

Assignment 2

Assignment 2

Biomedical Data Science

Due on Thursday 18th March 2020, 5:00pm

The assignment is marked out of 100 points, and will contribute to 30% of your final mark. Please knit this document in PDF format and submit using the gradescope link on Learn. If you can't knit to PDF directly, knit it to word and you should be able to either convert to PDF or print it and scan to PDF using a scanning app on your phone. If you have any code that doesn't run you won't be able to knit the document so comment it as you might still get some grades for partial code. Clear and reusable code will be rewarded so pay attention to indentation, choice of variable identifiers, comments, error checking, etc. An initial code chunk is provided after each subquestion but create as many chunks as you feel is necessary to make a clear report. Add plain text explanations in between the chunks as and when required and any comments necessary within code chunks to make it easier to follow your code/reasoning.

Problem 1 (27 points)

File wdbc2.csv (available from the accompanying zip folder on Learn) refers to a study of breast cancer where the outcome of interest is the type of the tumour (benign or malignant, recorded in column "diagnosis"). The study collected 30 imaging biomarkers on 569 patients.

Problem 1.a (7 points)

Using package caret, create a data partition so that the training set contains 70% of the observations (set the random seed to 984065 beforehand). Fit both a ridge regression model and a lasso model which uses cross-validation on the training set to diagnose the type of tumour from the 30 biomarkers. Then use a plot to help identify the penalty parameter λ that maximizes the AUC. Note: There is no need to use the prepare.glmnet() function from lab 4, using as.matrix() with the required columns is sufficient.

```
# Enter code here.
set.seed(984065)
wdbc2.dt <- fread("data/wdbc2.csv")
wdbc2.dt$diagnosis <- ifelse(wdbc2.dt$diagnosis=='malignant',1,0)

ind <- createDataPartition(wdbc2.dt$diagnosis, p=0.7, list=FALSE)
data.train <- wdbc2.dt[ind,]
data.test <- wdbc2.dt[-ind,]

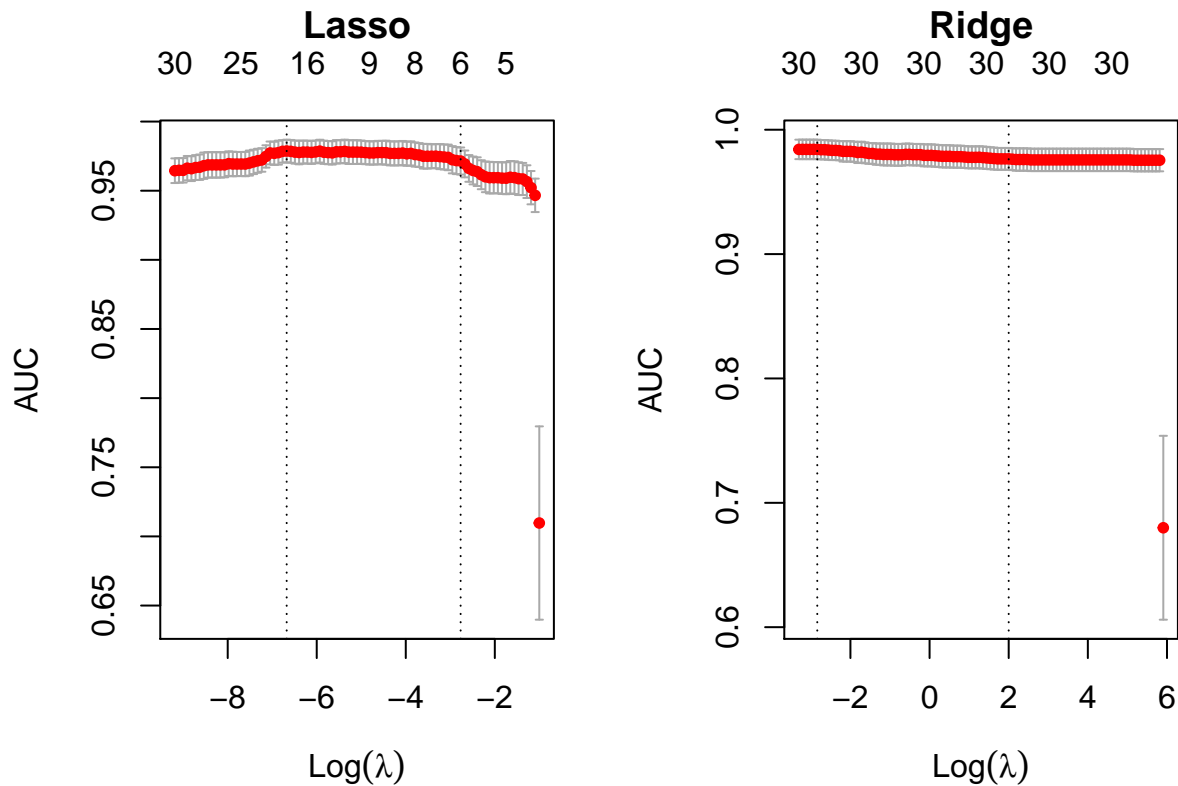
# check that the split is actually 70-30
# table(wdbc2.dt$diagnosis)[1] / (table(wdbc2.dt$diagnosis)[1] + table(wdbc2.dt$diagnosis)[2])
# table(data1.train$diagnosis)[1] / (table(data1.train$diagnosis)[1] + table(data1.train$diagnosis)[2])
# table(data1.test$diagnosis)[1] / (table(data1.test$diagnosis)[1] + table(data1.test$diagnosis)[2])

X.train <- data.train[, !c("diagnosis","id"), with=FALSE]
X.test <- data.test[, !c("diagnosis","id"), with=FALSE]
y.train <- data.train[, c("diagnosis"), with=FALSE]
y.test <- data.test[, c("diagnosis"), with=FALSE]
```

```

fit.cv.lasso <- cv.glmnet(as.matrix(X.train), as.matrix(y.train), family='binomial', type.measure = c('auc'))
fit.cv.ridge <- cv.glmnet(as.matrix(X.train), as.matrix(y.train), family='binomial', type.measure = c('auc'))
par(mfrow=c(1,2), mar=c(4,4,5,2))
plot(fit.cv.lasso, main="Lasso")
plot(fit.cv.ridge, main="Ridge")

```



Problem 1.b (2 points)

Create a data table that for each value of 'lambda.min' and 'lambda.1se' for each model fitted in problem 1.a reports: * the corresponding AUC, * the corresponding model size. Use 3 significant digits for floating point values and comment on these results. Hint: The AUC values are stored in the field called 'cvm'.

```

# Enter code here.
lasso.min.pos <- which(fit.cv.lasso$lambda==fit.cv.lasso$lambda.min)
lasso.1se.pos <- which(fit.cv.lasso$lambda==fit.cv.lasso$lambda.1se)
lasso.model <- 'lasso'
lasso.lambda.min <- round(fit.cv.lasso$lambda.min,3)
lasso.lambda.1se <- round(fit.cv.lasso$lambda.1se,3)
lasso.model.min <- round(fit.cv.lasso$nzzero[lasso.min.pos],3)
lasso.model.1se <- round(fit.cv.lasso$nzzero[lasso.1se.pos],3)
lasso.auc.min <- round(fit.cv.lasso$cvm[lasso.min.pos],3)
lasso.auc.1se <- round(fit.cv.lasso$cvm[lasso.1se.pos],3)

ridge.min.pos <- which(fit.cv.ridge$lambda==fit.cv.ridge$lambda.min)
ridge.1se.pos <- which(fit.cv.ridge$lambda==fit.cv.ridge$lambda.1se)
ridge.model <- 'ridge'
ridge.lambda.min <- round(fit.cv.ridge$lambda.min,3)
ridge.lambda.1se <- round(fit.cv.ridge$lambda.1se,3)
ridge.model.min <- round(fit.cv.ridge$nzzero[ridge.min.pos],3)

```

```

ridge.model.1se <- round(fit.cv.ridge$nzero[ridge.1se.pos],3)
ridge.auc.min <- round(fit.cv.ridge$cvm[ridge.min.pos],3)
ridge.auc.1se <- round(fit.cv.ridge$cvm[ridge.1se.pos],3)

model.lasso.row <- c(lasso.model, lasso.lambda.min, lasso.model.min, lasso.auc.min, lasso.lambda.1se,
model.ridge.row <- c(ridge.model, ridge.lambda.min, ridge.model.min, ridge.auc.min, ridge.lambda.1se,
results.train <- as.data.table(rbind(model.lasso.row, model.ridge.row))
cols <- c('model', 'lambda.min', 'variables.min', 'auc.min', 'lambda.1se', 'variables.1se',
setnames(results.train, cols)

results.train

##      model lambda.min variables.min auc.min lambda.1se variables.1se auc.1se
## 1: lasso      0.001          20  0.979      0.063          6  0.971
## 2: ridge      0.059          30  0.984      7.389         30  0.977

```

Problem 1.c (7 points)

Perform both backward (we'll later refer to this as model B) and forward (model S) stepwise selection on the same training set derived in problem 1.a. Report the variables selected and their standardized regression coefficients in decreasing order of the absolute value of their standardized regression coefficient. Discuss the results and how the different variables entering or leaving the model influenced the final result.

```

full.model <- suppressWarnings(glm(data.train$diagnosis ~ . , data=data.train, family='binomial'))
modelB <- suppressWarnings(stepAIC(full.model, direction="back", trace=FALSE))
null.model <- suppressWarnings(glm(data.train$diagnosis ~ 1 , data=data.train, family='binomial'))
modelS <- suppressWarnings(stepAIC(null.model, scope=list(upper=full.model), direction="forward", t

modelB

##
## Call: glm(formula = data.train$diagnosis ~ radius + perimeter + concavepoints +
##      radius.stderr + texture.stderr + radius.worst + texture.worst +
##      area.worst + smoothness.worst + compactness.worst + concavity.worst +
##      concavepoints.worst, family = "binomial", data = data.train)
##
## Coefficients:
##      (Intercept)          radius          perimeter
##      -59.98039          1.08925          -0.38156
##      concavepoints      radius.stderr      texture.stderr
##      103.44514          14.28442          -2.94382
##      radius.worst      texture.worst          area.worst
##      5.39339           0.43813          -0.03597
##      smoothness.worst      compactness.worst      concavity.worst
##      43.34720          -16.81214          20.07203
##      concavepoints.worst
##      -28.09322
##
## Degrees of Freedom: 398 Total (i.e. Null); 386 Residual
## Null Deviance: 527.3
## Residual Deviance: 73.47 AIC: 99.47

modelS

##
## Call: glm(formula = data.train$diagnosis ~ perimeter.worst + concavity +

```

```
## texture.worst + radius.stderr + area.stderr + smoothness.worst +
## radius + concavity.worst + perimeter.stderr + area.worst +
## compactness.worst + perimeter + radius.worst + texture.stderr,
## family = "binomial", data = data.train)
##
## Coefficients:
## (Intercept) perimeter.worst concavity texture.worst
## -64.81578 0.23889 33.09024 0.38552
## radius.stderr area.stderr smoothness.worst radius
## 19.83368 0.03095 57.43884 0.81858
## concavity.worst perimeter.stderr area.worst compactness.worst
## 10.18660 -1.25851 -0.03928 -18.73717
## perimeter radius.worst texture.stderr
## -0.27491 3.97715 -2.39510
##
## Degrees of Freedom: 398 Total (i.e. Null); 384 Residual
## Null Deviance: 527.3
## Residual Deviance: 75.29 AIC: 105.3
```

Problem 1.d (3 points)

Compare the goodness of fit of model B and model S in an appropriate way.

```
# Enter code here.
# Chi-square goodness of fit tests and deviance
signif(pchisq(modelB$null.deviance - modelB$deviance, df=12, lower.tail=FALSE),2)

## [1] 1.5e-89

signif(pchisq(modelS$null.deviance - modelS$deviance, df=14, lower.tail=FALSE),2)

## [1] 1.4e-87
```

Problem 1.e (2 points)

Compute the training AUC for model B and model S.

```
# Enter code here.
auc.modelB <- roc(data.train$diagnosis, modelB$fitted.values)

## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
auc.modelS <- roc(data.train$diagnosis, modelS$fitted.values)

## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
auc.modelB$auc

## Area under the curve: 0.9936
auc.modelS$auc

## Area under the curve: 0.9929
```

Problem 1.f (6 points)

Use the four models to predict the outcome for the observations in the test set (use the lambda at 1 standard error for the penalised models). Plot the ROC curves of these models (on the same plot, using different colours) and report their test AUCs. Compare the training AUCs obtained in problems 1.b and 1.e with the test AUCs and discuss the fit of the different models.

Enter code here.

```
modelB.pred <- predict(modelB, newdata=data.test, type='response')
modelS.pred <- predict(modelS, newdata=data.test, type='response')
lasso.pred  <- predict(fit.cv.lasso, newx=as.matrix(X.test), s=lasso.lambda.1se, type='response')
ridge.pred  <- predict(fit.cv.ridge, newx=as.matrix(X.test), s=ridge.lambda.1se, type='response')

roc.modelB <- roc(data.test$diagnosis, modelB.pred , plot=TRUE, col='blue4', direction="<")

## Setting levels: control = 0, case = 1
roc.modelS <- roc(data.test$diagnosis, modelS.pred , plot=TRUE, col='red4', direction="<", add=TRUE, qu

## Setting levels: control = 0, case = 1
roc.lasso  <- roc(data.test$diagnosis, lasso.pred  , plot=TRUE, col='orange4', direction="<", add=TRUE,

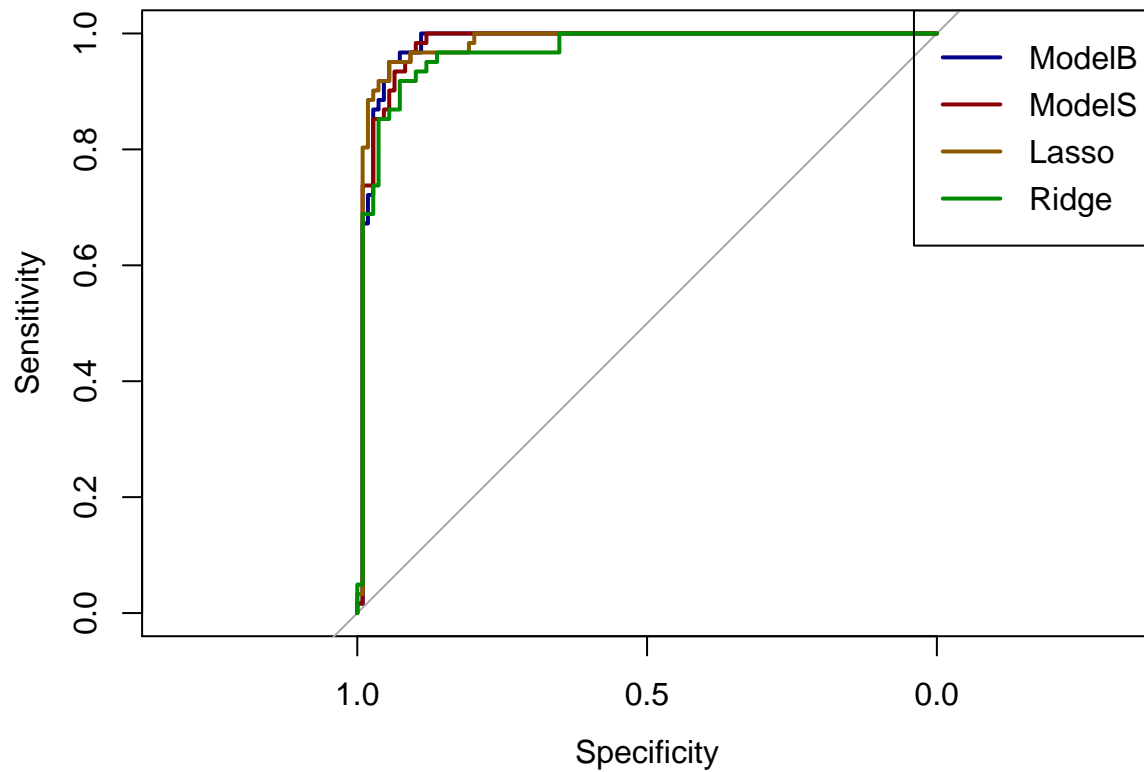
## Setting levels: control = 0, case = 1

## Warning in roc.default(data.test$diagnosis, lasso.pred, plot = TRUE, col =
## "orange4", : Deprecated use a matrix as predictor. Unexpected results may be
## produced, please pass a numeric vector.
roc.ridge  <- roc(data.test$diagnosis, ridge.pred  , plot=TRUE, col='green4', direction="<", add=TRUE,

## Setting levels: control = 0, case = 1

## Warning in roc.default(data.test$diagnosis, ridge.pred, plot = TRUE, col =
## "green4", : Deprecated use a matrix as predictor. Unexpected results may be
## produced, please pass a numeric vector.

legend(x = 'topright', legend = c('ModelB', 'ModelS', 'Lasso', 'Ridge'),
      col=c('blue4', 'red4', 'orange4', 'green4'), lwd=2)
```



```
row1 <- c('lasso' , signif(roc.lasso$auc,4), signif(lasso.auc.1se,4))
row2 <- c('ridge' , signif(roc.ridge$auc,4), signif(ridge.auc.1se,4))
row3 <- c('modelB', signif(roc.modelB$auc,4), signif(auc.modelB$auc,4))
row4 <- c('modelS', signif(roc.modelS$auc,4), signif(auc.modelS$auc,4))
results.final <- as.data.table(rbind(row1,row2,row3,row4))
cols <- c('model', 'AUC.test', 'AUC.train')
setnames(results.final, cols)
results.final[order(-AUC.test),]
```

```
##      model AUC.test AUC.train
## 1:  lasso  0.9806    0.971
## 2: modelB  0.9803    0.9936
## 3: modelS  0.9791    0.9929
## 4:  ridge  0.9668    0.977
```

Problem 2 (40 points)

File GDM.raw.txt (available from the accompanying zip folder on Learn) contains 176 SNPs to be studied for association with incidence of gestational diabetes (a form of diabetes that is specific to pregnant women). SNP names are given in the form “rs1234_X” where “rs1234” is the official identifier (rsID), and “X” (one of A, C, G, T) is the reference allele.

Problem 2.a (3 points)

Read file GDM.raw.txt into a data table named gdm.dt. Impute missing values in gdm.dt according to SNP-wise median allele count.

```
#' This is a function that takes as impute a column of a data.table and imputes  
#' the NAs with its mean / mode if the vector is numeric or categorical respectively.  
#' @param x A vector of numeric or categorical values for which the NAs will be imputed.  
impute.to.median <- function(x) {  
  if (all(na.omit(x) %in% 0L:2L)){  
    x[is.na(x)] = median(x, na.rm=TRUE)  
  }  
  return(x)  
}
```

```
# Enter code here.  
gdm.dt <- fread("data/GDM.raw.txt")  
numcols <- colnames(gdm.dt)  
gdm.dt %>% .[, (numcols) := lapply(.SD, impute.to.median), .SDcols = numcols]
```

Problem 2.b (8 points)

Write function univ.glm.test <- function(x, y, order = FALSE) where x is a data table of SNPs, y is a binary outcome vector, and order is a boolean. The function should fit a logistic regression model for each SNP in x, and return a data table containing SNP names, regression coefficients, odds ratios, standard errors and p-values. If order is set to TRUE, the output data table should be ordered by increasing p-value.

```
# run univariate tests of associations for all SNPs(columns of az)  
univ.glm.test <- function(x, y, ordering=FALSE) {  
  stopifnot(all(na.omit(y) %in% 0L:1L))  
  output <- NULL  
  for (i in 1:ncol(x)){  
    regr <- glm(y ~ x[[i]], family='binomial')  
  
    data <- transpose(as.data.table(coef(summary(regr))[-1, -3]))  
    data <- cbind(data, exp(coef(regr))[2]) # odds ration calculation  
    data <- cbind(data, colnames(X[1,])[i]) # keep column name as argument on the output  
    output <- rbind(output, data)  
  }  
  # assign better column names  
  colnames(output) <- c("beta", "std.error", "p.value", "odds ratio", "snp_full")  
  return(output[order(output$"p.value"*ordering)])  
  # The requirement is strictly to write the function with an argument called  
# 'order', not 'ordering'. When the argument was called 'order', there was a  
# problem because there is the function 'order()' as well. In any case,  
# strictly speaking with the function argument 'order', I would solve it like:  
#  
# if(!order) {return(output)} else {return(output[order(output$"p.value"), ])}  
}
```

Problem 2.c (5 points)

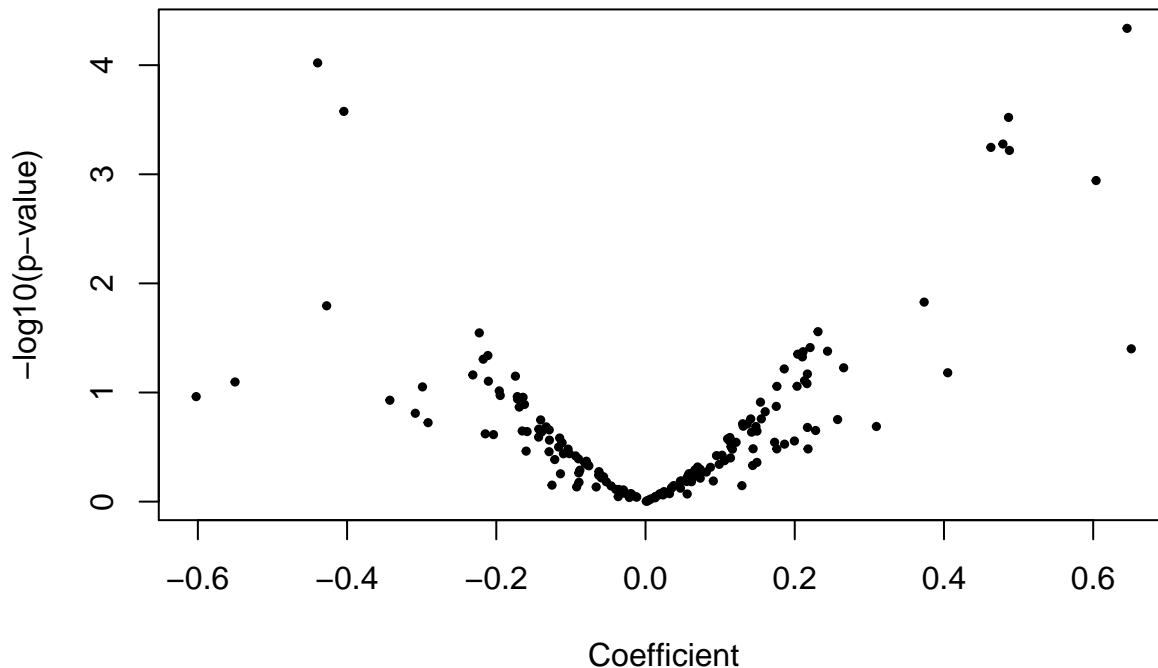
Using function `univ.glm.test()`, run an association study for all the SNPs in `gdm.dt` against having gestational diabetes (column “pheno”). For the SNP that is most strongly associated to increased risk of gestational diabetes and the one with most significant protective effect, report the summary statistics from the GWAS as well as the 95% and 99% confidence intervals on the odds ratio.

```
X <- as.data.table(gdm.dt[,4:ncol(gdm.dt)])
target <- gdm.dt$pheno
association <- data.table(univ.glm.test(x=X,y=target, ordering=FALSE), key=c('snp_full'))
association

##           beta  std.error   p.value odds ratio   snp_full
##  1:  0.14214661 0.11864045 0.23086663  1.1527456 rs10150332_A
##  2: -0.07876094 0.10208514 0.44039753  0.9242609 rs10488683_A
##  3:  0.07335711 0.14381095 0.60998558  1.0761148 rs1052248_G
##  4: -0.03621755 0.13986052 0.79567012  0.9644305 rs10767664_C
##  5: -0.06274131 0.11130078 0.57295182  0.9391864 rs10770141_A
##  ---
## 172: -0.21128464 0.10579572 0.04581431  0.8095436 rs972283_A
## 173: -0.15998626 0.16926370 0.34456217  0.8521555 rs9816226_C
## 174: -0.17436723 0.09651276 0.07081291  0.8399884 rs987237_C
## 175: -0.04611920 0.12793644 0.71848429  0.9549281 rs9939609_A
## 176:  0.11644920 0.11969475 0.33061059  1.1235004 rs9941349_A

plot(association[, .(beta, -log10(p.value))],
     pch = 19, cex = 0.5,
     main = "Volcano plot",
     xlab = "Coefficient",
     ylab = "-log10(p-value)"
    )
abline(h = -log10(5e-8), lty = 2, col = "red") # genome-wide significance threshold
```


Volcano plot



```
# Biggest risk
threshold = 0.05
risk <- association[p.value < threshold,]
risk <- risk[order(-beta),]
biggest_risk <- risk[1,]
biggest_protect <- risk[dim(risk)[1],]
sns_risk <- biggest_risk[,snp_full][1]
sns_protect <- biggest_protect[,snp_full][1]

sns_risk.dt <- gdm.dt[,..sns_risk]
sns_protect.dt <- gdm.dt[,..sns_protect]
data <- cbind(target, sns_risk.dt, sns_protect.dt)

risk_logistic <- glm(data[[1]] ~ data[[2]], family='binomial')
protect_logistic <- glm(data[[1]] ~ data[[3]], family='binomial')

results <- as.data.table(coef(summary(risk_logistic))[, -3])
results <- cbind(results, confint(risk_logistic, level=0.95), confint(risk_logistic, level=0.99))

## Waiting for profiling to be done...
## Waiting for profiling to be done...

temp <- as.data.table(coef(summary(protect_logistic))[, -3])
temp <- cbind(temp, confint(protect_logistic, level=0.95), confint(protect_logistic, level=0.99))

## Waiting for profiling to be done...
## Waiting for profiling to be done...

results <- rbind(results, temp)
sns_name <- c(sns_risk, sns_protect, sns_protect, sns_protect)
sns_role <- c('risk', 'risk', 'protect', 'protect')
```

```

results <- cbind(sns_name, sns_role, results)
beta <- c('Intercept', 'beta1', 'Intercept', 'beta1')
results <- cbind(beta, results)
results

```

```

##          beta    sns_name sns_role    Estimate Std. Error    Pr(>|z|)
## 1: Intercept rs1423096_T    risk    0.08241388 0.07340542 2.615556e-01
## 2:      beta1 rs1423096_T    risk    0.65106408 0.31665472 3.977583e-02
## 3: Intercept rs2237897_T protect    0.37439772 0.09727068 1.185867e-04
## 4:      beta1 rs2237897_T protect   -0.43944560 0.11261333 9.530178e-05
##          2.5 %    97.5 %    0.5 %    99.5 %
## 1: -0.06137965 0.2264890 -0.1065641 0.2718783
## 2: 0.04920779 1.3002071 -0.1347336 1.5188279
## 3: 0.18468070 0.5662477 0.1253780 0.6271024
## 4: -0.66191949 -0.2200563 -0.7326623 -0.1515496

```

Problem 2.d (4points)

Merge your GWAS results with the table of gene names provided in file GDM.annot.txt (available from the accompanying zip folder on Learn). For SNPs that have p-value $< 10^{-4}$ (hit SNPs) report SNP name, effect allele, chromosome number and corresponding gene name. Separately, report for each 'hit SNP' the names of the genes that are within a 1Mb window from the SNP position on the chromosome. Note: That's genes that fall within $\pm 1,000,000$ positions using the 'pos' column in the dataset.

```

# Enter code here.
gdm.annot.dt <- data.table(fread('data/GDM.annot.txt'), key=c('snp'))
pk <- c('snp')
association[,snp:=substring(snp_full, 1, nchar(snp_full)-2)]
association[,allele:=substring(snp_full, nchar(snp_full),nchar(snp_full))]
# association<- association[,-'snp_full']
association.ext <- merge(association,
                        gdm.annot.dt,
                        by=pk,
                        all=TRUE)[order(snp)]
association.ext

```

```

##          snp          beta std.error    p.value odds ratio    snp_full
## 1: rs10150332 0.14214661 0.11864045 0.23086663 1.1527456 rs10150332_A
## 2: rs10488683 -0.07876094 0.10208514 0.44039753 0.9242609 rs10488683_A
## 3: rs1052248 0.07335711 0.14381095 0.60998558 1.0761148 rs1052248_G
## 4: rs10767664 -0.03621755 0.13986052 0.79567012 0.9644305 rs10767664_C
## 5: rs10770141 -0.06274131 0.11130078 0.57295182 0.9391864 rs10770141_A
## ---
## 172: rs972283 -0.21128464 0.10579572 0.04581431 0.8095436 rs972283_A
## 173: rs9816226 -0.15998626 0.16926370 0.34456217 0.8521555 rs9816226_C
## 174: rs987237 -0.17436723 0.09651276 0.07081291 0.8399884 rs987237_C
## 175: rs9939609 -0.04611920 0.12793644 0.71848429 0.9549281 rs9939609_A
## 176: rs9941349 0.11644920 0.11969475 0.33061059 1.1235004 rs9941349_A
##          allele chrom      pos      gene
## 1:      A      14  79936964      NRXN3
## 2:      A      11  18053545      TPH1
## 3:      G       6  31556581      NFKBIL1
## 4:      C      11  27725986      BDNF
## 5:      A      11   2193840       TH
## ---

```

```
## 172:      A      7 130466854 LOC105375508
## 173:      C      3 185834499
## 174:      C      6 50803050      TFAP2B
## 175:      A     16 53820527      FTO
## 176:      A     16 53825488      FTO
```

```
report1 <- association.ext[p.value < 1e-4, c('snp','allele','chrom','gene','pos')]
report1[,c('snp','allele','chrom','gene')]
```

```
##          snp allele chrom  gene
## 1: rs12243326      A    10 TCF7L2
## 2:  rs2237897      T    11  KCNQ1
```

```
report2 <- association.ext[p.value < 1e-4 & (pos >= report1[,pos][1] - 1000000 & pos <=report1[,pos][1]
| (pos >= report1[,pos][2] - 1000000 & pos <=report1[,pos][2] + 1000000),
c('snp','gene')]
report2
```

```
##          snp      gene
## 1: rs10770141      TH
## 2: rs12243326  TCF7L2
## 3:  rs163184   KCNQ1
## 4:  rs2041139 CACNA2D4
## 5:  rs2237892   KCNQ1
## 6:  rs2237897   KCNQ1
## 7:  rs231362   KCNQ1
## 8:  rs391300   SMG6
## 9:  rs4523957   SMG6
```

Problem 2.e (8 points)

Build a weighted genetic risk score that includes all SNPs with p -value $< 10^{-4}$, a score with all SNPs with p -value $< 10^{-3}$, and a score that only includes SNPs on the FTO gene (hint: ensure that the ordering of SNPs is respected). Add the three scores as columns to the gdm.dt data table. Fit the three scores in separate logistic regression models to test their association with gestational diabetes, and for each report odds ratio, 95% confidence interval and p -value.

```
# Genetic risk score
snps.grs.3 <- association.ext[p.value < 1e-3]
snps.grs.4 <- association.ext[p.value < 1e-4]
snps.grs.FTO <- association.ext[gene == 'FTO']

gdm.grs.3 <- gdm.dt[, .SD, .SDcols = snps.grs.3$snp_full]
gdm.grs.4 <- gdm.dt[, .SD, .SDcols = snps.grs.4$snp_full]
gdm.grs.FTO <- gdm.dt[, .SD, .SDcols = snps.grs.FTO$snp_full]

weighted.score.3 <- as.matrix(gdm.grs.3) %*% snps.grs.3$beta
weighted.score.4 <- as.matrix(gdm.grs.4) %*% snps.grs.4$beta
weighted.score.FTO <- as.matrix(gdm.grs.FTO) %*% snps.grs.FTO$beta

gdm.dt[,weighted.risk.3:=weighted.score.3]
gdm.dt[,weighted.risk.4:=weighted.score.4]
gdm.dt[,weighted.risk.FTO:=weighted.score.FTO]
gdm.dt

##          ID  sex pheno rs7513574_T rs1627238_A rs1171278_C rs1137100_A
##   1:      1 FALSE      0              1              0              0              2
```

```

## 2: 2 FALSE 0 0 0 0 1
## 3: 4 FALSE 1 2 1 1 1
## 4: 5 FALSE 1 0 1 1 1
## 5: 6 FALSE 1 0 1 1 1
## ---
## 785: 1054 FALSE 0 0 1 1 1
## 786: 1055 FALSE 0 0 0 0 0
## 787: 1056 FALSE 1 1 0 0 1
## 788: 1058 FALSE 0 1 0 0 1
## 789: 1059 FALSE 1 1 0 0 1
## rs2568958_A rs1514175_A rs1555543_C rs10923931_C rs516636_A rs574367_G
## 1: 0 1 2 0 0 0
## 2: 0 0 1 0 1 0
## 3: 1 1 2 0 0 0
## 4: 0 2 2 1 0 0
## 5: 1 0 0 0 0 0
## ---
## 785: 1 1 2 0 1 1
## 786: 0 0 2 0 1 1
## 787: 1 0 0 0 1 1
## 788: 1 0 2 1 0 0
## 789: 0 1 1 0 0 0
## rs543874_C rs7554506_A rs340874_G rs2867125_A rs6548238_A rs7561317_C
## 1: 0 0 0 0 0 0
## 2: 1 0 1 0 0 0
## 3: 0 0 1 0 0 0
## 4: 0 0 1 0 0 0
## 5: 0 0 0 0 0 0
## ---
## 785: 1 0 1 0 0 0
## 786: 1 1 0 0 0 0
## 787: 1 0 1 1 1 1
## 788: 0 1 2 0 0 0
## 789: 0 0 2 1 1 1
## rs6545814_T rs713586_C rs11899863_C rs7578597_C rs887912_C rs243021_C
## 1: 0 0 0 0 0 1
## 2: 0 0 0 0 0 1
## 3: 0 0 0 0 1 1
## 4: 1 1 1 0 0 0
## 5: 1 1 1 1 0 0
## ---
## 785: 0 0 0 0 0 1
## 786: 1 1 0 0 0 0
## 787: 0 1 0 0 0 1
## 788: 0 2 0 1 0 1
## 789: 1 1 0 0 0 2
## rs2890652_T rs2925757_C rs3923113_C rs13389219_T rs7578326_A rs2943641_A
## 1: 0 0 0 1 0 1
## 2: 0 0 0 0 1 0
## 3: 0 0 1 1 1 0
## 4: 0 0 0 0 0 0
## 5: 0 0 0 0 0 0
## ---
## 785: 1 0 1 0 1 0

```

## 786:	0	1	0	0	1	0
## 787:	0	0	1	0	0	0
## 788:	0	0	0	0	1	0
## 789:	0	1	1	0	2	0
##	rs1801282_C	rs6780569_C	rs831571_T	rs4607103_G	rs13078807_T	rs11708067_G
## 1:	0	0	0	1	0	1
## 2:	0	0	0	1	0	0
## 3:	0	0	0	0	0	1
## 4:	1	0	0	0	0	2
## 5:	0	1	0	1	0	0
## ---						
## 785:	0	0	0	0	0	2
## 786:	0	0	0	1	0	0
## 787:	0	0	0	0	0	1
## 788:	0	1	0	2	0	0
## 789:	0	0	0	0	0	1
##	rs187230_A	rs4402960_T	rs1470579_C	rs7647305_G	rs9816226_C	rs266729_G
## 1:	1	0	0	0	0	1
## 2:	1	0	0	1	0	0
## 3:	0	2	2	1	0	2
## 4:	1	0	0	0	0	0
## 5:	1	0	0	0	0	0
## ---						
## 785:	1	1	1	0	0	0
## 786:	2	0	1	1	0	0
## 787:	0	0	0	0	0	0
## 788:	2	0	0	2	1	0
## 789:	0	0	0	0	0	1
##	rs1501299_C	rs16861329_C	rs6815464_A	rs4688985_A	rs1801214_A	rs10938397_T
## 1:	1	0	0	1	2	0
## 2:	2	1	0	0	0	0
## 3:	1	1	1	0	0	0
## 4:	2	1	0	0	0	0
## 5:	2	1	0	0	0	0
## ---						
## 785:	1	1	1	0	0	1
## 786:	0	1	1	1	2	1
## 787:	0	0	0	0	0	0
## 788:	1	0	1	0	0	0
## 789:	1	1	2	0	1	0
##	rs2227306_G	rs2886920_G	rs13107325_T	rs459193_G	rs2112347_A	rs4457053_C
## 1:	1	1	0	0	0	2
## 2:	1	1	0	0	1	0
## 3:	1	1	0	1	1	1
## 4:	0	0	0	0	0	1
## 5:	0	0	0	1	0	1
## ---						
## 785:	0	0	0	1	1	1
## 786:	1	1	0	0	1	1
## 787:	1	1	0	0	0	0
## 788:	0	0	0	0	0	0
## 789:	0	0	0	0	0	2
##	rs261967_G	rs4836133_A	rs7754840_G	rs7756992_A	rs9356744_C	rs2206734_T
## 1:	2	0	0	0	0	0

##	2:	0	1	0	0	0	0
##	3:	0	0	0	0	0	0
##	4:	1	1	1	1	1	0
##	5:	1	2	0	0	0	0
##	---						
##	785:	0	1	1	1	1	1
##	786:	1	0	1	1	1	0
##	787:	0	0	1	1	1	1
##	788:	1	2	1	1	1	1
##	789:	2	0	1	0	0	0
##		rs1052248_G	rs11575839_C	rs206936_G	rs9470794_A	rs1535500_T	rs987237_C
##	1:	1	0	1	0	1	1
##	2:	1	0	1	0	2	2
##	3:	0	0	0	0	2	0
##	4:	1	0	1	0	1	1
##	5:	1	1	1	0	1	0
##	---						
##	785:	1	0	1	0	2	1
##	786:	0	0	0	0	0	1
##	787:	0	0	2	0	0	2
##	788:	0	0	1	0	0	0
##	789:	1	0	1	1	2	0
##		rs9395950_T	rs17168486_T	rs2191349_T	rs6954897_G	rs864745_A	rs1635852_C
##	1:	0	2	1	1	0	0
##	2:	0	0	1	0	1	1
##	3:	0	1	1	0	1	1
##	4:	0	2	1	0	0	0
##	5:	1	1	2	0	0	0
##	---						
##	785:	0	2	1	0	2	2
##	786:	0	0	1	1	1	1
##	787:	0	2	2	0	1	1
##	788:	0	0	1	0	0	0
##	789:	0	0	1	1	1	1
##		rs849134_G	rs4607517_A	rs6467136_T	rs2167270_G	rs972283_A	rs516946_C
##	1:	1	1	0	2	1	0
##	2:	1	2	1	1	1	0
##	3:	1	0	1	2	2	1
##	4:	0	0	2	1	0	0
##	5:	0	0	0	2	1	0
##	---						
##	785:	2	0	0	0	1	0
##	786:	1	1	1	1	1	1
##	787:	1	1	0	1	0	0
##	788:	0	1	2	1	1	1
##	789:	1	0	0	1	1	0
##		rs896854_C	rs13266634_G	rs3802177_A	rs7041847_G	rs17584499_T	rs2383208_A
##	1:	0	1	1	1	1	0
##	2:	1	1	1	1	0	0
##	3:	1	1	1	1	1	0
##	4:	2	1	1	0	2	0
##	5:	1	1	1	2	1	0
##	---						
##	785:	0	0	0	0	2	0

```

## 786:      0      0      0      0      1      0
## 787:      0      0      0      0      0      0
## 788:      1      1      1      2      0      0
## 789:      1      1      1      1      1      0
##      rs10965250_T rs10811661_A rs2183825_T rs824248_G rs11142387_A rs13292136_A
## 1:      0      0      1      1      2      0
## 2:      0      0      0      0      1      0
## 3:      0      0      0      1      1      0
## 4:      0      0      1      0      0      0
## 5:      0      0      1      0      1      1
## ---
## 785:      0      0      0      0      1      1
## 786:      0      0      0      0      1      1
## 787:      0      0      0      1      1      2
## 788:      0      0      0      1      0      1
## 789:      0      0      0      0      1      0
##      rs2796441_T rs12779790_T rs10882066_C rs1111875_A rs5015480_G rs7087591_T
## 1:      1      0      0      1      1      1
## 2:      0      1      1      1      0      0
## 3:      2      1      1      2      0      0
## 4:      0      1      0      2      0      0
## 5:      0      1      2      0      0      0
## ---
## 785:      1      0      0      2      0      0
## 786:      1      0      1      1      0      0
## 787:      0      1      1      0      1      1
## 788:      1      0      1      1      0      1
## 789:      0      0      0      2      0      0
##      rs7901695_T rs4506565_T rs7903146_C rs12243326_A rs2334499_T rs10770141_A
## 1:      0      0      0      1      1      1
## 2:      0      0      0      0      0      1
## 3:      0      0      0      0      1      1
## 4:      0      0      0      0      1      0
## 5:      0      0      0      0      1      1
## ---
## 785:      0      0      0      0      1      0
## 786:      0      0      0      0      2      1
## 787:      0      0      0      0      1      0
## 788:      1      1      1      1      1      1
## 789:      0      0      0      0      0      1
##      rs231362_T rs2237892_C rs163184_T rs2237897_T rs4929949_C rs5215_C
## 1:      1      2      2      2      1      1
## 2:      0      2      2      2      1      1
## 3:      1      0      0      0      1      0
## 4:      1      0      1      1      2      1
## 5:      1      0      1      0      1      2
## ---
## 785:      0      0      1      0      1      0
## 786:      0      1      1      1      0      0
## 787:      1      1      1      1      2      0
## 788:      0      1      1      1      0      1
## 789:      1      0      0      0      0      2
##      rs2056246_A rs10488683_A rs685249_T rs508924_C rs4923461_T rs6265_G
## 1:      2      0      2      2      1      1

```

##	2:	1	1	1	1	0	0
##	3:	1	1	1	1	0	0
##	4:	0	1	0	0	0	0
##	5:	2	0	2	2	0	0
##	---						
##	785:	1	1	1	1	1	0
##	786:	0	1	0	0	0	0
##	787:	1	0	1	1	0	0
##	788:	1	0	1	1	0	0
##	789:	1	0	1	1	1	1
##		rs10767664_C	rs2030323_C	rs3817334_T	rs10838738_G	rs1552224_T	rs1387153_A
##	1:	1	1	0	0	0	1
##	2:	0	0	0	0	0	0
##	3:	0	0	0	0	0	1
##	4:	0	0	1	1	0	1
##	5:	0	0	0	0	0	0
##	---						
##	785:	0	0	1	1	0	2
##	786:	0	0	2	2	0	0
##	787:	0	0	1	1	0	0
##	788:	0	0	1	0	0	0
##	789:	1	1	0	0	0	1
##		rs10830962_T	rs10830963_A	rs2041139_T	rs73040004_C	rs10842994_G	
##	1:	1	0	0	0	0	
##	2:	0	0	0	1	0	
##	3:	1	1	0	0	0	
##	4:	1	1	0	0	0	
##	5:	0	0	1	1	0	
##	---						
##	785:	1	1	0	0	1	
##	786:	1	0	0	1	0	
##	787:	0	0	0	0	0	
##	788:	0	0	0	1	0	
##	789:	2	1	0	1	1	
##		rs7138803_C	rs1531343_T	rs7961581_C	rs7957197_A	rs4771122_G	rs1359790_A
##	1:	1	0	1	0	1	0
##	2:	1	0	1	0	0	1
##	3:	0	0	0	0	1	2
##	4:	0	0	0	1	0	2
##	5:	0	0	0	0	0	1
##	---						
##	785:	0	0	0	1	1	1
##	786:	0	0	0	1	1	1
##	787:	0	0	0	1	1	2
##	788:	1	0	0	1	1	1
##	789:	1	0	1	0	1	2
##		rs11847697_A	rs10150332_A	rs1884082_G	rs7172432_G	rs2241423_G	rs12898654_T
##	1:	0	0	0	1	2	1
##	2:	0	0	0	2	0	0
##	3:	0	0	1	1	0	0
##	4:	0	0	0	1	0	0
##	5:	0	0	0	1	0	0
##	---						
##	785:	0	0	1	1	1	1

## 786:	0	0	0	2	0	0
## 787:	0	1	1	2	1	1
## 788:	0	1	1	1	2	0
## 789:	0	0	0	0	1	0
##	rs7178572_G	rs7177055_A	rs11634397_A	rs2028299_C	rs8042680_A	rs7359397_G
## 1:	0	0	1	0	1	0
## 2:	1	1	1	0	0	1
## 3:	0	0	1	0	1	0
## 4:	2	2	2	0	0	1
## 5:	0	0	0	0	0	1
## ---						
## 785:	1	2	1	0	2	1
## 786:	0	1	2	1	0	2
## 787:	0	0	2	0	0	1
## 788:	0	0	0	1	2	1
## 789:	0	0	0	0	0	2
##	rs1421085_T	rs1558902_C	rs1121980_G	rs17817449_T	rs8050136_A	rs9939609_A
## 1:	0	0	0	0	0	0
## 2:	1	1	1	1	1	1
## 3:	0	0	0	0	0	0
## 4:	1	1	1	1	1	1
## 5:	0	0	0	0	0	0
## ---						
## 785:	1	1	1	0	0	0
## 786:	0	0	0	0	0	0
## 787:	1	1	2	1	1	1
## 788:	2	2	2	2	2	2
## 789:	0	0	0	0	0	0
##	rs9941349_A	rs12149832_A	rs11642841_G	rs6499500_C	rs7202877_T	rs4523957_G
## 1:	0	0	0	0	0	1
## 2:	1	1	1	0	2	1
## 3:	0	0	0	1	0	0
## 4:	1	1	1	0	0	1
## 5:	0	0	0	2	1	2
## ---						
## 785:	0	0	0	0	0	1
## 786:	0	0	0	1	0	0
## 787:	2	1	0	2	0	2
## 788:	2	2	2	0	1	1
## 789:	0	0	0	1	0	1
##	rs391300_C	rs75493593_C	rs75418188_T	rs13342232_A	rs13342692_C	
## 1:	1	0	0	0	0	
## 2:	1	1	1	1	1	
## 3:	0	0	0	0	0	
## 4:	1	0	0	0	0	
## 5:	2	0	0	0	0	
## ---						
## 785:	0	1	1	2	2	
## 786:	0	0	0	0	0	
## 787:	1	1	1	1	1	
## 788:	1	0	0	0	0	
## 789:	2	1	1	1	1	
##	rs117767867_T	rs757210_T	rs4430796_T	rs7501939_C	rs2331841_C	rs6567160_G
## 1:	0	1	1	1	0	0

```

##      2:      1      1      1      1      0      0
##      3:      0      1      1      1      0      0
##      4:      0      0      0      0      1      0
##      5:      0      1      1      1      1      0
## ---
## 785:      1      1      1      1      1      1
## 786:      0      1      1      1      1      1
## 787:      1      0      1      0      0      0
## 788:      0      0      0      0      1      0
## 789:      1      0      0      0      1      0
##      rs571312_G rs17782313_T rs12970134_C rs1423096_T rs3786897_A rs29941_T
##      1:      0      0      1      0      0      1
##      2:      0      0      0      0      0      1
##      3:      0      0      0      0      0      1
##      4:      0      0      0      0      0      2
##      5:      0      0      0      0      0      0
## ---
## 785:      1      1      2      0      0      1
## 786:      1      1      1      0      1      1
## 787:      0      0      1      0      0      0
## 788:      0      0      1      0      0      0
## 789:      1      1      1      0      1      1
##      rs8108269_T rs2287019_A rs3810291_T rs6017317_G rs1800961_G rs5945326_C
##      1:      0      0      0      1      0      1
##      2:      0      0      2      0      0      0
##      3:      1      0      1      0      0      1
##      4:      2      0      1      2      0      2
##      5:      0      0      0      2      0      0
## ---
## 785:      0      0      2      1      0      0
## 786:      1      1      2      0      0      1
## 787:      1      0      2      0      0      0
## 788:      1      1      0      0      0      1
## 789:      0      0      0      0      0      0
##      weighted.risk.3 weighted.risk.4 weighted.risk.FTO
##      1:      -1.0420490      -0.2334714      0.0000000
##      2:      -1.6874688      -0.8788912      0.4740752
##      3:      0.0000000      0.0000000      0.0000000
##      4:      -0.4394456      -0.4394456      0.4740752
##      5:      0.0000000      0.0000000      0.0000000
## ---
## 785:      0.0000000      0.0000000      0.3599666
## 786:      -0.3808404      -0.4394456      0.0000000
## 787:      -0.8437344      -0.4394456      0.6840916
## 788:      1.2550123      0.2059742      0.9481504
## 789:      0.4628940      0.0000000      0.0000000

risk.3.logistic <- glm(gdm.dt$pheno ~ gdm.dt$weighted.risk.3, family='binomial')
risk.4.logistic <- glm(gdm.dt$pheno ~ gdm.dt$weighted.risk.4, family='binomial')
risk.FTO.logistic <- glm(gdm.dt$pheno ~ gdm.dt$weighted.risk.FTO, family='binomial')

report.3 <- NULL
report.3 <- transpose(as.data.table(coef(summary(risk.3.logistic))[-1, -3]))
report.3 <- cbind(report.3,

```

```

exp(coef(risk.3.logistic))[2],
exp(confint(risk.3.logistic, level=0.95)[2,1]),
exp(confint(risk.3.logistic, level=0.95)[2,2]),
"p.value 1e-3")

## Waiting for profiling to be done...
## Waiting for profiling to be done...

colnames(report.3) <- c("beta","std.error", "p.value", "odds ratio", "odds ratio 2.5%", "odds ratio 97.5%")
report.4 <- NULL
report.4 <- transpose(as.data.table(coef(summary(risk.4.logistic))[-1, -3]))
report.4 <- cbind(report.4,
exp(coef(risk.4.logistic))[2],
exp(confint(risk.4.logistic, level=0.95)[2,1]),
exp(confint(risk.4.logistic, level=0.95)[2,2]),
"p.value 1e-4")

## Waiting for profiling to be done...
## Waiting for profiling to be done...

colnames(report.4) <- c("beta","std.error", "p.value", "odds ratio", "odds ratio 2.5%", "odds ratio 97.5%")
report.FT0 <- NULL
report.FT0 <- transpose(as.data.table(coef(summary(risk.3.logistic))[-1, -3]))
report.FT0 <- cbind(report.FT0,
exp(coef(risk.FT0.logistic))[2],
exp(confint(risk.FT0.logistic, level=0.95)[2,1]),
exp(confint(risk.FT0.logistic, level=0.95)[2,2]),
"gene FT0")

## Waiting for profiling to be done...
## Waiting for profiling to be done...

colnames(report.FT0) <- c("beta","std.error", "p.value", "odds ratio", "odds ratio 2.5%", "odds ratio 97.5%")

report <- rbind(report.3, report.4, report.FT0)
report[,3:7]

##           p.value odds ratio odds ratio 2.5% odds ratio 97.5%  identifier
## 1: 7.813912e-09   1.451854      1.2814405      1.651126 p.value 1e-3
## 2: 2.759214e-08   2.729432      1.9243530      3.911052 p.value 1e-4
## 3: 7.813912e-09   1.413857      0.8191201      2.452615   gene FT0

```

Problem 2.f (4 points)

File GDM.test.txt (available from the accompanying zip folder on Learn) contains genotypes of another 40 pregnant women with and without gestational diabetes (assume that the reference allele is the same one that was specified in file GDM.raw.txt). Read the file into variable gdm.test. For the set of patients in gdm.test, compute the three genetic risk scores as defined in problem 2.e using the same set of SNPs and corresponding weights. Add the three scores as columns to gdm.test (hint: use the same columnnames as before).

```

# Enter code here.
gdm.test <- fread("data/GDM.test.txt")
X <- as.data.table(gdm.test[,4:ncol(gdm.test)])
target <- gdm.test$pheno

association.test <- data.table(univ.glm.test(x=X,y=target, ordering=TRUE), key=c('snp_full'))

```

```

pk <- c('snp')
setnames(association.test, "snp_full", "snp")
association.test.ext <- merge(association.test,
                             gdm.annot.dt,
                             by=pk,
                             all=TRUE)[order(snp)]

snps.grs.3 <- association.test.ext[p.value < 1e-3]
snps.grs.4 <- association.test.ext[p.value < 1e-4]
snps.grs.FT0 <- association.test.ext[gene == 'FT0']

gdm.grs.3 <- gdm.test[, .SD, .SDcols = snps.grs.3$snp]
gdm.grs.4 <- gdm.test[, .SD, .SDcols = snps.grs.4$snp]
gdm.grs.FT0 <- gdm.test[, .SD, .SDcols = snps.grs.FT0$snp]

weighted.score.3 <- as.matrix(gdm.grs.3) %*% snps.grs.3$beta
weighted.score.4 <- as.matrix(gdm.grs.4) %*% snps.grs.4$beta
weighted.score.FT0 <- as.matrix(gdm.grs.FT0) %*% snps.grs.FT0$beta

gdm.test[,weighted.risk.3:=weighted.score.3]
gdm.test[,weighted.risk.4:=weighted.score.4]
gdm.test[,weighted.risk.FT0:=weighted.score.FT0]
gdm.test

```

##	ID	sex	pheno	rs7513574	rs1627238	rs1171278	rs1137100	rs2568958	rs1514175
##	1: 1101	F	0	0	0	0	2	0	1
##	2: 1102	F	0	1	0	0	1	0	0
##	3: 1104	F	1	1	1	1	1	1	1
##	4: 1105	F	1	0	0	1	1	0	2
##	5: 1106	F	1	0	1	1	1	1	0
##	6: 1107	F	0	1	1	1	0	0	0
##	7: 1108	F	0	0	0	0	1	2	1
##	8: 1112	F	1	1	1	1	1	0	2
##	9: 1113	F	0	2	0	0	2	0	0
##	10: 1118	F	0	1	0	0	0	0	1
##	11: 1119	F	1	0	1	1	1	0	1
##	12: 1120	F	0	0	0	0	1	1	1
##	13: 1122	F	0	0	2	2	0	0	0
##	14: 1123	F	1	0	2	2	0	1	1
##	15: 1124	F	0	1	0	0	1	1	0
##	16: 1125	F	1	1	1	1	1	0	1
##	17: 1126	F	1	1	2	2	0	1	1
##	18: 1127	F	0	0	0	0	2	0	1
##	19: 1128	F	0	0	1	1	1	0	1
##	20: 1131	F	1	1	1	1	0	1	0
##	21: 1133	F	0	0	1	1	0	0	1
##	22: 1134	F	1	1	1	1	0	0	1
##	23: 1135	F	0	2	0	0	2	0	0
##	24: 1137	F	0	1	0	0	0	0	1
##	25: 1140	F	1	2	1	1	1	0	0
##	26: 1141	F	0	2	0	0	1	0	1
##	27: 1142	F	1	1	1	1	0	1	0
##	28: 1143	F	1	0	1	1	0	1	2
##	29: 1144	F	0	1	0	0	2	0	1

## 30:	1145	F	1	2	1	2	0	1	1
## 31:	1146	F	0	1	0	2	0	0	1
## 32:	1147	F	1	0	1	1	0	1	0
## 33:	1148	F	0	1	1	1	0	1	1
## 34:	1149	F	0	0	0	0	1	0	1
## 35:	1151	F	0	0	1	1	1	0	0
## 36:	1152	F	1	1	0	0	0	1	2
## 37:	1155	F	0	1	1	0	0	0	1
## 38:	1156	F	1	1	0	0	1	0	0
## 39:	1157	F	0	1	1	1	1	0	0
## 40:	1159	F	0	0	1	1	0	1	0
##	ID	sex	pheno	rs7513574	rs1627238	rs1171278	rs1137100	rs2568958	rs1514175
##	rs1555543	rs10923931	rs516636	rs574367	rs543874	rs7554506	rs340874		
## 1:	2	0	0	0	0	0	0	0	
## 2:	1	0	1	0	1	0	1		
## 3:	2	0	0	0	0	0	0	1	
## 4:	2	1	0	0	0	0	0	1	
## 5:	0	0	0	0	0	0	0	0	
## 6:	0	0	2	2	2	0	0		
## 7:	1	0	1	1	1	0	0		
## 8:	0	0	0	0	0	0	0		
## 9:	1	0	1	1	1	1	0		
## 10:	0	0	0	0	0	0	1		
## 11:	1	0	1	1	1	0	1		
## 12:	0	0	0	0	0	0	1		
## 13:	2	0	1	1	1	1	1		
## 14:	0	0	0	0	0	1	1		
## 15:	1	1	2	2	2	1	1		
## 16:	1	0	1	1	1	0	0		
## 17:	0	0	1	1	1	0	0		
## 18:	0	1	1	1	1	2	1		
## 19:	1	0	1	1	1	0	0		
## 20:	0	0	1	1	1	0	0		
## 21:	0	0	0	0	0	0	0		
## 22:	0	0	1	1	1	0	1		
## 23:	1	1	0	0	0	0	1		
## 24:	1	1	0	0	0	0	2		
## 25:	2	1	1	1	1	0	1		
## 26:	1	0	1	1	1	0	2		
## 27:	1	0	0	0	0	0	1		
## 28:	2	0	1	1	1	0	0		
## 29:	1	0	1	1	1	0	1		
## 30:	0	0	1	1	1	1	0		
## 31:	2	0	0	0	0	0	1		
## 32:	1	0	1	1	1	0	0		
## 33:	1	1	1	1	1	1	1		
## 34:	1	0	0	0	1	0	0		
## 35:	1	0	0	0	0	0	1		
## 36:	0	0	0	0	0	0	1		
## 37:	1	0	0	0	0	0	1		
## 38:	1	0	0	0	0	0	1		
## 39:	1	1	0	0	0	0	2		
## 40:	0	0	0	0	0	0	1		
##	rs1555543	rs10923931	rs516636	rs574367	rs543874	rs7554506	rs340874		

##	rs2867125	rs6548238	rs7561317	rs6545814	rs713586	rs11899863	rs7578597
## 1:	0	0	0	0	0	0	0
## 2:	0	0	0	0	0	0	0
## 3:	0	0	0	0	0	0	0
## 4:	0	0	0	1	1	1	0
## 5:	0	0	0	1	1	1	1
## 6:	0	0	0	0	0	0	0
## 7:	0	0	0	0	0	0	0
## 8:	1	1	0	0	0	0	0
## 9:	0	0	0	2	2	0	0
## 10:	0	0	0	1	1	0	0
## 11:	0	0	0	0	0	0	0
## 12:	0	0	0	0	0	0	0
## 13:	0	0	0	1	1	0	0
## 14:	0	0	0	0	0	0	0
## 15:	0	0	0	1	1	0	1
## 16:	0	0	0	1	1	0	0
## 17:	0	0	0	0	1	0	0
## 18:	0	0	0	0	0	0	0
## 19:	0	0	0	1	1	0	0
## 20:	0	1	1	1	1	0	0
## 21:	0	0	0	0	0	0	0
## 22:	0	0	0	0	1	0	0
## 23:	0	0	0	0	0	0	0
## 24:	0	0	0	1	1	0	0
## 25:	1	1	1	0	0	0	0
## 26:	0	0	0	0	0	0	0
## 27:	0	0	0	0	0	0	0
## 28:	1	1	0	0	0	0	0
## 29:	0	0	0	0	0	0	0
## 30:	0	0	0	1	1	0	0
## 31:	0	0	0	0	0	0	0
## 32:	0	0	0	0	0	0	0
## 33:	0	0	0	0	0	1	1
## 34:	0	0	0	0	1	0	0
## 35:	0	0	0	0	1	0	0
## 36:	0	0	0	0	0	0	0
## 37:	0	0	0	0	0	0	0
## 38:	1	1	0	0	0	0	1
## 39:	0	0	0	0	0	0	0
## 40:	0	0	0	0	0	0	0
##	rs2867125	rs6548238	rs7561317	rs6545814	rs713586	rs11899863	rs7578597
##	rs887912	rs243021	rs2890652	rs2925757	rs3923113	rs13389219	rs7578326
## 1:	0	1	0	0	0	1	0
## 2:	0	1	0	0	0	0	1
## 3:	1	1	0	0	1	1	1
## 4:	0	0	0	0	0	0	0
## 5:	0	0	0	0	0	0	0
## 6:	0	0	0	0	0	0	0
## 7:	0	1	0	1	0	0	0
## 8:	0	0	0	0	0	0	0
## 9:	0	0	0	0	0	0	1
## 10:	0	1	0	1	1	1	1
## 11:	0	2	0	1	1	1	0

## 12:	0	1	0	0	0	0	0
## 13:	0	2	1	0	0	1	1
## 14:	0	1	0	0	0	0	1
## 15:	1	1	0	0	0	0	1
## 16:	1	1	0	0	0	0	0
## 17:	0	0	0	0	0	0	0
## 18:	0	1	0	0	1	1	1
## 19:	0	0	0	0	0	0	0
## 20:	1	0	1	0	1	1	0
## 21:	0	1	0	0	0	2	1
## 22:	0	0	0	0	0	0	2
## 23:	0	1	0	1	0	0	0
## 24:	0	2	0	0	0	0	0
## 25:	0	0	1	0	1	1	0
## 26:	0	0	0	0	0	0	0
## 27:	1	0	0	0	1	1	0
## 28:	0	0	0	0	0	0	1
## 29:	0	0	0	0	0	0	1
## 30:	0	1	1	0	0	0	0
## 31:	1	1	0	0	1	1	0
## 32:	0	1	0	0	0	0	0
## 33:	0	1	1	0	0	0	1
## 34:	0	0	0	0	1	1	0
## 35:	0	0	0	1	0	0	0
## 36:	0	1	0	0	0	0	0
## 37:	0	1	1	0	1	0	0
## 38:	0	1	0	0	0	0	0
## 39:	0	2	1	0	0	0	1
## 40:	0	1	0	1	1	1	2
##	rs887912 rs243021 rs2890652 rs2925757 rs3923113 rs13389219 rs7578326						
##	rs2943641 rs1801282 rs6780569 rs831571 rs4607103 rs13078807 rs11708067						
## 1:	1	0	0	0	1	0	1
## 2:	0	0	0	0	1	0	0
## 3:	0	0	0	0	0	0	1
## 4:	0	1	0	0	0	0	2
## 5:	0	0	1	0	1	0	0
## 6:	0	0	0	0	0	0	1
## 7:	0	0	0	0	0	0	1
## 8:	0	0	0	0	1	1	1
## 9:	1	0	0	0	2	0	0
## 10:	1	0	0	0	0	0	0
## 11:	0	1	0	0	1	0	0
## 12:	0	1	0	0	0	0	0
## 13:	0	0	0	0	1	0	0
## 14:	1	1	0	0	0	0	1
## 15:	1	0	0	0	1	0	1
## 16:	0	1	0	0	1	0	1
## 17:	0	0	0	0	1	0	0
## 18:	0	1	0	0	2	0	0
## 19:	0	0	0	0	0	0	2
## 20:	1	0	0	0	0	0	0
## 21:	0	0	0	0	0	0	0
## 22:	1	1	0	0	0	0	1
## 23:	0	0	0	0	1	0	0

## 24:	0	1	0	0	1	0	1
## 25:	1	1	1	0	0	0	0
## 26:	0	0	0	0	2	1	1
## 27:	0	0	0	0	2	0	1
## 28:	0	1	0	0	0	0	0
## 29:	0	1	0	0	1	0	1
## 30:	1	0	0	0	1	0	0
## 31:	0	0	0	1	1	0	0
## 32:	0	0	0	0	0	0	1
## 33:	0	0	0	0	1	0	0
## 34:	0	0	0	0	1	0	2
## 35:	0	0	0	0	0	0	1
## 36:	0	0	0	0	0	1	1
## 37:	0	0	1	0	0	0	1
## 38:	0	0	0	0	0	0	0
## 39:	0	0	1	1	1	1	0
## 40:	1	0	0	0	2	0	2
##	rs2943641	rs1801282	rs6780569	rs831571	rs4607103	rs13078807	rs11708067
##	rs187230	rs4402960	rs1470579	rs7647305	rs9816226	rs266729	rs1501299
## 1:	1	0	0	0	0	1	1
## 2:	1	0	0	1	0	0	2
## 3:	0	2	2	1	0	2	1
## 4:	1	0	0	0	0	0	2
## 5:	1	0	0	0	0	0	2
## 6:	1	1	1	0	0	0	0
## 7:	1	0	0	1	1	0	0
## 8:	1	0	0	2	1	1	0
## 9:	1	0	0	0	0	0	2
## 10:	0	0	2	2	0	0	0
## 11:	1	0	0	0	0	1	0
## 12:	1	1	1	0	0	0	1
## 13:	2	1	1	0	0	0	0
## 14:	1	1	1	0	0	1	1
## 15:	1	2	2	1	1	1	0
## 16:	2	2	2	0	0	0	0
## 17:	1	1	1	0	0	0	1
## 18:	0	0	0	0	0	0	0
## 19:	1	1	1	0	0	1	0
## 20:	1	0	0	0	0	1	1
## 21:	0	0	0	0	0	1	0
## 22:	1	1	1	0	0	1	1
## 23:	0	0	0	0	0	1	1
## 24:	1	0	0	0	0	1	1
## 25:	1	0	0	0	0	1	0
## 26:	0	0	0	0	0	1	0
## 27:	1	1	1	0	0	1	0
## 28:	0	0	0	0	0	0	0
## 29:	1	0	0	0	0	1	0
## 30:	1	1	1	0	0	1	0
## 31:	2	0	0	1	1	0	1
## 32:	0	1	1	0	0	0	0
## 33:	1	0	0	1	1	0	0
## 34:	1	0	0	1	0	2	0
## 35:	2	1	1	0	0	0	1

## 36:	1	1	1	2	1	1	1
## 37:	2	0	0	0	0	1	1
## 38:	1	0	0	0	0	2	0
## 39:	0	1	1	2	2	0	0
## 40:	0	0	0	0	0	2	0
##	rs187230	rs4402960	rs1470579	rs7647305	rs9816226	rs266729	rs1501299
##	rs16861329	rs6815464	rs4688985	rs1801214	rs10938397	rs2227306	rs2886920
## 1:	0	0	1	2	0	1	1
## 2:	1	0	0	0	0	1	1
## 3:	1	1	0	0	0	1	1
## 4:	1	0	0	0	0	0	0
## 5:	1	0	0	0	0	0	0
## 6:	1	0	0	0	0	1	1
## 7:	1	1	0	0	2	1	2
## 8:	1	1	0	0	0	0	0
## 9:	1	0	1	1	2	0	1
## 10:	0	1	0	1	0	0	0
## 11:	0	0	0	0	2	0	0
## 12:	0	1	0	0	1	1	1
## 13:	0	0	0	0	0	0	0
## 14:	1	2	0	0	1	2	2
## 15:	0	1	1	0	1	1	1
## 16:	1	1	0	0	0	1	1
## 17:	1	1	0	0	0	0	1
## 18:	1	0	0	0	1	1	1
## 19:	2	2	0	0	0	0	0
## 20:	2	2	0	0	0	1	1
## 21:	0	2	0	1	0	0	0
## 22:	0	0	0	1	0	2	2
## 23:	0	2	0	2	2	1	1
## 24:	2	1	0	1	0	1	0
## 25:	0	1	0	0	0	0	0
## 26:	1	0	0	0	2	0	0
## 27:	0	0	0	0	0	0	1
## 28:	0	0	0	0	1	1	1
## 29:	1	1	0	0	0	0	0
## 30:	1	0	0	0	1	0	0
## 31:	1	0	0	0	1	0	0
## 32:	1	0	0	0	1	0	0
## 33:	0	1	0	1	1	1	1
## 34:	1	2	1	1	1	0	0
## 35:	1	1	0	0	1	1	1
## 36:	1	1	1	1	1	2	2
## 37:	1	1	0	0	2	1	1
## 38:	1	1	0	1	1	0	0
## 39:	0	1	0	1	0	0	0
## 40:	0	2	0	0	1	0	1
##	rs16861329	rs6815464	rs4688985	rs1801214	rs10938397	rs2227306	rs2886920
##	rs13107325	rs459193	rs2112347	rs4457053	rs261967	rs4836133	rs7754840
## 1:	0	0	0	2	2	0	0
## 2:	0	0	1	0	0	1	0
## 3:	0	1	1	1	0	0	0
## 4:	0	0	0	1	1	1	1
## 5:	0	1	0	1	1	2	0

## 6:	0	0	1	0	0	0	0
## 7:	0	1	0	1	1	0	1
## 8:	0	1	1	1	0	1	0
## 9:	0	0	0	1	0	2	0
## 10:	0	2	0	0	0	0	1
## 11:	0	0	1	1	2	0	1
## 12:	0	0	2	1	2	0	1
## 13:	0	1	1	0	0	0	1
## 14:	0	0	0	0	0	0	1
## 15:	0	0	1	2	1	0	2
## 16:	0	1	0	0	2	0	1
## 17:	0	1	0	1	1	0	1
## 18:	0	1	1	1	2	2	1
## 19:	0	0	1	1	1	0	1
## 20:	0	1	0	1	1	1	0
## 21:	0	2	1	0	0	0	1
## 22:	0	1	1	0	1	0	1
## 23:	0	1	0	1	0	0	0
## 24:	0	2	1	2	1	0	1
## 25:	0	1	2	2	1	0	1
## 26:	0	0	0	1	0	0	1
## 27:	0	1	0	1	1	0	1
## 28:	0	1	0	0	0	1	0
## 29:	0	0	1	0	0	0	0
## 30:	0	0	2	1	0	1	1
## 31:	0	1	1	1	0	2	1
## 32:	0	0	0	0	1	0	0
## 33:	0	1	0	2	0	0	1
## 34:	0	1	1	1	2	0	1
## 35:	0	1	0	1	0	1	0
## 36:	0	0	2	0	1	1	2
## 37:	1	0	0	1	1	0	1
## 38:	0	0	1	1	1	1	0
## 39:	0	1	0	0	2	0	0
## 40:	0	0	1	1	1	1	2
##	rs13107325	rs459193	rs2112347	rs4457053	rs261967	rs4836133	rs7754840
##	rs7756992	rs9356744	rs2206734	rs1052248	rs11575839	rs206936	rs9470794
## 1:	0	0	0	1	0	1	0
## 2:	0	0	0	1	0	1	0
## 3:	0	0	0	0	0	0	0
## 4:	1	1	0	1	0	1	0
## 5:	0	0	0	1	1	1	0
## 6:	0	0	0	0	0	0	0
## 7:	1	1	1	0	0	1	0
## 8:	0	0	0	0	0	0	0
## 9:	0	0	0	2	0	2	0
## 10:	1	1	0	0	0	0	1
## 11:	1	1	0	0	0	0	0
## 12:	1	1	0	0	0	0	0
## 13:	1	1	1	0	0	1	1
## 14:	1	1	0	1	0	1	0
## 15:	2	2	1	1	1	1	0
## 16:	1	1	0	0	0	1	0
## 17:	1	1	0	1	0	1	1

## 18:	1	1	1	1	0	0	0
## 19:	1	1	1	0	0	1	0
## 20:	0	0	0	0	0	1	0
## 21:	1	1	0	1	0	0	0
## 22:	1	1	1	0	0	1	0
## 23:	0	0	0	2	1	2	0
## 24:	1	1	1	0	0	0	0
## 25:	2	1	1	0	0	1	0
## 26:	1	1	1	0	0	0	0
## 27:	1	1	0	1	0	0	1
## 28:	0	1	0	1	0	1	0
## 29:	0	0	0	1	0	1	0
## 30:	2	1	1	0	0	1	0
## 31:	1	1	1	1	0	1	0
## 32:	0	0	0	0	0	0	0
## 33:	1	1	1	0	0	2	0
## 34:	1	1	1	0	0	0	0
## 35:	0	0	0	0	0	0	0
## 36:	2	2	2	0	0	1	0
## 37:	1	1	1	1	0	0	0
## 38:	0	0	0	0	0	1	0
## 39:	0	1	0	0	0	0	1
## 40:	2	2	0	0	0	1	0
##	rs7756992	rs9356744	rs2206734	rs1052248	rs11575839	rs206936	rs9470794
##	rs1535500	rs987237	rs9395950	rs17168486	rs2191349	rs6954897	rs864745
## 1:	1	1	0	2	1	1	0
## 2:	2	2	0	0	1	0	1
## 3:	2	0	0	1	1	0	1
## 4:	1	1	0	2	1	0	0
## 5:	1	0	1	1	2	0	0
## 6:	0	0	0	0	1	0	1
## 7:	1	0	0	1	1	0	1
## 8:	1	0	0	2	1	0	1
## 9:	1	1	0	1	1	1	1
## 10:	1	2	0	1	2	1	1
## 11:	0	1	0	1	0	1	2
## 12:	0	2	0	2	0	0	2
## 13:	2	1	0	1	0	1	0
## 14:	0	0	0	0	0	2	2
## 15:	2	0	0	2	1	1	1
## 16:	1	1	0	0	0	1	0
## 17:	1	1	0	1	0	0	1
## 18:	1	1	0	1	0	0	0
## 19:	1	2	0	1	1	0	1
## 20:	2	1	0	2	2	0	2
## 21:	1	1	0	1	0	0	0
## 22:	1	1	1	1	2	1	1
## 23:	2	0	0	1	2	1	2
## 24:	1	0	0	1	2	0	0
## 25:	0	0	0	2	1	1	1
## 26:	1	1	0	1	1	0	2
## 27:	0	2	1	1	1	1	1
## 28:	2	1	0	1	2	0	0
## 29:	0	1	0	1	0	0	0

## 30:	0	2	0	2	2	1	2	
## 31:	0	1	0	2	1	1	1	
## 32:	0	2	1	1	0	0	1	
## 33:	0	1	0	1	0	0	1	
## 34:	1	0	0	0	1	0	2	
## 35:	0	0	0	2	1	1	1	
## 36:	1	0	0	0	0	1	2	
## 37:	1	0	0	1	0	1	1	
## 38:	2	0	1	1	1	0	1	
## 39:	1	1	0	1	2	1	1	
## 40:	1	2	0	2	1	1	0	
##	rs1535500	rs987237	rs9395950	rs17168486	rs2191349	rs6954897	rs864745	
##	rs1635852	rs849134	rs4607517	rs6467136	rs2167270	rs972283	rs516946	rs896854
## 1:	0	1	1	0	2	1	0	0
## 2:	1	1	2	1	1	1	0	1
## 3:	1	1	0	1	2	2	1	1
## 4:	0	0	0	2	1	0	0	2
## 5:	0	0	0	0	2	1	0	1
## 6:	1	1	0	0	2	0	1	0
## 7:	1	1	1	1	1	1	0	2
## 8:	1	1	0	1	2	0	1	1
## 9:	1	1	0	1	2	0	0	1
## 10:	1	1	1	1	1	1	0	1
## 11:	2	2	1	0	0	1	0	2
## 12:	2	1	0	0	1	2	0	1
## 13:	0	0	1	2	0	0	1	0
## 14:	2	2	0	2	0	1	0	1
## 15:	1	1	1	2	1	1	1	0
## 16:	0	0	1	2	2	1	1	2
## 17:	1	1	0	2	2	1	0	0
## 18:	0	0	0	1	0	0	2	1
## 19:	1	1	0	0	0	1	2	1
## 20:	2	2	0	2	0	0	0	1
## 21:	0	0	0	1	1	1	0	2
## 22:	1	1	1	0	0	1	0	2
## 23:	2	2	0	1	1	0	0	0
## 24:	0	0	0	2	1	2	0	1
## 25:	1	1	2	1	0	1	0	1
## 26:	2	2	0	1	0	1	0	1
## 27:	1	1	1	1	2	1	1	1
## 28:	0	0	0	2	1	0	1	2
## 29:	0	0	1	0	2	0	0	2
## 30:	2	2	0	1	1	0	0	1
## 31:	1	1	0	2	1	1	0	1
## 32:	1	1	0	0	1	1	1	1
## 33:	1	1	0	2	1	1	0	1
## 34:	2	2	0	1	2	2	0	1
## 35:	1	1	0	0	1	0	0	2
## 36:	2	2	0	1	2	0	2	1
## 37:	1	1	0	0	2	0	0	2
## 38:	2	2	1	0	2	1	0	1
## 39:	1	1	0	1	1	0	0	2
## 40:	0	0	1	2	2	1	0	1
##	rs1635852	rs849134	rs4607517	rs6467136	rs2167270	rs972283	rs516946	rs896854

	rs13266634	rs3802177	rs7041847	rs17584499	rs2383208	rs10965250	rs10811661
## 1:	1	1	1	1	0	0	0
## 2:	1	1	1	0	0	0	0
## 3:	1	1	1	1	0	0	0
## 4:	1	1	0	2	0	0	0
## 5:	1	1	2	1	0	0	0
## 6:	0	0	1	0	0	0	0
## 7:	0	0	1	0	0	0	0
## 8:	1	1	1	0	0	0	0
## 9:	0	0	2	0	0	2	2
## 10:	0	0	1	1	0	0	0
## 11:	0	0	0	1	0	0	0
## 12:	1	1	0	0	1	1	1
## 13:	0	0	1	1	1	1	1
## 14:	0	0	1	0	0	0	0
## 15:	0	0	1	1	0	0	0
## 16:	0	0	1	1	1	1	1
## 17:	1	2	0	1	0	0	0
## 18:	1	1	2	1	1	1	1
## 19:	0	0	1	0	1	1	1
## 20:	0	0	2	1	0	0	0
## 21:	1	1	0	0	0	0	0
## 22:	1	1	0	1	0	0	0
## 23:	0	0	0	0	1	1	1
## 24:	1	1	0	1	0	0	0
## 25:	0	0	2	0	0	0	0
## 26:	1	1	0	1	0	0	0
## 27:	0	0	2	0	0	0	0
## 28:	0	0	1	1	1	1	1
## 29:	2	2	2	0	0	0	0
## 30:	0	0	0	0	0	0	0
## 31:	1	1	2	1	0	0	0
## 32:	0	0	2	1	0	0	0
## 33:	1	1	0	0	0	0	0
## 34:	0	0	1	1	0	0	0
## 35:	0	0	1	0	0	0	0
## 36:	0	0	0	0	0	0	0
## 37:	0	0	0	1	0	0	0
## 38:	0	0	1	0	0	0	0
## 39:	0	0	1	0	0	0	0
## 40:	1	0	0	1	0	0	0
##	rs13266634	rs3802177	rs7041847	rs17584499	rs2383208	rs10965250	rs10811661
##	rs2183825	rs824248	rs11142387	rs13292136	rs2796441	rs12779790	rs10882066
## 1:	1	1	2	0	1	0	0
## 2:	0	0	1	0	0	1	1
## 3:	0	1	1	0	2	1	1
## 4:	1	0	0	0	0	1	0
## 5:	1	0	1	1	0	1	2
## 6:	1	0	1	0	0	1	0
## 7:	1	0	0	1	1	1	2
## 8:	0	0	1	1	1	1	2
## 9:	0	2	1	1	1	0	0
## 10:	0	1	1	0	0	0	0
## 11:	1	1	1	1	1	0	1

## 12:	0	1	1	0	0	0	1
## 13:	0	1	1	0	2	0	1
## 14:	0	0	1	0	0	2	1
## 15:	1	1	1	0	2	0	0
## 16:	1	2	1	0	2	0	0
## 17:	0	1	1	0	0	0	1
## 18:	1	0	1	0	2	1	0
## 19:	0	0	2	0	2	0	0
## 20:	0	1	1	0	2	0	0
## 21:	0	0	1	1	1	1	0
## 22:	0	1	0	1	2	0	1
## 23:	0	1	2	0	1	0	1
## 24:	1	1	0	0	2	0	0
## 25:	1	1	2	0	1	0	0
## 26:	0	0	0	0	0	0	1
## 27:	0	0	0	0	1	0	0
## 28:	0	0	2	0	1	0	0
## 29:	1	2	0	1	0	0	0
## 30:	2	0	0	0	1	0	0
## 31:	0	2	1	0	2	0	0
## 32:	0	0	2	0	2	1	1
## 33:	0	1	1	0	0	0	1
## 34:	1	2	1	2	0	0	2
## 35:	0	2	1	0	1	0	1
## 36:	0	0	0	0	0	1	0
## 37:	0	1	2	0	0	0	1
## 38:	0	0	2	0	1	1	0
## 39:	0	2	0	0	1	1	1
## 40:	1	0	0	1	1	0	1
##	rs2183825	rs824248	rs11142387	rs13292136	rs2796441	rs12779790	rs10882066
##	rs1111875	rs5015480	rs7087591	rs7901695	rs4506565	rs7903146	rs12243326
## 1:	1	1	1	0	0	0	1
## 2:	1	0	0	0	0	0	0
## 3:	2	0	0	0	0	0	0
## 4:	2	0	0	0	0	0	0
## 5:	0	0	0	0	0	0	0
## 6:	1	1	1	0	0	0	0
## 7:	0	0	0	0	0	0	0
## 8:	0	0	0	0	0	0	0
## 9:	0	2	2	0	0	0	0
## 10:	1	1	1	0	0	0	0
## 11:	0	1	1	1	1	1	1
## 12:	0	1	1	0	0	0	0
## 13:	1	0	0	1	1	1	0
## 14:	1	0	0	0	0	0	0
## 15:	0	2	2	1	1	1	1
## 16:	0	1	1	0	0	0	0
## 17:	1	0	0	0	0	0	0
## 18:	1	1	2	0	0	0	0
## 19:	0	1	1	0	0	0	0
## 20:	0	2	2	1	1	1	1
## 21:	1	1	1	0	0	0	0
## 22:	1	0	1	1	1	1	0
## 23:	1	0	1	0	0	0	0

## 24:	2	0	0	0	0	0	0
## 25:	1	1	1	0	0	0	0
## 26:	1	0	0	0	0	0	0
## 27:	2	0	0	1	1	1	0
## 28:	2	0	0	0	0	0	0
## 29:	2	0	2	0	0	0	0
## 30:	1	1	2	1	2	2	2
## 31:	1	1	1	0	0	0	0
## 32:	1	0	0	0	0	0	0
## 33:	0	1	1	0	0	0	0
## 34:	0	0	0	0	0	0	0
## 35:	0	1	1	0	0	0	0
## 36:	1	1	1	1	1	1	1
## 37:	1	0	0	1	1	1	0
## 38:	1	1	2	0	0	0	0
## 39:	1	0	0	0	0	0	0
## 40:	1	0	0	0	0	0	0
##	rs1111875	rs5015480	rs7087591	rs7901695	rs4506565	rs7903146	rs12243326
##	rs2334499	rs10770141	rs231362	rs2237892	rs163184	rs2237897	rs4929949
## 1:	1	1	1	2	2	2	1
## 2:	0	1	0	2	2	2	1
## 3:	1	1	1	0	0	0	1
## 4:	1	0	1	0	1	1	2
## 5:	1	1	1	0	1	0	1
## 6:	1	0	0	2	2	2	1
## 7:	0	2	1	2	2	2	1
## 8:	0	0	1	1	1	1	1
## 9:	2	0	1	0	1	0	1
## 10:	1	2	0	1	2	1	2
## 11:	1	2	1	0	0	0	1
## 12:	0	2	2	0	1	0	1
## 13:	2	0	1	0	1	0	1
## 14:	2	0	1	0	1	0	1
## 15:	0	0	1	0	1	0	1
## 16:	0	0	0	0	0	0	2
## 17:	2	1	0	1	0	0	1
## 18:	1	0	0	1	1	1	1
## 19:	2	0	2	0	0	0	0
## 20:	2	0	0	0	1	0	1
## 21:	1	0	2	1	1	0	0
## 22:	2	1	1	0	1	0	1
## 23:	1	0	0	2	2	2	1
## 24:	1	1	2	0	2	0	0
## 25:	0	0	0	0	0	0	1
## 26:	1	2	1	1	2	1	2
## 27:	1	1	0	0	2	0	1
## 28:	0	0	0	2	2	2	1
## 29:	1	0	1	1	2	1	0
## 30:	1	0	0	0	1	1	1
## 31:	2	1	0	0	0	0	0
## 32:	1	1	1	0	1	0	1
## 33:	2	2	0	1	1	1	0
## 34:	0	1	2	0	1	0	0
## 35:	0	1	0	1	1	1	1

## 36:	2	0	1	0	1	0	0	1
## 37:	1	1	0	1	2	1	1	0
## 38:	2	0	0	0	1	0	0	1
## 39:	1	0	1	2	2	2	1	0
## 40:	0	0	2	1	2	1	1	1
##	rs2334499	rs10770141	rs231362	rs2237892	rs163184	rs2237897	rs4929949	rs5215
##	rs2056246	rs10488683	rs685249	rs508924	rs4923461	rs6265	rs10767664	
## 1:	2	0	2	2	1	1	1	
## 2:	1	1	1	1	0	0	0	
## 3:	1	1	1	1	0	0	0	
## 4:	0	1	0	0	0	0	0	
## 5:	2	0	2	2	0	0	0	
## 6:	1	1	1	1	0	0	0	
## 7:	2	0	2	2	1	0	0	
## 8:	0	1	0	0	0	0	0	
## 9:	0	1	0	0	2	1	2	
## 10:	1	1	1	1	1	1	1	
## 11:	0	2	0	0	1	1	1	
## 12:	0	2	0	0	1	1	1	
## 13:	1	1	1	1	0	0	0	
## 14:	1	1	1	1	1	1	1	
## 15:	1	0	1	1	1	1	1	
## 16:	2	0	2	2	1	1	1	
## 17:	1	1	2	2	0	0	0	
## 18:	0	2	0	0	0	0	0	
## 19:	0	1	0	0	0	0	0	
## 20:	2	0	2	2	0	0	0	
## 21:	1	1	1	1	0	0	0	
## 22:	1	1	1	1	0	0	0	
## 23:	2	0	2	2	0	0	0	
## 24:	0	1	0	0	2	1	1	
## 25:	1	1	1	1	1	1	1	
## 26:	1	1	1	1	1	1	1	
## 27:	0	2	0	0	1	1	1	
## 28:	1	0	1	1	0	0	0	
## 29:	1	1	1	1	1	0	0	
## 30:	0	2	0	0	0	0	0	
## 31:	1	1	1	1	2	2	2	
## 32:	2	0	2	2	1	1	1	
## 33:	0	2	0	0	0	0	0	
## 34:	1	1	1	1	0	0	0	
## 35:	2	0	2	2	0	0	0	
## 36:	0	1	1	1	0	0	0	
## 37:	1	1	1	1	1	1	1	
## 38:	1	1	1	1	0	0	0	
## 39:	0	1	0	1	0	0	0	
## 40:	0	2	0	0	0	0	0	
##	rs2056246	rs10488683	rs685249	rs508924	rs4923461	rs6265	rs10767664	
##	rs2030323	rs3817334	rs10838738	rs1552224	rs1387153	rs10830962	rs10830963	
## 1:	1	0	0	0	1	1	0	
## 2:	0	0	0	0	0	0	0	
## 3:	0	0	0	0	1	1	1	
## 4:	0	1	1	0	1	1	1	
## 5:	0	0	0	0	0	0	0	

## 6:	0	1	1	2	0	0	0
## 7:	0	1	1	0	0	0	0
## 8:	0	0	0	0	1	1	1
## 9:	2	1	0	0	1	1	1
## 10:	1	0	0	0	0	0	0
## 11:	1	0	0	0	0	0	0
## 12:	1	0	0	0	0	0	0
## 13:	0	1	1	0	0	1	0
## 14:	1	1	1	0	0	0	0
## 15:	1	0	0	0	0	0	1
## 16:	1	1	1	0	0	0	0
## 17:	0	0	0	0	1	2	1
## 18:	0	1	1	0	0	0	0
## 19:	0	1	1	0	1	1	1
## 20:	0	0	0	0	1	1	1
## 21:	0	1	0	0	0	0	0
## 22:	0	1	1	0	0	0	0
## 23:	0	1	1	1	0	0	0
## 24:	1	1	1	0	1	2	1
## 25:	1	1	1	0	0	1	0
## 26:	1	0	0	0	1	1	0
## 27:	1	0	0	1	2	2	2
## 28:	0	0	0	0	0	0	0
## 29:	0	1	0	0	0	0	0
## 30:	0	2	2	0	0	0	0
## 31:	0	1	1	0	0	1	0
## 32:	1	0	0	0	0	0	0
## 33:	0	1	1	0	0	0	0
## 34:	0	0	0	0	0	0	0
## 35:	0	1	1	0	1	1	1
## 36:	0	0	0	0	0	0	0
## 37:	1	0	0	0	0	0	0
## 38:	0	0	0	0	0	2	1
## 39:	0	2	2	0	0	1	0
## 40:	0	1	1	0	0	1	1
##	rs2030323	rs3817334	rs10838738	rs1552224	rs1387153	rs10830962	rs10830963
##	rs2041139	rs73040004	rs10842994	rs7138803	rs1531343	rs7961581	rs7957197
## 1:	0	0	0	1	0	1	0
## 2:	0	1	0	1	0	1	0
## 3:	0	0	0	0	0	0	0
## 4:	0	0	0	0	0	0	1
## 5:	1	1	0	0	0	0	0
## 6:	0	0	0	1	1	0	0
## 7:	0	0	1	0	0	0	1
## 8:	0	0	1	1	0	2	1
## 9:	0	0	0	1	0	0	0
## 10:	0	1	0	2	0	0	1
## 11:	0	2	0	0	0	2	0
## 12:	0	1	0	0	0	1	0
## 13:	1	0	0	0	0	1	0
## 14:	0	1	0	1	0	1	0
## 15:	0	0	1	0	0	0	0
## 16:	0	1	0	0	0	0	0
## 17:	0	0	1	1	0	0	0

## 18:	0	0	0	2	0	1	0
## 19:	0	0	0	0	0	1	0
## 20:	0	0	1	1	0	0	0
## 21:	0	0	0	0	0	0	0
## 22:	0	0	0	0	0	1	1
## 23:	0	0	0	0	0	0	0
## 24:	0	0	2	0	0	1	0
## 25:	0	1	0	0	0	0	0
## 26:	0	0	0	0	0	0	0
## 27:	0	0	0	0	0	0	2
## 28:	0	0	1	1	0	0	0
## 29:	0	0	1	0	0	0	0
## 30:	0	0	0	1	0	0	0
## 31:	0	1	0	0	0	0	0
## 32:	0	1	1	1	0	1	0
## 33:	0	1	1	1	0	0	0
## 34:	0	1	1	0	0	0	0
## 35:	0	0	1	0	0	1	0
## 36:	0	0	0	0	0	0	0
## 37:	0	0	0	1	0	1	0
## 38:	0	0	0	1	0	0	0
## 39:	0	0	1	2	1	0	0
## 40:	0	0	0	1	0	0	0
##	rs2041139	rs73040004	rs10842994	rs7138803	rs1531343	rs7961581	rs7957197
##	rs4771122	rs1359790	rs11847697	rs10150332	rs1884082	rs7172432	rs2241423
## 1:	1	0	0	0	0	1	2
## 2:	0	1	0	0	0	2	0
## 3:	1	2	0	0	1	1	0
## 4:	0	2	0	0	0	1	0
## 5:	0	1	0	0	0	1	0
## 6:	0	1	0	1	0	1	1
## 7:	0	1	0	0	0	2	0
## 8:	0	1	0	2	1	2	1
## 9:	0	1	0	1	1	1	1
## 10:	0	1	0	1	0	1	1
## 11:	0	0	0	0	1	0	1
## 12:	0	1	0	0	1	0	0
## 13:	1	0	1	0	0	1	0
## 14:	0	1	0	0	2	1	0
## 15:	0	1	0	0	2	1	0
## 16:	0	0	0	0	0	1	0
## 17:	1	0	0	1	0	2	0
## 18:	0	1	0	0	0	1	1
## 19:	1	1	0	0	0	0	2
## 20:	0	1	0	1	1	0	1
## 21:	0	0	0	0	0	1	2
## 22:	0	1	0	0	0	0	2
## 23:	0	1	0	0	1	1	1
## 24:	0	1	0	1	1	0	0
## 25:	1	1	0	0	2	0	0
## 26:	1	2	1	0	0	1	1
## 27:	1	1	0	1	1	0	0
## 28:	0	0	0	1	0	1	0
## 29:	1	2	0	1	1	1	1

## 30:	0	0	1	0	0	1	2
## 31:	0	0	0	1	1	0	0
## 32:	0	0	0	0	0	0	0
## 33:	0	1	0	0	2	1	1
## 34:	0	0	0	1	0	2	0
## 35:	0	0	0	1	1	1	2
## 36:	1	0	0	0	1	1	0
## 37:	0	0	0	0	1	2	0
## 38:	0	2	0	0	0	0	1
## 39:	0	1	0	0	0	0	1
## 40:	0	1	0	0	0	1	1
##	rs4771122	rs1359790	rs11847697	rs10150332	rs1884082	rs7172432	rs2241423
##	rs12898654	rs7178572	rs7177055	rs11634397	rs2028299	rs8042680	rs7359397
## 1:	1	0	0	1	0	1	0
## 2:	0	1	1	1	0	0	1
## 3:	0	0	0	1	0	1	0
## 4:	0	2	2	2	0	0	1
## 5:	0	0	0	0	0	0	1
## 6:	1	0	0	1	0	0	0
## 7:	0	0	0	1	0	0	0
## 8:	0	0	0	1	0	0	2
## 9:	0	1	1	2	0	1	1
## 10:	0	1	2	2	0	0	2
## 11:	0	1	1	2	0	0	0
## 12:	0	1	1	2	0	0	0
## 13:	0	1	0	1	0	0	0
## 14:	0	1	1	1	0	0	1
## 15:	0	1	1	1	0	1	1
## 16:	0	1	1	0	0	1	1
## 17:	0	1	1	0	0	1	1
## 18:	0	0	1	0	1	2	2
## 19:	0	2	2	2	0	0	1
## 20:	0	0	0	2	1	0	1
## 21:	0	0	0	1	0	0	1
## 22:	1	0	0	1	2	1	2
## 23:	1	1	1	2	1	1	1
## 24:	0	0	0	1	0	0	1
## 25:	0	0	0	1	0	0	0
## 26:	0	1	1	1	1	1	2
## 27:	0	1	1	1	1	2	1
## 28:	0	2	2	2	1	0	1
## 29:	0	2	2	1	0	0	2
## 30:	1	0	0	0	0	1	2
## 31:	0	0	0	0	0	0	1
## 32:	0	0	0	2	0	0	1
## 33:	1	0	1	0	1	0	0
## 34:	0	2	2	2	0	0	0
## 35:	0	0	1	1	1	0	1
## 36:	0	2	2	0	0	0	2
## 37:	0	2	2	1	1	0	2
## 38:	0	0	0	2	1	0	2
## 39:	0	1	1	0	0	1	2
## 40:	0	1	1	0	1	0	2
##	rs12898654	rs7178572	rs7177055	rs11634397	rs2028299	rs8042680	rs7359397

##	rs1421085	rs1558902	rs1121980	rs17817449	rs8050136	rs9939609	rs9941349
## 1:	0	0	0	0	0	0	0
## 2:	1	1	1	1	1	1	1
## 3:	0	0	0	0	0	0	0
## 4:	1	1	1	1	1	1	1
## 5:	0	0	0	0	0	0	0
## 6:	0	0	0	0	0	0	0
## 7:	0	0	1	0	0	0	1
## 8:	0	0	0	0	0	0	0
## 9:	1	1	2	1	1	1	0
## 10:	0	0	0	0	0	0	0
## 11:	1	1	1	1	1	1	1
## 12:	0	0	0	0	0	0	0
## 13:	0	0	0	0	0	0	0
## 14:	1	1	1	1	1	1	1
## 15:	0	0	0	0	0	0	0
## 16:	0	0	0	0	0	0	0
## 17:	0	0	0	0	0	0	0
## 18:	1	1	1	1	1	1	1
## 19:	0	0	0	0	0	0	0
## 20:	1	1	1	0	0	0	0
## 21:	0	0	0	0	0	0	0
## 22:	0	0	0	0	0	0	0
## 23:	1	1	1	1	1	1	1
## 24:	2	2	2	2	2	2	2
## 25:	1	1	1	1	1	1	1
## 26:	0	0	0	0	0	0	0
## 27:	1	1	1	1	1	1	1
## 28:	0	0	0	0	0	0	0
## 29:	0	0	0	0	0	0	0
## 30:	1	1	2	2	2	2	1
## 31:	1	1	1	1	1	1	1
## 32:	0	0	0	0	0	0	0
## 33:	0	0	1	1	1	1	0
## 34:	0	0	0	0	0	0	0
## 35:	0	0	0	0	0	0	0
## 36:	0	0	0	0	0	0	0
## 37:	0	0	0	0	0	0	0
## 38:	1	1	1	1	1	1	1
## 39:	1	1	1	1	1	1	1
## 40:	0	0	0	0	0	0	0
##	rs1421085	rs1558902	rs1121980	rs17817449	rs8050136	rs9939609	rs9941349
##	rs12149832	rs11642841	rs6499500	rs7202877	rs4523957	rs391300	rs75493593
## 1:	0	0	0	0	1	1	0
## 2:	1	1	0	2	1	1	1
## 3:	0	0	1	0	0	0	0
## 4:	1	1	0	0	1	1	0
## 5:	0	0	2	1	2	2	0
## 6:	0	0	1	0	0	0	1
## 7:	0	0	0	0	2	2	1
## 8:	0	0	1	0	1	1	1
## 9:	0	0	1	0	0	0	0
## 10:	0	0	0	0	0	0	1
## 11:	1	1	0	0	0	0	2

## 12:	0	0	0	0	0	0	2
## 13:	0	0	0	0	0	0	0
## 14:	1	1	1	0	0	0	0
## 15:	0	0	1	0	0	0	0
## 16:	0	0	0	0	2	1	0
## 17:	0	0	2	1	1	1	1
## 18:	1	1	1	0	1	1	0
## 19:	0	0	0	0	0	0	2
## 20:	0	0	0	0	0	0	0
## 21:	0	0	0	0	0	0	0
## 22:	0	0	1	0	0	0	1
## 23:	1	0	0	0	1	1	0
## 24:	2	2	2	0	1	2	0
## 25:	1	1	1	1	1	1	2
## 26:	1	1	0	0	1	0	0
## 27:	1	1	0	0	1	1	1
## 28:	0	0	2	0	0	0	0
## 29:	0	0	1	1	0	0	1
## 30:	1	1	1	1	0	0	0
## 31:	1	1	0	0	1	1	2
## 32:	0	0	0	1	1	1	0
## 33:	0	0	0	0	1	1	1
## 34:	0	0	1	0	0	1	0
## 35:	0	0	0	1	0	0	0
## 36:	0	0	1	1	1	1	0
## 37:	0	0	1	0	2	2	1
## 38:	1	1	1	0	1	1	0
## 39:	1	1	0	2	1	1	1
## 40:	0	0	0	0	0	0	2
##	rs12149832	rs11642841	rs6499500	rs7202877	rs4523957	rs391300	rs75493593
##	rs75418188	rs13342232	rs13342692	rs117767867	rs757210	rs4430796	rs7501939
## 1:	0	0	0	0	1	1	1
## 2:	1	1	1	1	1	1	1
## 3:	0	0	0	0	1	1	1
## 4:	0	0	0	0	0	0	0
## 5:	0	0	0	0	1	1	1
## 6:	1	1	1	1	1	1	1
## 7:	1	1	1	1	0	1	0
## 8:	1	1	1	1	0	0	0
## 9:	1	0	0	0	1	1	1
## 10:	1	1	1	1	1	1	1
## 11:	2	2	2	2	1	1	0
## 12:	2	2	2	2	2	1	1
## 13:	0	0	0	0	2	1	1
## 14:	0	1	1	0	1	1	1
## 15:	0	0	0	0	0	0	0
## 16:	0	0	0	0	0	0	0
## 17:	1	1	1	1	1	2	1
## 18:	0	0	0	0	0	0	0
## 19:	2	2	2	2	0	0	0
## 20:	0	0	0	0	0	0	0
## 21:	0	0	0	0	0	0	0
## 22:	1	1	1	1	1	2	1
## 23:	0	0	0	0	0	0	0

## 24:	0	0	0	0	0	0	0
## 25:	2	2	2	2	1	1	1
## 26:	0	0	0	0	1	1	1
## 27:	1	1	1	1	0	0	0
## 28:	0	0	0	0	1	1	1
## 29:	1	2	2	1	0	0	0
## 30:	0	0	0	0	1	1	1
## 31:	2	2	2	2	1	1	1
## 32:	0	0	0	0	0	1	1
## 33:	1	1	1	1	0	0	0
## 34:	0	0	0	0	0	0	0
## 35:	0	0	0	0	1	2	1
## 36:	0	0	0	0	1	2	2
## 37:	1	1	1	1	1	1	1
## 38:	0	0	0	0	1	1	1
## 39:	1	1	1	1	1	2	1
## 40:	2	2	2	2	1	1	1
##	rs75418188	rs13342232	rs13342692	rs117767867	rs757210	rs4430796	rs7501939
##	rs2331841	rs6567160	rs571312	rs17782313	rs12970134	rs1423096	rs3786897
## 1:	0	0	0	0	1	0	0
## 2:	0	0	0	0	0	0	0
## 3:	0	0	0	0	0	0	0
## 4:	1	0	0	0	1	0	0
## 5:	1	0	0	0	0	0	0
## 6:	0	0	0	0	0	0	0
## 7:	0	0	0	0	0	0	0
## 8:	2	1	1	1	1	0	1
## 9:	0	0	0	0	1	0	0
## 10:	2	0	0	0	0	0	0
## 11:	0	0	0	0	0	0	0
## 12:	0	0	0	0	0	1	0
## 13:	0	0	0	0	0	0	1
## 14:	0	0	0	0	0	0	1
## 15:	0	0	0	0	0	0	1
## 16:	0	0	0	0	2	0	0
## 17:	1	0	0	0	1	0	1
## 18:	0	0	0	0	0	0	0
## 19:	0	0	0	0	0	0	0
## 20:	0	0	0	0	0	0	1
## 21:	1	0	0	0	0	0	0
## 22:	0	0	0	0	0	0	0
## 23:	0	0	0	0	0	0	0
## 24:	1	0	0	0	0	0	0
## 25:	0	0	1	1	0	0	0
## 26:	0	0	0	0	0	0	0
## 27:	0	0	0	0	0	1	0
## 28:	1	0	0	0	0	0	1
## 29:	1	0	0	0	0	0	0
## 30:	0	1	1	1	2	0	0
## 31:	2	0	0	0	0	0	0
## 32:	0	0	0	0	0	0	0
## 33:	2	0	0	0	0	0	0
## 34:	1	0	0	0	0	0	0
## 35:	1	0	0	0	0	0	1

## 36:	0	0	0	0	0	0	2
## 37:	0	0	0	0	0	1	1
## 38:	2	0	0	0	1	0	0
## 39:	0	0	0	0	1	0	0
## 40:	0	0	0	0	0	0	0
##	rs2331841	rs6567160	rs571312	rs17782313	rs12970134	rs1423096	rs3786897
##	rs29941	rs8108269	rs2287019	rs3810291	rs6017317	rs1800961	rs5945326
## 1:	1	0	0	0	1	0	1
## 2:	1	0	0	2	0	1	0
## 3:	1	1	0	1	0	2	1
## 4:	2	2	0	1	2	0	2
## 5:	0	0	0	0	2	1	0
## 6:	2	1	1	0	1	1	0
## 7:	1	2	0	0	1	0	0
## 8:	1	2	0	0	0	0	0
## 9:	0	1	0	2	0	0	1
## 10:	1	1	1	0	0	1	1
## 11:	1	1	0	1	2	0	1
## 12:	0	0	0	2	2	0	0
## 13:	1	1	0	2	0	0	1
## 14:	1	1	0	1	1	0	0
## 15:	0	1	0	1	1	0	0
## 16:	1	0	0	1	2	0	1
## 17:	0	1	1	0	0	0	0
## 18:	2	1	0	1	0	0	1
## 19:	1	1	0	1	1	0	1
## 20:	2	0	0	0	0	0	1
## 21:	1	1	0	0	0	0	1
## 22:	1	1	0	0	1	0	0
## 23:	1	1	0	0	0	0	1
## 24:	1	0	0	2	1	0	0
## 25:	1	1	0	1	1	0	0
## 26:	0	1	0	2	1	0	0
## 27:	1	1	1	1	1	0	0
## 28:	1	1	0	2	1	0	1
## 29:	2	2	0	0	1	1	1
## 30:	2	0	1	1	0	0	1
## 31:	0	0	0	0	1	1	1
## 32:	0	1	0	0	1	1	1
## 33:	2	0	0	1	1	0	0
## 34:	1	2	1	2	0	0	2
## 35:	0	0	0	0	2	0	1
## 36:	1	0	0	2	1	0	0
## 37:	0	1	0	1	1	0	0
## 38:	1	2	1	1	0	0	1
## 39:	1	1	0	1	2	0	1
## 40:	1	2	1	1	0	0	1
##	rs29941	rs8108269	rs2287019	rs3810291	rs6017317	rs1800961	rs5945326
##	weighted.risk.3	weighted.risk.4	weighted.risk.FTD				
## 1:	NA	NA	0.0000000				
## 2:	NA	NA	2.4896550				
## 3:	NA	NA	0.0000000				
## 4:	NA	NA	2.4896550				
## 5:	NA	NA	0.0000000				

```
## 6:      NA      NA      0.0000000
## 7:      NA      NA      0.3509844
## 8:      NA      NA      0.0000000
## 9:      NA      NA      1.7851171
## 10:     NA      NA      0.0000000
## 11:     NA      NA      2.4896550
## 12:     NA      NA      0.0000000
## 13:     NA      NA      0.0000000
## 14:     NA      NA      2.4896550
## 15:     NA      NA      0.0000000
## 16:     NA      NA      0.0000000
## 17:     NA      NA      0.0000000
## 18:     NA      NA      2.4896550
## 19:     NA      NA      0.0000000
## 20:     NA      NA      0.9710653
## 21:     NA      NA      0.0000000
## 22:     NA      NA      0.0000000
## 23:     NA      NA      2.1049461
## 24:     NA      NA      4.9793101
## 25:     NA      NA      2.4896550
## 26:     NA      NA      0.6083134
## 27:     NA      NA      2.4896550
## 28:     NA      NA      0.0000000
## 29:     NA      NA      0.0000000
## 30:     NA      NA      3.3037068
## 31:     NA      NA      2.4896550
## 32:     NA      NA      0.0000000
## 33:     NA      NA      0.8140518
## 34:     NA      NA      0.0000000
## 35:     NA      NA      0.0000000
## 36:     NA      NA      0.0000000
## 37:     NA      NA      0.0000000
## 38:     NA      NA      2.4896550
## 39:     NA      NA      2.4896550
## 40:     NA      NA      0.0000000
##      weighted.risk.3 weighted.risk.4 weighted.risk.FTO
```

Problem 2.g (4 points)

Use the logistic regression models fitted in problem 2.e to predict the outcome of patients in `gdm.test`. Compute the test log-likelihood for the predicted probabilities from the three genetic risk score models.

```
# Enter code here.
```

Problem 2.h (4points)

File `GDM.study2.txt` (available from the accompanying zip folder on Learn) contains the summary statistics from a different study on the same set of SNPs. Perform a meta-analysis with the results obtained in problem 2.c (hint: remember that the effect alleles should correspond) and produce a summary of the meta-analysis results for the set of SNPs with meta-analysis p-value $< 10^{-4}$ sorted by increasing p-value.

```
# Enter code here.
```

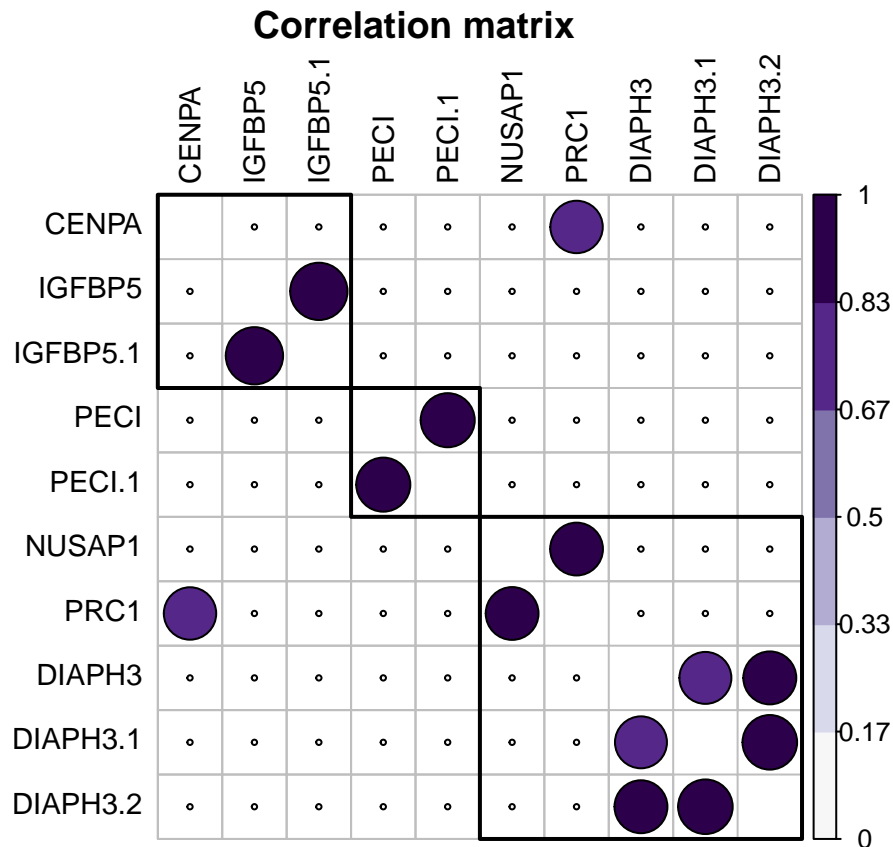

Problem 3 (33 points)

File `nki.csv` (available from the accompanying zip folder on Learn) contains data for 144 breast cancer patients. The dataset contains a binary outcome variable (“Event”, indicating the insurgence of further complications after operation), covariates describing the tumour and the age of the patient, and gene expressions for 70 genes found to be prognostic of survival.

Problem 3.a (6 points)

Compute the matrix of correlations between the gene expression variables, and display it so that a block structure is highlighted. Discuss what you observe. Write some code to identify the unique pairs of (distinct) variables that have correlation coefficient greater than 0.80 in absolute value and report their correlation coefficients.

```
# Enter code here.
nki.dt <- fread("data/nki.csv")
numcols <- sapply(nki.dt, is.numeric)
cor.nki <- nki.dt[, ..numcols] %>% cor(use="pairwise.complete")
cor.nki <- cor.nki*(abs(cor.nki)>0.8)
# remove rows where they only have autocorrelation present
cor.nki <- cor.nki[-which(abs(rowSums(cor.nki))==1),-which(abs(colSums(cor.nki))==1)]
corrplot(cor.nki,
          order="hclust",
          addrect=3,
          diag=FALSE,
          tl.col="black",
          tl.cex = 0.9,
          outline=TRUE,
          title="Correlation matrix",
          col = brewer.pal(n=11, name="PuOr"),
          cl.lim=c(0, 1),
          mar=c(0,0,1.5,0))
```



Problem 3.b (8 points)

Run PCA (only over the columns containing gene expressions), in order to derive a patient-wise summary of all gene expressions (dimensionality reduction). Decide which components to keep and justify your decision. Test if those principal components are associated with the outcome in unadjusted logistic regression models and in models adjusted for age, estrogen receptor and grade. Justify the difference in results between unadjusted and adjusted models.

```
# Enter code here.
numcols[c('Event', 'Diam', 'LymphNodes', 'EstrogenReceptor', 'Grade', 'Age')] <- FALSE
```

```
pca.vars <- prcomp(nki.dt[, ..numcols], center=T, scale=T)
var.expl <- cumsum(pca.vars$sdev^2 / sum(pca.vars$sdev^2))
```

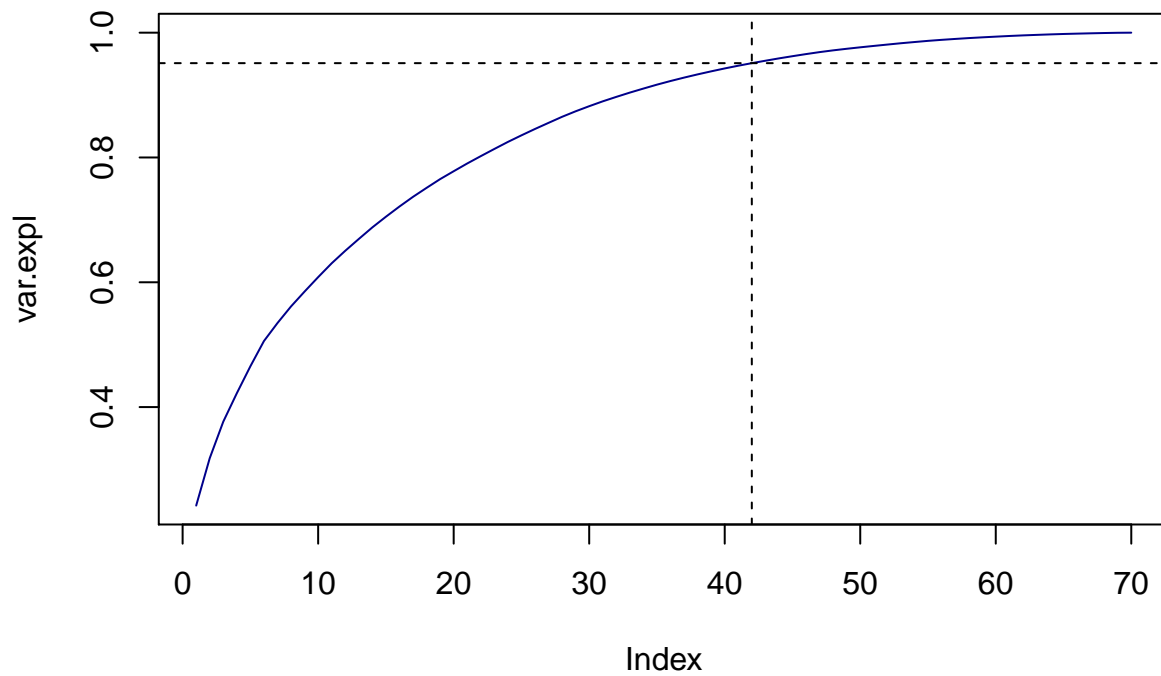
```
summary(pca.vars)
```

```
## Importance of components:
##              PC1      PC2      PC3      PC4      PC5      PC6      PC7
## Standard deviation    4.1171 2.30541 2.02437 1.78597 1.73982 1.68091 1.42309
## Proportion of Variance 0.2422 0.07593 0.05854 0.04557 0.04324 0.04036 0.02893
## Cumulative Proportion 0.2422 0.31808 0.37662 0.42219 0.46543 0.50580 0.53473
##              PC8      PC9      PC10     PC11     PC12     PC13     PC14
## Standard deviation    1.36441 1.29119 1.2715 1.24741 1.18388 1.15101 1.13883
## Proportion of Variance 0.02659 0.02382 0.0231 0.02223 0.02002 0.01893 0.01853
## Cumulative Proportion 0.56132 0.58514 0.6082 0.63046 0.65049 0.66941 0.68794
##              PC15     PC16     PC17     PC18     PC19     PC20     PC21
## Standard deviation    1.09473 1.07016 1.04187 1.00234 0.99086 0.94095 0.93322
## Proportion of Variance 0.01712 0.01636 0.01551 0.01435 0.01403 0.01265 0.01244
```

```
## Cumulative Proportion 0.70506 0.72142 0.73693 0.75128 0.76531 0.77796 0.79040
## PC22 PC23 PC24 PC25 PC26 PC27 PC28
## Standard deviation 0.90727 0.89675 0.88859 0.86019 0.84462 0.82782 0.82368
## Proportion of Variance 0.01176 0.01149 0.01128 0.01057 0.01019 0.00979 0.00969
## Cumulative Proportion 0.80216 0.81364 0.82492 0.83549 0.84569 0.85548 0.86517
## PC29 PC30 PC31 PC32 PC33 PC34 PC35
## Standard deviation 0.78694 0.75594 0.73942 0.70569 0.69414 0.67129 0.6639
## Proportion of Variance 0.00885 0.00816 0.00781 0.00711 0.00688 0.00644 0.0063
## Cumulative Proportion 0.87401 0.88218 0.88999 0.89710 0.90399 0.91042 0.9167
## PC36 PC37 PC38 PC39 PC40 PC41 PC42
## Standard deviation 0.63815 0.61964 0.59947 0.58447 0.57195 0.55097 0.53820
## Proportion of Variance 0.00582 0.00549 0.00513 0.00488 0.00467 0.00434 0.00414
## Cumulative Proportion 0.92254 0.92802 0.93316 0.93804 0.94271 0.94705 0.95118
## PC43 PC44 PC45 PC46 PC47 PC48 PC49
## Standard deviation 0.52029 0.51211 0.49533 0.48712 0.47079 0.44565 0.41879
## Proportion of Variance 0.00387 0.00375 0.00351 0.00339 0.00317 0.00284 0.00251
## Cumulative Proportion 0.95505 0.95880 0.96230 0.96569 0.96886 0.97170 0.97420
## PC50 PC51 PC52 PC53 PC54 PC55 PC56
## Standard deviation 0.40556 0.39328 0.3925 0.38502 0.36669 0.36205 0.33734
## Proportion of Variance 0.00235 0.00221 0.0022 0.00212 0.00192 0.00187 0.00163
## Cumulative Proportion 0.97655 0.97876 0.9810 0.98308 0.98500 0.98687 0.98850
## PC57 PC58 PC59 PC60 PC61 PC62 PC63
## Standard deviation 0.32150 0.30744 0.28898 0.28186 0.27274 0.25622 0.24118
## Proportion of Variance 0.00148 0.00135 0.00119 0.00113 0.00106 0.00094 0.00083
## Cumulative Proportion 0.98998 0.99133 0.99252 0.99365 0.99472 0.99565 0.99649
## PC64 PC65 PC66 PC67 PC68 PC69 PC70
## Standard deviation 0.23024 0.21442 0.19886 0.19371 0.17927 0.1677 0.09833
## Proportion of Variance 0.00076 0.00066 0.00056 0.00054 0.00046 0.0004 0.00014
## Cumulative Proportion 0.99724 0.99790 0.99846 0.99900 0.99946 0.9999 1.00000
```

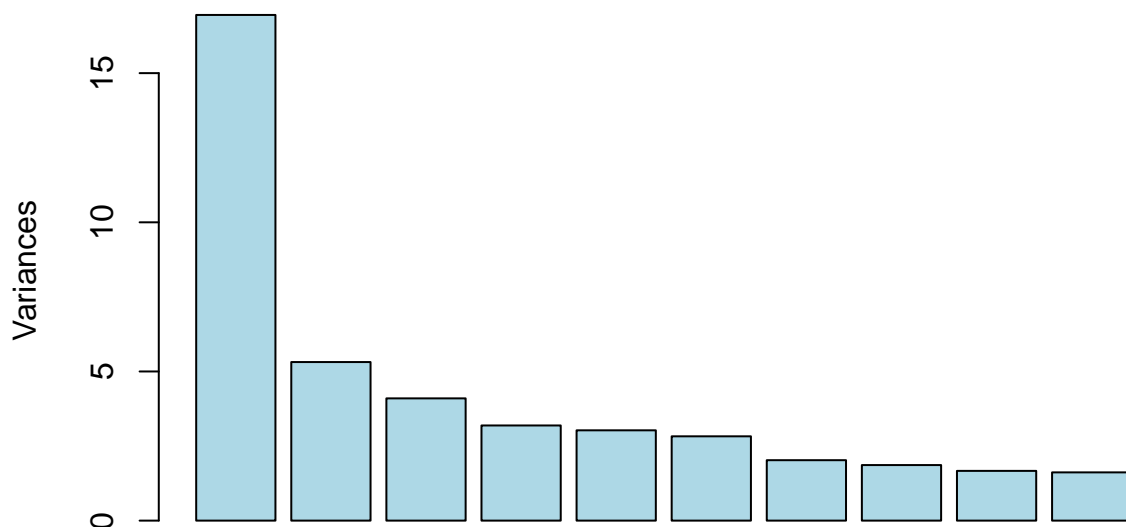
```
# cumulative variance explained plot
plot(var.expl, type='l', col='blue4')
```

```
# calculate first 90%, 95% variance explained automatically.
abline(h=0.9511847, v=42, lty=2)
```



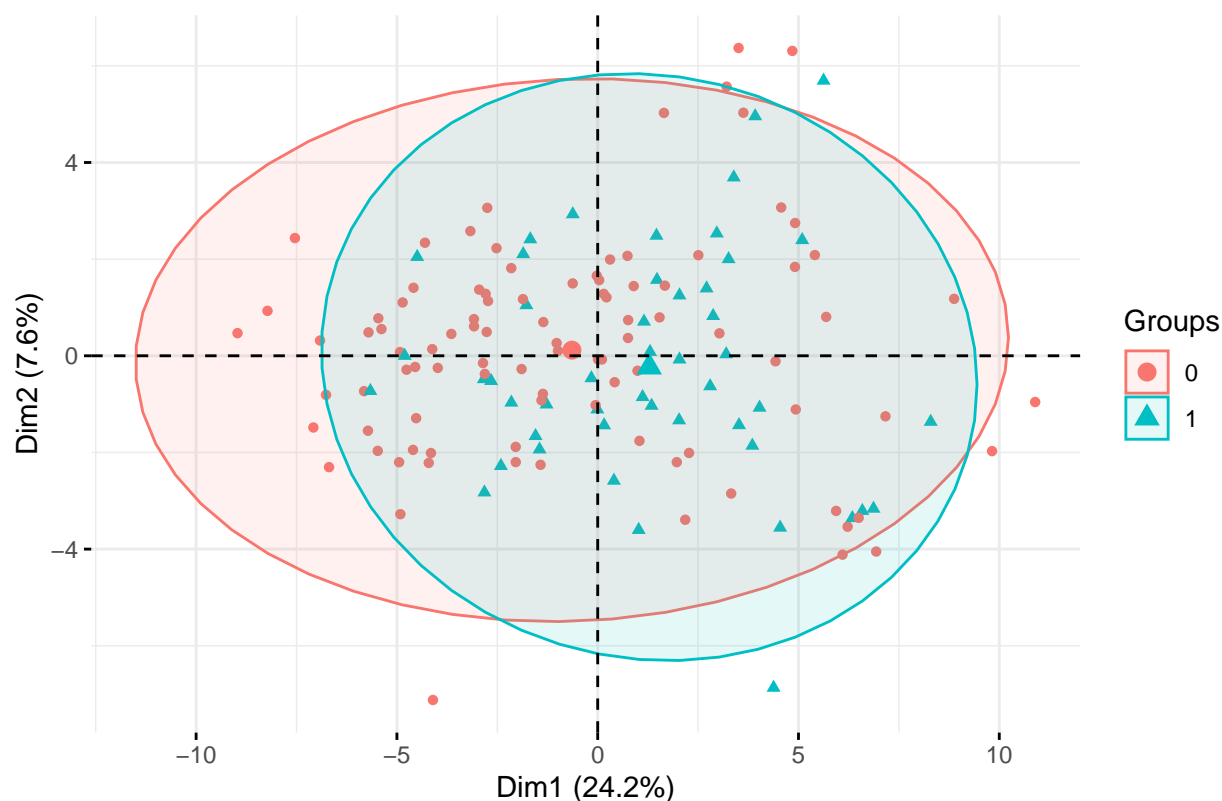
```
# scree plot
screeplot(pca.vars, main="Scree plot", col='lightblue')
```

Scree plot



```
# PCA plot
fviz_pca_ind(pca.vars, geom='point',
             habillage=nki.dt$Event,
             addEllipses=T,
             ellipse.level=0.95)
```

Individuals – PCA



```
# PCA biplot
# fviz_pca_biplot(pca.vars, geom='point', repel = T)

pca.embeddings.95 <- as.data.frame(pca.vars$x[,1:42])

# all PCs are othogonal, checking that the correlation matrix is all white except autocorrelations.
# res1 <- cor(pca.embeddings.95, method='pearson')
# corplot(res1, method= "color", order = "hclust", tl.pos = 'n')

## Models
#
# beta.Z <- as.matrix(lmodel$coefficients[2:123])
# V <- as.matrix(crimeData.pca1$rotation)
# beta.X <- V %*% beta.Z
# beta.X

data.embedded <- as.data.frame(cbind(nki.dt[,1], pca.embeddings.95))
data.embedded.adj <- as.data.frame(cbind(nki.dt[,1], nki.dt[,4:6], pca.embeddings.95))

model <- glm(Event~., data=data.embedded, family='binomial')
model.adj <- glm(Event~., data=data.embedded.adj, family='binomial')

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
summary(model)

##
## Call:
```

```
## glm(formula = Event ~ ., family = "binomial", data = data.embedded)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5622  -0.4036  -0.0104   0.0675   3.4493
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.69481    0.79564  -3.387 0.000707 ***
## PC1          0.55978    0.18355   3.050 0.002290 **
## PC2         -0.06842    0.15515  -0.441 0.659221
## PC3          0.62519    0.24568   2.545 0.010935 *
## PC4         -1.25179    0.48186  -2.598 0.009382 **
## PC5         -0.08599    0.23513  -0.366 0.714565
## PC6          0.74780    0.33238   2.250 0.024461 *
## PC7          0.02495    0.34292   0.073 0.941998
## PC8          0.04694    0.27135   0.173 0.862653
## PC9          0.47010    0.35968   1.307 0.191216
## PC10         -1.04938    0.48219  -2.176 0.029536 *
## PC11         -1.54897    0.53098  -2.917 0.003532 **
## PC12          0.07232    0.43895   0.165 0.869132
## PC13         -0.36607    0.36062  -1.015 0.310046
## PC14         -0.31123    0.40088  -0.776 0.437543
## PC15         -0.47155    0.37796  -1.248 0.212176
## PC16         -1.18771    0.52651  -2.256 0.024081 *
## PC17         -0.81375    0.38486  -2.114 0.034479 *
## PC18         -0.75850    0.46976  -1.615 0.106384
## PC19          3.17912    0.99653   3.190 0.001422 **
## PC20         -0.21795    0.46738  -0.466 0.640984
## PC21         -0.80290    0.53328  -1.506 0.132172
## PC22          0.62281    0.64242   0.969 0.332307
## PC23          1.97124    0.75226   2.620 0.008782 **
## PC24         -1.54956    0.66614  -2.326 0.020008 *
## PC25         -0.36892    0.49271  -0.749 0.454009
## PC26          0.11901    0.56651   0.210 0.833608
## PC27          0.78966    0.48303   1.635 0.102089
## PC28         -1.43775    0.70439  -2.041 0.041239 *
## PC29         -0.42265    0.59864  -0.706 0.480178
## PC30         -0.52763    0.55293  -0.954 0.339966
## PC31          1.75629    0.80495   2.182 0.029120 *
## PC32         -0.28186    0.51983  -0.542 0.587669
## PC33         -2.00846    0.76640  -2.621 0.008777 **
## PC34         -0.92011    0.60905  -1.511 0.130861
## PC35         -0.41835    0.69394  -0.603 0.546598
## PC36         -0.18634    0.67284  -0.277 0.781828
## PC37          0.70620    0.70401   1.003 0.315806
## PC38          2.15027    0.98875   2.175 0.029651 *
## PC39         -1.56093    0.75960  -2.055 0.039884 *
## PC40          1.09829    0.66805   1.644 0.100174
## PC41          2.37649    1.07157   2.218 0.026571 *
## PC42         -1.06355    0.86688  -1.227 0.219872
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 183.316 on 143 degrees of freedom
## Residual deviance: 71.416 on 101 degrees of freedom
## AIC: 157.42
##
## Number of Fisher Scoring iterations: 9
```

summary(model.adj)

```
##
## Call:
## glm(formula = Event ~ ., family = "binomial", data = data.embedded.adj)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.95896  -0.31596  -0.00462   0.02414   2.73979
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      8.9235     5.4584   1.635  0.10209
## EstrogenReceptorPositive  0.9137     2.9675   0.308  0.75816
## GradePoorly diff    0.8489     1.3982   0.607  0.54377
## GradeWell diff     0.9822     1.2850   0.764  0.44465
## Age              -0.3050     0.1248  -2.443  0.01455 *
## PC1               0.7326     0.2973   2.464  0.01372 *
## PC2              -0.1089     0.2947  -0.369  0.71182
## PC3               0.7543     0.3289   2.293  0.02182 *
## PC4              -1.5600     0.5964  -2.616  0.00890 **
## PC5              -0.1001     0.2996  -0.334  0.73830
## PC6               0.8508     0.4448   1.913  0.05579 .
## PC7               0.2613     0.4130   0.633  0.52690
## PC8               0.2602     0.3506   0.742  0.45802
## PC9               0.4646     0.4486   1.036  0.30041
## PC10             -1.3649     0.5977  -2.284  0.02239 *
## PC11             -1.6256     0.5543  -2.933  0.00336 **
## PC12              0.1567     0.5411   0.290  0.77217
## PC13             -0.2706     0.4454  -0.607  0.54354
## PC14             -0.7907     0.5492  -1.440  0.14993
## PC15             -0.5473     0.4637  -1.180  0.23792
## PC16             -1.4157     0.5943  -2.382  0.01721 *
## PC17             -0.6467     0.4489  -1.441  0.14970
## PC18             -1.1272     0.5916  -1.905  0.05673 .
## PC19              4.3515     1.3403   3.247  0.00117 **
## PC20             -0.2178     0.6464  -0.337  0.73613
## PC21             -1.1895     0.7461  -1.594  0.11087
## PC22              0.2722     0.8581   0.317  0.75109
## PC23              2.4944     0.9286   2.686  0.00723 **
## PC24             -1.5903     0.7029  -2.262  0.02367 *
## PC25             -0.2657     0.5461  -0.487  0.62654
## PC26              0.6941     0.7415   0.936  0.34921
## PC27              0.7377     0.5655   1.305  0.19205
## PC28             -2.3176     0.9264  -2.502  0.01236 *
## PC29             -0.5082     0.7014  -0.725  0.46867
## PC30             -0.2429     0.6660  -0.365  0.71532
```

```
## PC31          1.9403      0.9225   2.103  0.03543 *
## PC32          -0.3864      0.5788  -0.668  0.50433
## PC33          -2.0100      0.8543  -2.353  0.01864 *
## PC34          -1.6495      0.8443  -1.954  0.05073 .
## PC35          -0.8643      1.0053  -0.860  0.38990
## PC36          -0.5447      0.8716  -0.625  0.53201
## PC37           1.0922      0.9860   1.108  0.26797
## PC38           2.3179      1.1272   2.056  0.03976 *
## PC39          -1.7144      0.8660  -1.980  0.04773 *
## PC40           1.0340      0.8062   1.283  0.19963
## PC41           4.0163      1.5948   2.518  0.01179 *
## PC42          -1.6523      1.0158  -1.627  0.10384
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 183.316  on 143  degrees of freedom
## Residual deviance:  63.498  on  97  degrees of freedom
## AIC: 157.5
##
## Number of Fisher Scoring iterations: 9
```

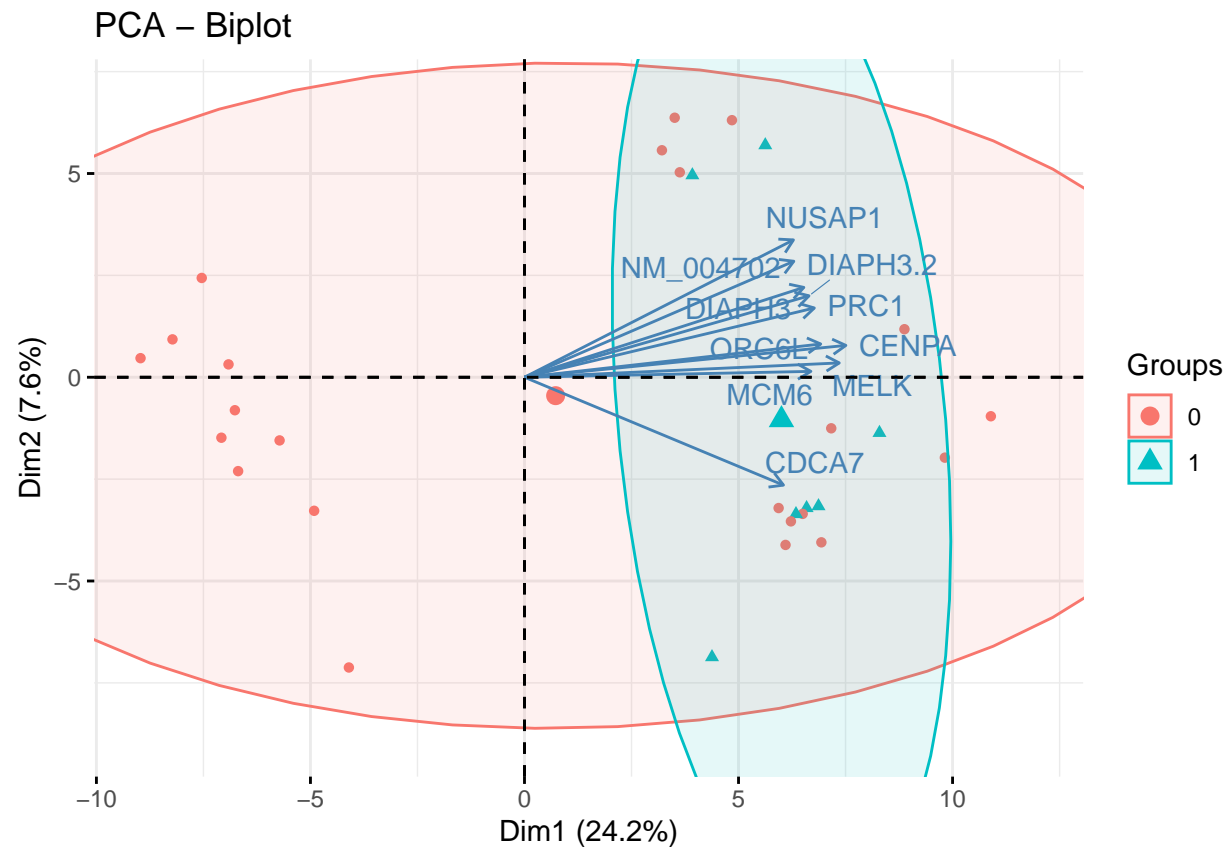
Problem 3.c (8 points)

Use plots to compare with the correlation structure observed in problem 2.a and to examine how well the dataset may explain your outcome. Discuss your findings and suggest any further steps if needed.

Enter code here.

```
fviz_pca_biplot(pca.vars,
  repel=T,
  select.var=list(contrib=10),
  select.ind = list(contrib=30),
  label="var",
  habillage = nki.dt$Event,
  addEllipses=TRUE,
  ellipse.level=0.90,
  xlim=c(-9,12),
  ylim=c(-9,7))
```

Coordinate system already present. Adding new coordinate system, which will replace the existing one



```
pc1.rotations.top <- sort(pca.vars$rotation[,1], decreasing=TRUE)[1:10]
pc2.rotations.top <- sort(pca.vars$rotation[,2], decreasing=TRUE)[1:10]
```

pc1.rotations.top

Gene	Rotation 1	Rotation 2
CENPA	0.2130018	0.2086196
MELK	0.1963327	0.1920987
ORC6L	0.1898039	0.1885517
PRC1	0.1851385	0.1784957
MCM6	0.1782456	0.1773431
DIAPH3.2		
DIAPH3		
NM_004702		
NUSAP1		
C16orf61		

pc2.rotations.top

Gene	Rotation 1	Rotation 2
PECI	0.2869100	0.2735517
PECI.1	0.1741105	0.1707437
ECT2	0.1631555	0.1442509
NUSAP1	0.1439098	0.1184746
RTN4RL1		
NM_004702		
SERF1A		
SCUBE2		
DTL		
DIAPH3		

Problem 3.d (11 points)

Based on the models we examined in the labs, fit an appropriate model with the aim to provide the most accurate prognosis you can for patients. Discuss and justify your decisions.

Enter code here.

TODO: split dataset, train models, measure accuracy, compare results.