RAT-ANALYSIS

Benoit Liquet

February 11, 2017

R Markdown

DATA RAT (Data in R2GUESS Package)

Dimension of the Y ($n \times q$) matrix

```
dim(Y)
```

```
## [1] 29  4
```

Dimension of X ($n \times p$) matrix and group structure (by chromosomes)

```
dim(X)
```

```
## [1]  29 770
```

```
(Xdata <- data.frame(size=as.vector(table(MAP.file[,2])),name=paste("Cromo",1:20)))
```

```
##    size     name
## 1    74  Cromo 1
## 2    67  Cromo 2
## 3    63  Cromo 3
## 4    60  Cromo 4
## 5    39  Cromo 5
## 6    45  Cromo 6
## 7    52  Cromo 7
## 8    43  Cromo 8
## 9    31  Cromo 9
## 10   51 Cromo 10
## 11   21 Cromo 11
## 12   26 Cromo 12
## 13   33 Cromo 13
## 14   22 Cromo 14
## 15   15 Cromo 15
## 16   27 Cromo 16
## 17   18 Cromo 17
## 18   30 Cromo 18
## 19   34 Cromo 19
## 20   19 Cromo 20
```
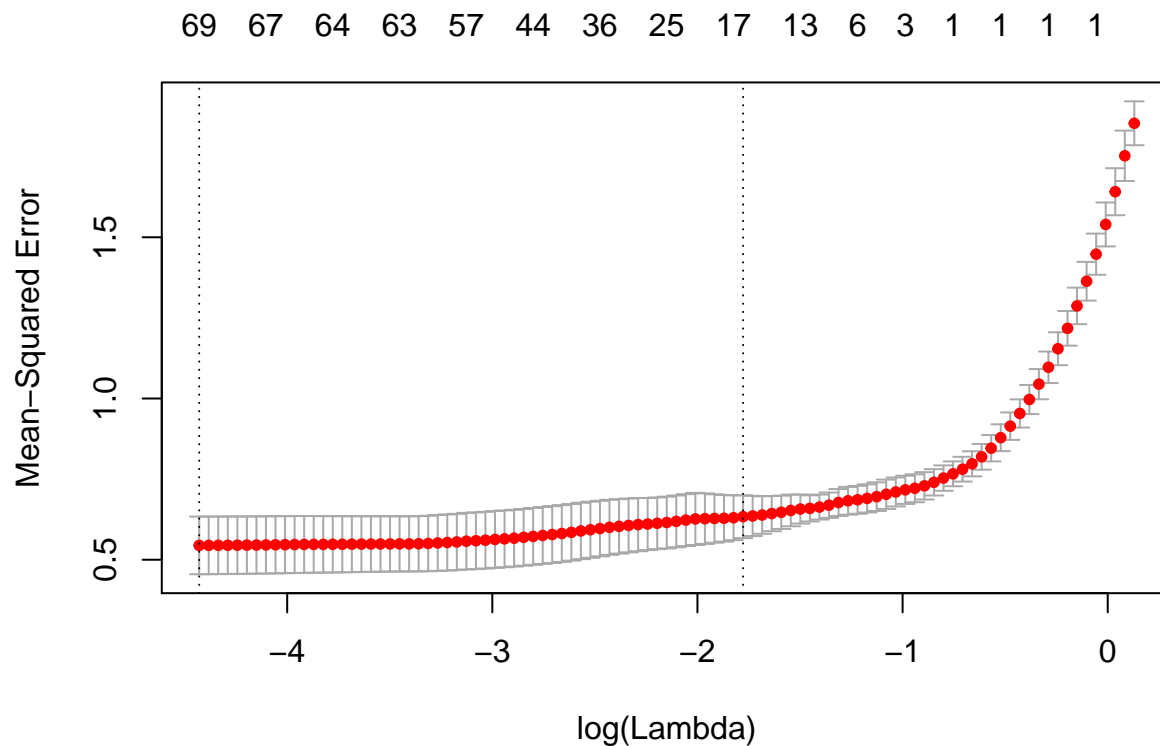
Correlation of the multivariate phenotype

```
Plotpairwise(Y)
```

Pairwise correlation between the phenotypes

	ADR	Fat	Heart	Kidney
ADR				
Fat	0.46			
Heart	0.44	0.24		
Kidney	0.7	0.42	0.44	
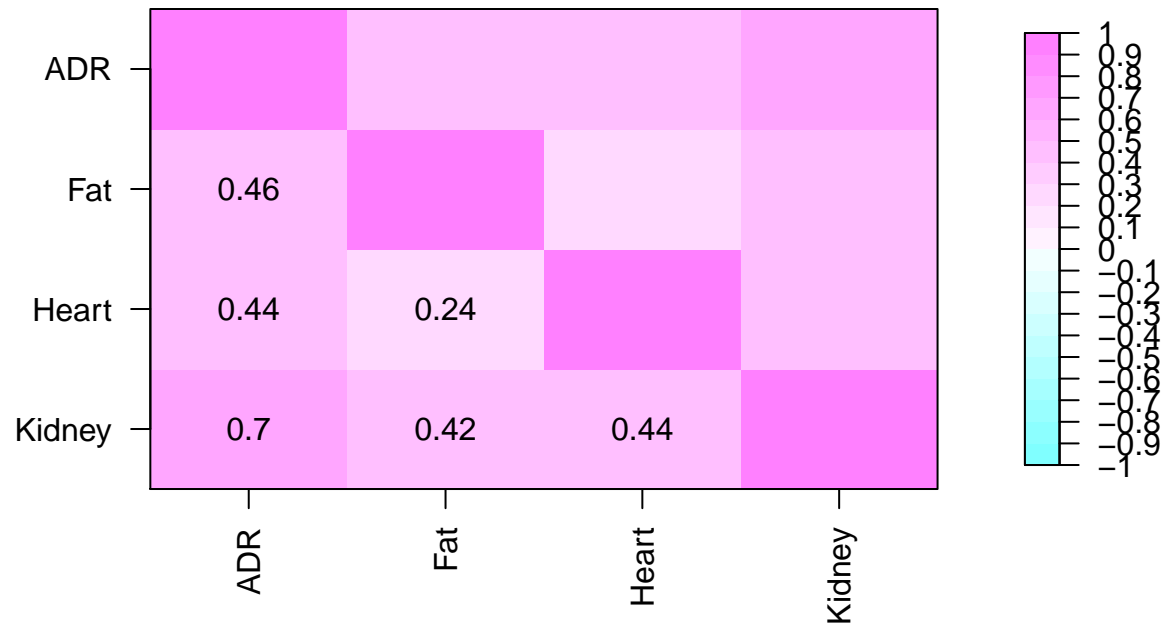
mlasso results

```
#Plotpairwise(Y)
### mlasso model
cvFit = cv.glmnet(X,Y,family="mgaussian",nfold=5)
plot(cvFit)
```

```
best.lam <- cvFit$lambda.min
Fit <- glmnet(X,Y,family="mgaussian",lambda=best.lam)
model_GL = (Fit$beta[[1]][,1]!=0)
sum(model_GL) -> nbr.gene.lasso
nbr.gene.lasso # selected by lasso
```

```
## [1] 68
```

```
#### Which comes from the following chromosomes
unique(MAP.file[model_GL,2]) -> res.lasso
```

Bayesian result

- MBGL-SS

```
result.GF$res.MG ## chromosome selected
```

```
## [1] 1 2
```

```
gsize[result.GF$res.MG] ## chromosome selected
```

```
##
##  1  2
## 74 67
```

- MBSGS-SS

```
#chromosomes selected
result.GF$res.MSG
```

```
## [1]  2  3  4  7 10 14 15 19
```

```r
#Names of the snps
(nameSNP <- as.character(sort(unique(MAP.file[unique(which(result.GF$MBSGS$pos_median!=0,arr.ind = TRUE)
```

```
##  [1] "Cyp11b2"       "D10Cebr39s2"   "D10Mit3"       "D10Ntr32"
##  [5] "D10Rat102"     "D10Rat226"     "D10Rat31"      "D14Cebrp312s2"
##  [9] "D14Mit3"       "D14Rat36"      "D14Rat52"      "D14Rat8"
## [13] "D15Rat21"      "D19Utr1"       "D2CebrP476s2"  "D2Mit16"
## [17] "D2Rat147"      "D2Rat222"      "D2Rat69"       "D2Rat70"
## [21] "D3Cebr204s4"   "D4Rat252"      "D4Rat49"       "D4Ucsf2"
## [25] "D7Cebr14C16s2" "D7Cebr205s3"   "D7Mit6"        "D7Rat112"
## [29] "D7Rat19"       "Ednra"         "Es13"          "Myc"
```

```r
# Number of snps selected
length(nameSNP)
```

```
## [1] 32
```

```r
#distribution of the snps selected
table(sort((MAP.file[unique(which(result.GF$MBSGS$pos_median!=0,arr.ind = TRUE)[,1]),2])))
```

```
##
##  2  3  4  7 10 14 15 19
##  6  1  3  7  7  5  1  2
```

```r
name.beta <- rep(result.GF$res.MSG ,times=table(sort((MAP.file[unique(which(result.GF$MBSGS$pos_median!=
```

Median estimator

```r
res <-result.GF$MBSGS$pos_median[unique(which(result.GF$MBSGS$pos_median!=0,arr.ind = TRUE)[,1]),]
pos <- unique(which(result.GF$MBSGS$pos_median!=0,arr.ind = TRUE)[,1])
colnames(res) <- colnames(Y)
res1 <- data.frame(Chromosome=name.beta,SNP.NAME=MAP.file[pos,1],signif(res,digit=4))
rownames(res1) <- NULL
res1
```

```
   Chromosome      SNP.NAME       ADR        Fat      Heart     Kidney
1           2       D2Rat147 5.530e-03 2.385e-03  0.0000000 0.0032880
2           2       D2Rat222 4.423e-03 1.160e-03  0.0000000 0.0030540
3           2   D2CebrP476s2 1.234e-03 0.000e+00  0.0000000 0.0000000
4           2        D2Rat69 7.149e-03 1.748e-02  0.0072990 0.0061970
5           2        D4Ucsf2 5.412e-04 0.000e+00  0.0000000 0.0000000
6           2    D7Cebr205s3 2.459e-03 0.000e+00  0.0095040 0.0046110
7           3  D7Cebr14C16s2 2.087e-03 3.264e-03  0.0000000 0.0004852
8           4       D7Rat112 3.485e-04 8.165e-06  0.0000000 0.0000000
9           4        D7Rat19 1.113e-02 1.800e-02  0.0368000 0.0182800
10          4        Cyp11b2 7.506e-04 3.738e-03  0.0000000 0.0039360
11          7       D10Ntr32 1.228e-03 0.000e+00  0.0111200 0.0014310
12          7        D10Rat31 3.063e-04 5.726e-03  0.0044210 0.0031610
13          7    D10Cebr39s2 2.798e-03 4.900e-03  0.0082070 0.0058590
14          7           Es13 5.395e-03 0.000e+00  0.0092440 0.0041860
15          7       D10Rat226 4.150e-03 6.342e-05  0.0098670 0.0037230
16          7        D14Rat36 3.648e-04 0.000e+00  0.0307600 0.0000000
17          7  D14Cebrp312s2 4.329e-05 0.000e+00  0.0542700 0.0000000
18         10        D14Mit3 4.963e-02 5.415e-02  0.3343000 0.0749100
19         10        D15Rat21 9.366e-03 5.692e-03  0.0314000 0.0170400
```

```
20      10         D19Utr1 1.487e-03 2.974e-03  0.0025090 0.0048670
21      10           Ednra 2.593e-04 0.000e+00  0.0000000 0.0000000
22      10          D2Mit16 0.000e+00 7.690e-04  0.0000000 0.0000000
23      10          D2Rat70 0.000e+00 1.904e-03  0.0000000 0.0000000
24      10      D3Cebr204s4 0.000e+00 4.161e-04  0.0000000 0.0000000
25      14          D4Rat49 0.000e+00 1.022e-03  0.0009157 0.0040140
26      14           D7Mit6 0.000e+00 1.971e-05  0.0000000 0.0000000
27      14        D10Rat102 0.000e+00 1.116e-03  0.0000000 0.0000000
28      14         D4Rat252 0.000e+00 0.000e+00 -0.0018380 0.0000000
29      14              Myc 0.000e+00 0.000e+00  0.0066930 0.0000000
30      15          D10Mit3 0.000e+00 0.000e+00  0.0010380 0.0000000
31      19          D14Rat8 0.000e+00 0.000e+00  0.0005849 0.0000000
32      19         D14Rat52 0.000e+00 0.000e+00  0.0036050 0.0000000
```