gebvVec1, phenoValid$Yield))


17.   ##Here, use G-BLUP (leverage genomic relationships) rather than
      RR-BLUP (estimate marker effects individually)
18.   gebvVec2 <- kinship.BLUP(y=phenoEst$Yield, G.train=mrksEst,
      G.pred=mrksValid)$g.pred
19.   (predAb2 <- cor(gebvVec2, phenoValid$Yield))

20.   ##Compare the two accuracy estimates

21.   ##Actually, the phenotypes used above are simulated phenotypes.
      We can import the true genetic values and calculate prediction
      accuracy
22.   genoVal <- read.csv('geno.csv')

23.   genoValid <- genoVal[201:302, ]

24.   (predAcc <- cor(gebvVec1, genoValid$Yield_g))

25.   ##Use BLR package to implement Bayesian LASSO regression

26.   ##First, need to set prior on regularization parameter, lambda
27.   DF = 5
28.   h2 = 0.33
29.   Vy = var(phenoEst$Yield)
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30.   Se = Vy*(1-h2)*(DF-2)
31.   MSx = sum(apply(FUN=var, MARGIN=2, X=mrksEst))
32.   Sr = Vy*h2*(DF-2)/MSx

33.   ##Calculate starting point of lambda
34.   lambda = sqrt(2*(1-h2)/h2*MSx)

35.   ##Set shape and rate priors
36.   shape <- 1.01
37.   rate <- (shape-1)/lambda^2

38.   ##Create list with prior informatoin
39.   prior=list(varE=list(df=DF, S=Se), lambda=list(type='random',
      value=lambda, shape=shape, rate=rate))

40.   ##Here, we'll use a small number of iterations and burnin to save
      time. In real life, use 2000 burnin and ~10,000 iterations.
41.   model1 <- BLR(y=phenoEst$Yield, XL=mrksEst, nIter=1000,
      burnIn=200, prior=prior)
42.   str(model1)
43.   model1$bL

44.   ##Calculate GEBVs using Bayesian LASSO estimates
45.   gebvVec3 <- mrksValid%*%model1$bL

46.   plot(gebvVec1, gebvVec3)
47.   cor(gebvVec1, genoValid[, 2])
48.   cor(gebvVec3, genoValid[, 2])
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