The EPISbigRR package - a tutorial

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Introduction

This vignette gives an introduction to the EPISbigRR package. The package performs genomic predictions for models including marker interaction effects. It uses the same theory as for the bigRR package but extends bigRR to models including interaction effects. It allows several variance components to be fitted in the functions `bigRR`, `bigRR_update`, `hugeRR` and `hugeRR_update`. The `hugeRR` and `hugeRR_update` functions stores the design matrices in parts as DatABEL objects (see the GenABEL package on CRAN and the bigRR documentation). The EPISbigRR package is available upon request from the author.

Example using the Arabidopsis data

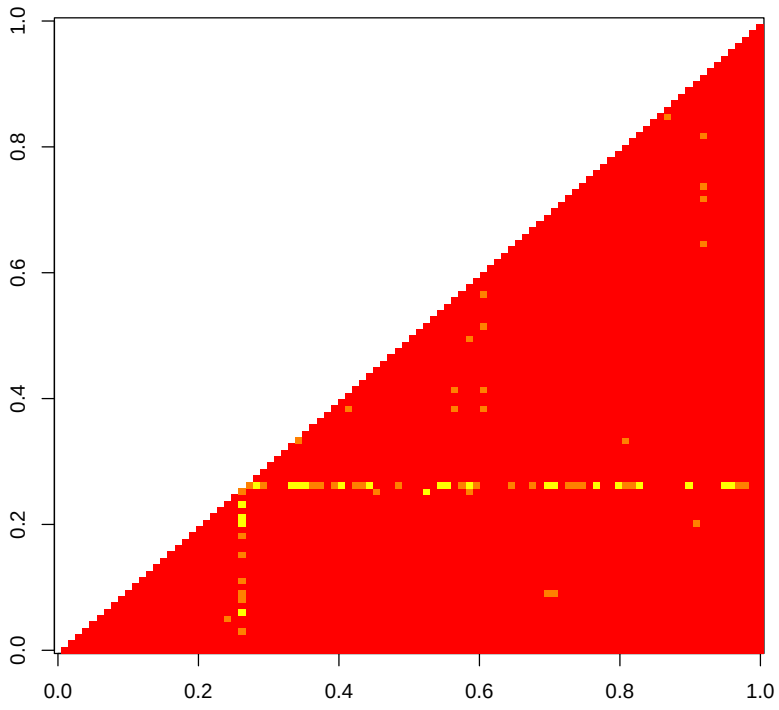
In this example there are 84 observations and we use the first 100 markers. The fitted pair-wise epistatic effects from the BLUP and updated BLUP models are plotted at the end of the file.

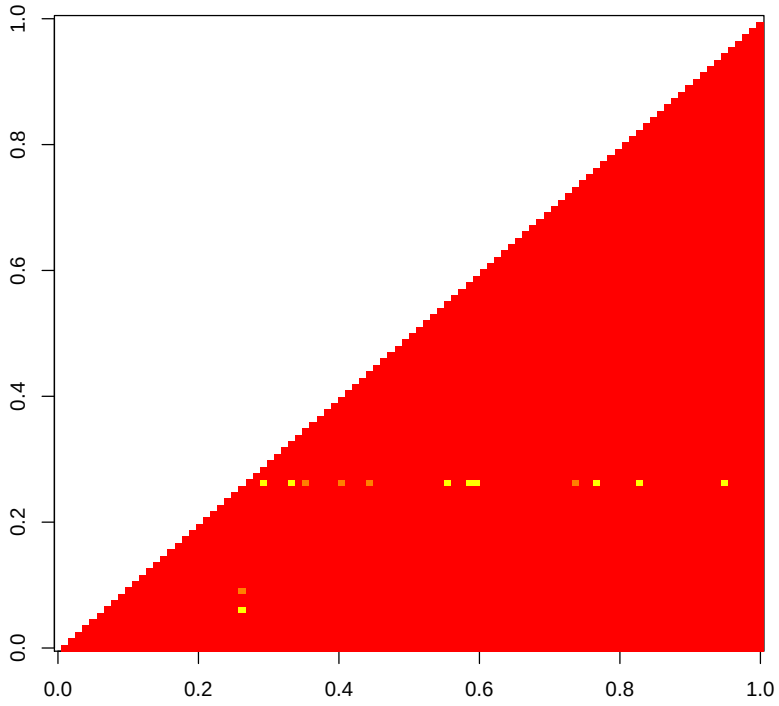
```
> library(EPISbigRR)
> data(Arabidopsis)
> N=length(y)
> X <- matrix(1, N, 1)
> p = 1e2 #We use the first 100 markers to make this example run fast
> Z = Z[,1:p]
> scZ <- scale(Z)/sqrt(p)
> #Store matrix for the main effects
> matrix2databel(scZ, paste('main_effects',1,sep=""))
uninames$unique.names = FALSE
uninames$unique.rownames = TRUE
uninames$unique.colnames = FALSE
backingfilename = main_effects1
cachesizeMb = 64
number of columns (variables) =  100
number of rows (observations) =  84
usedRowIndex: 1  2  3  4  5  ...
usedColIndex: 1  2  3  4  5  6  7  8  9  10  ...
Upper-left 10 columns and  5 rows:
          [,1]        [,2]        [,3]        [,4]
V1  0.06470583  0.06841382 -0.06470583  0.03654126
V4  0.06470583  0.06841382 -0.06470583  0.03654126
V7 -0.15270576 -0.14442918  0.15270576  0.03654126
V8  0.06470583  0.06841382 -0.06470583 -0.27040534
V9  0.06470583  0.06841382 -0.06470583  0.03654126
         [,5]        [,6]        [,7]        [,8]
V1 -0.0344342 -0.16188269 -0.02222718 -0.08608551
V4 -0.0344342  0.06103773 -0.02222718 -0.08608551
V7 -0.0344342  0.06103773 -0.02222718  0.11478067
V8  0.2869517  0.06103773 -0.02222718  0.11478067
V9 -0.0344342  0.06103773 -0.02222718 -0.08608551
          [,9]      [,10]
```

```
V1 -0.06286796  0.0405811
V4 -0.06286796  0.0405811
V7  0.15716991  0.0405811
V8 -0.06286796 -0.2434866
V9 -0.06286796  0.0405811
> #Create and store the scaled insidence matrix for the epistatic effects
> Zepi <- matrix(0, N, p*p)
> for (i in 1:(p-1)) {
      matrix2databel(matrix(scZ[,i]*scZ[,(i+1):p], N, (p-i)),
                     paste('epistatic_effects_data',i,sep=""))
      if (i%%10==0) print(i)
    }
[1] 10
[1] 20
[1] 30
[1] 40
[1] 50
[1] 60
[1] 70
[1] 80
[1] 90
> EPI2.BLUP.result <- hugeRR(y = y, X = X,
                           Z.name = list('main_effects','epistatic_effects_data'),
                           Z.index = list(1, 1:(p-1)), save.cache = TRUE)
Creating kinship matrix ...
1
Cholesky-decomposition & inversion ...
Creating kinship matrix ...
1         2         3         4         5         6         7         8         9
Cholesky-decomposition & inversion ...
Fitting HGLM ...
Calculating effects and leverages ...
1
 main_effects  Done.
1         2         3         4         5         6         7         8         9
 epistatic_effects_data  Done.

Done.
> mat.u <- matrix(NA,p,p)
> mat.u[lower.tri(mat.u)] <- abs(EPI2.BLUP.result$u[-(1:p)])
> pdf(file="EpistaticBLUP.pdf")
> image(mat.u, col = heat.colors(3)) #Plot the SNP interaction effects
> dev.off()
null device
          1
> #hugeRR_update
> EPI3.BLUP.result <- hugeRR_update(EPI2.BLUP.result,
                           Z.name = list('main_effects','epistatic_effects_data'),
                           Z.index = list(1, 1:(p-1)), save.cache = TRUE)
```

```
Creating kinship matrix ...
1
Cholesky-decomposition & inversion ...
Creating kinship matrix ...
1         2         3         4         5         6         7         8         9
Cholesky-decomposition & inversion ...
Fitting HGLM ...
Calculating effects and leverages ...
1
 main_effects  Done.
1         2         3         4         5         6         7         8         9
 epistatic_effects_data  Done.

Done.
> mat2.u <- matrix(NA,p,p)
> mat2.u[lower.tri(mat2.u)] <- abs(EPI3.BLUP.result$u[-(1:p)])
> pdf(file="EpistaticUpdatedBLUP.pdf")
> image(mat2.u, col = heat.colors(3))
> dev.off()
null device
          1
> #Remove working files
> file.remove(list.files()[substr(list.files(),1,3)=="tZi"])
  [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [12] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [23] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [34] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [45] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [56] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [67] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [78] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [89] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[100] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[111] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[122] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[133] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[144] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[155] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[166] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[177] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[188] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[199] TRUE TRUE
> file.remove(list.files()[substr(list.files(),1,3)=="epi"])
  [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [12] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [23] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [34] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [45] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [56] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

```
 [67] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [78] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
 [89] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[100] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[111] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[122] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[133] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[144] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[155] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[166] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[177] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[188] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
> file.remove(list.files()[substr(list.files(),1,3)=="G_s"])
[1] TRUE TRUE TRUE TRUE
> file.remove(list.files()[substr(list.files(),1,3)=="mai"])
[1] TRUE TRUE
```




0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0