Assignment 1

Assignment 1

Biomedical Data Science

Due on Thursday 25th February 2020, 5:00pm

The assignment is marked out of 100 points, and will contribute to 20% 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 (25 points)

Files longegfr1.csv and longegfr2.csv (available on Learn) contain information regarding a longitudinal dataset containing records on 250 patients. For each subject, eGFR (estimated glomerular filtration rate, a measure of kidney function) was collected at irregularly spaced time points: variable "fu.years" contains the follow-up time (that is, the distance from baseline to the date when each eGFR measurement was taken, expressed in years).

Problem 1.a (4 points)

Convert the files to data tables (or tibble) and merge in an appropriate way into a single data table, then order the observations according to subject identifier and follow-up time.

```
is.nan.data.frame = function(x)
  do.call(cbind, lapply(x, is.nan))
```

```
# Enter code here.

# reading datasets and setting primary keys
longegfr1 = data.table(fread('./data/longegfr1.csv'), key=c('id', 'fu.years'))
longegfr2 = data.table(fread('./data/longegfr2.csv'), key=c('ID', 'fu.years'))
colnames(longegfr2) = c('id','fu.years','egfr') # change column names to make joining easier
pk = c('id','fu.years')
longegfr = merge(longegfr1,
                 longegfr2,
                 by=pk,
                 all=TRUE)[order(id,fu.years)] # FULL OUTER JOIN
longegfr %>% summary()
```

```
##        id           fu.years           sex          baseline.age
##  Min.   :  1.0   Min.   :0.0000   Min.   :0.0000   Min.   :18.3
##  1st Qu.: 58.0   1st Qu.:0.8597   1st Qu.:0.0000   1st Qu.:54.7
##  Median :123.0   Median :2.3682   Median :0.0000   Median :63.5
##  Mean   :118.9   Mean   :2.6598   Mean   :0.4297   Mean   :63.2
##  3rd Qu.:177.0   3rd Qu.:4.4353   3rd Qu.:1.0000   3rd Qu.:74.4
##  Max.   :250.0   Max.   :6.6283   Max.   :1.0000   Max.   :91.4
##
##       egfr
##  Min.   :  4.83
##  1st Qu.: 41.05
##  Median : 61.08
##  Mean   : 66.31
##  3rd Qu.: 86.44
##  Max.   :174.94
##  NA's   :212
```

Problem 1.b (6 points)

Compute the average eGFR and length of follow-up for each patient, then tabulate the number of patients with average eGFR in the following ranges: (0, 15], (15, 30], (30, 60], (60, 90], (90, max(eGFR)). Count and report the number of patients with missing average eGFR.

```
# Enter code here.
longegfr[,mean_egfr:=mean(egfr),
         by=id]
longegfr[,count_egfr:=length(fu.years),
         by=id]
longegfr[,fu_total:=max(fu.years)-min(fu.years),
         by=id]
summary(longegfr)
```

```
##        id           fu.years           sex          baseline.age
##  Min.   :  1.0   Min.   :0.0000   Min.   :0.0000   Min.   :18.3
##  1st Qu.: 58.0   1st Qu.:0.8597   1st Qu.:0.0000   1st Qu.:54.7
##  Median :123.0   Median :2.3682   Median :0.0000   Median :63.5
##  Mean   :118.9   Mean   :2.6598   Mean   :0.4297   Mean   :63.2
##  3rd Qu.:177.0   3rd Qu.:4.4353   3rd Qu.:1.0000   3rd Qu.:74.4
##  Max.   :250.0   Max.   :6.6283   Max.   :1.0000   Max.   :91.4
##
##       egfr          mean_egfr        count_egfr       fu_total
##  Min.   :  4.83   Min.   : 14.87   Min.   : 1.00   Min.   :0.000
##  1st Qu.: 41.05   1st Qu.: 44.12   1st Qu.:13.00   1st Qu.:3.817
##  Median : 61.08   Median : 59.28   Median :24.00   Median :5.287
##  Mean   : 66.31   Mean   : 60.53   Mean   :28.09   Mean   :4.680
##  3rd Qu.: 86.44   3rd Qu.: 76.59   3rd Qu.:39.00   3rd Qu.:6.097
##  Max.   :174.94   Max.   :147.69   Max.   :88.00   Max.   :6.628
##  NA's   :212      NA's   :758
```

```
longegfr
```

```
##        id fu.years sex baseline.age   egfr mean_egfr count_egfr fu_total
##    1:   1   0.0000   0         65.5  76.48  43.04333         15   6.4586
##    2:   1   0.1533   0         65.5  47.36  43.04333         15   6.4586
##    3:   1   0.6899   0         65.5  94.87  43.04333         15   6.4586
##    4:   1   1.1882   0         65.5  52.12  43.04333         15   6.4586
##    5:   1   1.8398   0         65.5  91.91  43.04333         15   6.4586
##   ---
## 4027: 249   1.9521   1         50.2  91.94  75.59571          7   2.6174
## 4028: 249   2.1246   1         50.2  69.51  75.59571          7   2.6174
## 4029: 249   2.5982   1         50.2  53.28  75.59571          7   2.6174
## 4030: 249   2.6174   1         50.2  66.78  75.59571          7   2.6174
## 4031: 250   0.0000   1         48.6 101.23 101.23000          1   0.0000
```

```
longegfr$bag_egfr = cut(longegfr$mean_egfr, c(0,15,30,60,90,Inf))

longegfr_nas = longegfr[,sum(is.na(mean_egfr)), by=id]
longegfr_nas[,missing_ind:=ifelse(V1>0,1,0)]
patients_egfr_na = longegfr_nas[,sum(missing_ind)]
cat('There are', patients_egfr_na, 'patients with missing values for \'mean egfr\'')
```

```
## There are 39 patients with missing values for 'mean egfr'
```

Problem 1.c (6 points)

For patients with average eGFR in the (90,max(eGFR)) range, collect in a data table (or tibble) their identifier, sex, age at baseline, average eGFR, time of last eGFR reading and number of eGFR measurements taken.

```
# Enter code here.
egfr_90_plus = unique(longegfr[mean_egfr>90, .(id,sex,baseline.age,mean_egfr, count_egfr),])[order(mean_
egfr_90_plus
```

```
##      id sex baseline.age mean_egfr count_egfr
##  1: 120   0         90.9  90.04000          2
##  2: 170   0         87.0  90.56000          2
##  3: 157   0         63.8  90.57308         13
##  4: 140   0         51.6  90.60929         28
##  5: 112   1         77.8  90.66500          6
##  6:  45   1         24.9  91.25000          1
##  7:  79   0         65.6  91.45057         35
##  8:  52   1         56.3  93.31544         57
##  9: 196   1         62.5  94.26000          2
## 10: 115   0         70.3  94.56900         10
## 11: 177   1         78.7  94.85769         26
## 12:  25   0         40.1  95.35625          8
## 13: 169   0         82.8  97.12400         10
## 14: 250   1         48.6 101.23000          1
## 15:  92   1         41.2 101.33882         17
## 16: 100   0         63.0 101.86769         13
## 17: 242   0         54.3 102.24000          4
## 18: 241   1         62.3 105.25200          5
## 19: 102   0         38.7 105.96000         10
## 20: 220   1         47.0 106.00857          7
## 21: 215   1         45.4 106.08278         54
## 22:  80   0         67.7 106.09600          5
## 23:  10   0         50.4 107.00429          7
## 24:  81   0         38.8 108.32000          8
## 25: 245   1         50.5 111.02900         10
## 26: 238   1         55.1 113.37833          6
## 27:  31   0         74.8 113.59250          8
## 28: 205   0         59.9 114.84833          6
## 29:  14   0         65.1 116.09200         10
## 30:  33   0         74.2 116.35000          4
## 31: 234   1         55.3 116.38250          4
## 32: 218   0         56.6 117.65750          4
## 33: 247   0         48.4 118.70667          9
## 34:  49   1         68.2 128.25800          5
## 35: 134   0         31.7 133.29500          2
## 36: 173   0         22.1 147.69000          1
##      id sex baseline.age mean_egfr count_egfr
```

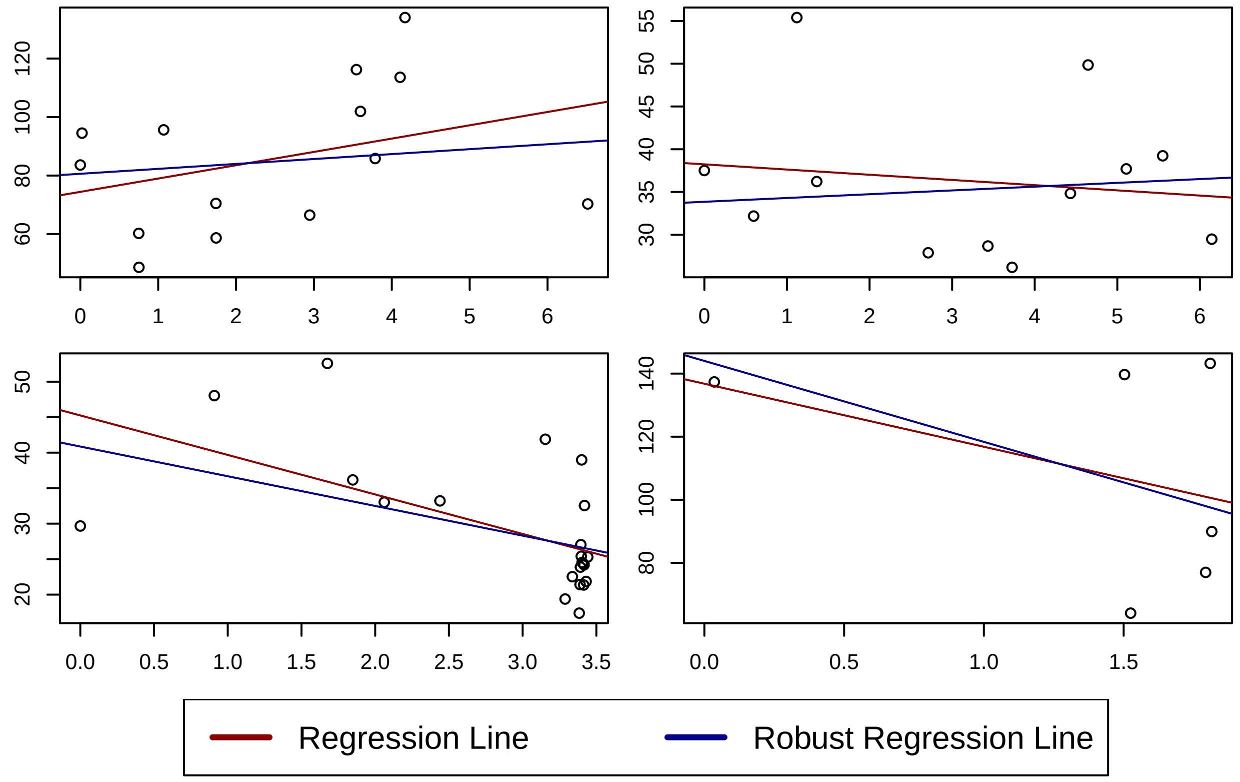
Problem 1.d (9 points)

For patients 3, 37, 162 and 223: * Plot the patient's eGFR measurements as a function of time. * Fit a linear regression model and add the regression line to the plot. * Report the 95% confidence interval for the regression coefficients of the fitted model. * Using a different colour, plot a second regression line computed after removing the extreme eGFR values (one each of the highest and the lowest value).

The plots should be appropriately labeled and the results should be accompanied by some explanation as you would communicate it to a colleague with a medical rather than statistical background.

```r
# Enter code here.
patient_id = c(3,37,162,223)
subset = longegfr[id %in% patient_id, .(id, fu.years, egfr)][order(id, fu.years)]
subset_1 = subset[id==patient_id[1]]
subset_2 = subset[id==patient_id[2]]
subset_3 = subset[id==patient_id[3]]
subset_4 = subset[id==patient_id[4]]
subset_1_rob = subset_1[!(egfr==max(egfr, na.rm=TRUE) | egfr==min(egfr, na.rm=TRUE))]
subset_2_rob = subset_2[!(egfr==max(egfr, na.rm=TRUE) | egfr==min(egfr, na.rm=TRUE))]
subset_3_rob = subset_3[!(egfr==max(egfr, na.rm=TRUE) | egfr==min(egfr, na.rm=TRUE))]
subset_4_rob = subset_4[!(egfr==max(egfr, na.rm=TRUE) | egfr==min(egfr, na.rm=TRUE))]

reg1 = lm(subset_1[,egfr] ~ subset_1[,fu.years])
reg2 = lm(subset_2[,egfr] ~ subset_2[,fu.years])
reg3 = lm(subset_3[,egfr] ~ subset_3[,fu.years])
reg4 = lm(subset_4[,egfr] ~ subset_4[,fu.years])
reg1_rob = lm(subset_1_rob[,egfr] ~ subset_1_rob[,fu.years])
reg2_rob = lm(subset_2_rob[,egfr] ~ subset_2_rob[,fu.years])
reg3_rob = lm(subset_3_rob[,egfr] ~ subset_3_rob[,fu.years])
reg4_rob = lm(subset_4_rob[,egfr] ~ subset_4_rob[,fu.years])

coef_1 = summary(reg1, conf.int=TRUE)$coefficients[2,1]
sd_1   = summary(reg1, conf.int=TRUE)$coefficients[2,2]
coef_2 = summary(reg2, conf.int=TRUE)$coefficients[2,1]
sd_2   = summary(reg2, conf.int=TRUE)$coefficients[2,2]
coef_3 = summary(reg3, conf.int=TRUE)$coefficients[2,1]
sd_3   = summary(reg3, conf.int=TRUE)$coefficients[2,2]
coef_4 = summary(reg4, conf.int=TRUE)$coefficients[2,1]
sd_4   = summary(reg4, conf.int=TRUE)$coefficients[2,2]

ci_1 = c(coef_1 - 2*sd_1 , coef_1 + 2*sd_1)
ci_2 = c(coef_2 - 2*sd_2 , coef_2 + 2*sd_2)
ci_3 = c(coef_3 - 2*sd_3 , coef_3 + 2*sd_3)
ci_4 = c(coef_4 - 2*sd_4 , coef_4 + 2*sd_4)

m = matrix(c(1,2,3,4,5,5),nrow = 3,ncol = 2,byrow = TRUE)

layout(mat = m,heights = c(0.4,0.4,0.2))
```

```r
par(mar = c(2,2,1,1))
plot(subset_1[,fu.years], subset_1[,egfr], xlab='years', ylab='patient 1 egfr')
abline(reg1, col='red4')
abline(reg1_rob, col='blue4')
plot(subset_2[,fu.years], subset_2[,egfr], xlab='years', ylab='patient 2 egfr')
abline(reg2, col='red4')
abline(reg2_rob, col='blue4')
plot(subset_3[,fu.years], subset_3[,egfr], xlab='years', ylab='patient 3 egfr')
abline(reg3, col='red4')
abline(reg3_rob, col='blue4')
plot(subset_4[,fu.years], subset_4[,egfr], xlab='years', ylab='patient 4 egfr')
abline(reg4, col='red4')
abline(reg4_rob, col='blue4')
plot(1, type = "n", axes=FALSE, xlab="", ylab="")
plot_colors = c("blue","black", "green", "orange", "pink")
legend(x = "top",inset = 0,
        legend = c("Regression Line", "Robust Regression Line"),
        col=c('red4', 'blue4'), lwd=3, cex=1.5, horiz = TRUE)
```



Problem 2 (25 points)

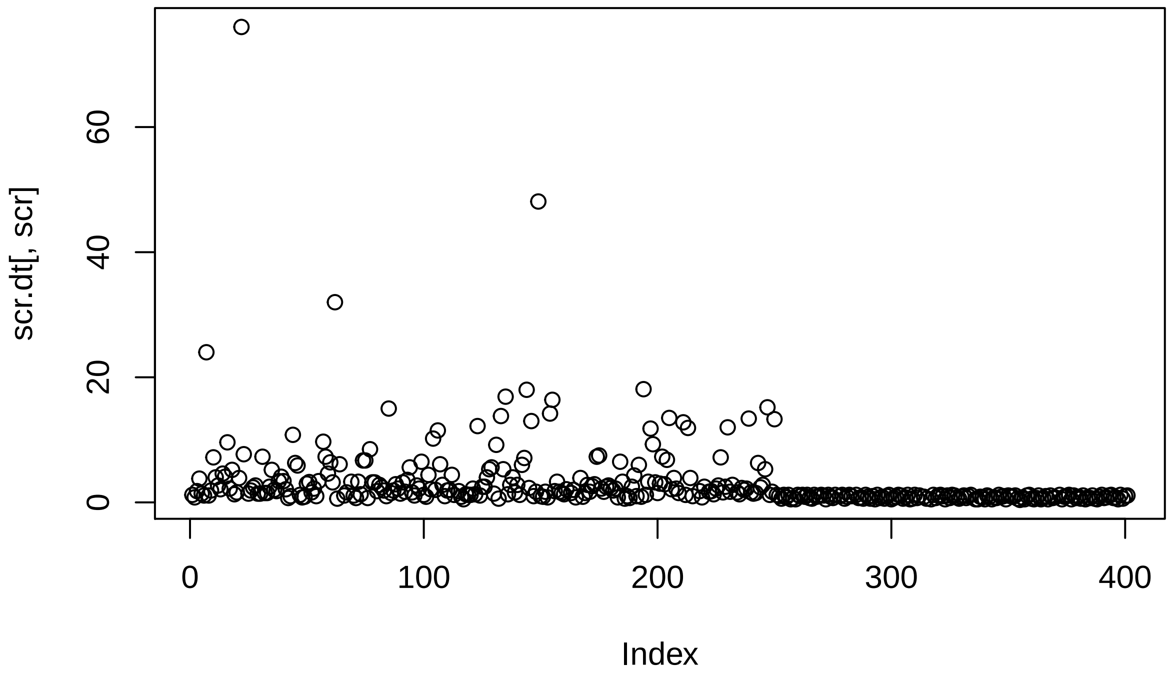
The MDRD4 and CKD-EPI equations are two different ways of estimating the glomerular filtration rate (eGFR) in adults: $MDRD4 = 175 \times Scr^{-1.154} \times Age^{-0.203}[\times 0.742 if female][\times 1.212 if black]$, and $CKD\_EPI = 141 \times \min(Scr/\kappa, 1)^{\alpha} \times \max(Scr/\kappa, 1)^{-1.209} \times 0.993^{Age}[\times 1.018\ \ if\ \ female][\times 1.158\ \ if\ black]$, (1)

where: * Scr is serum creatinine (in mg/dL) * κ is 0.7 for females and 0.9 for males * α is -0.329 for females and -0.411 for males

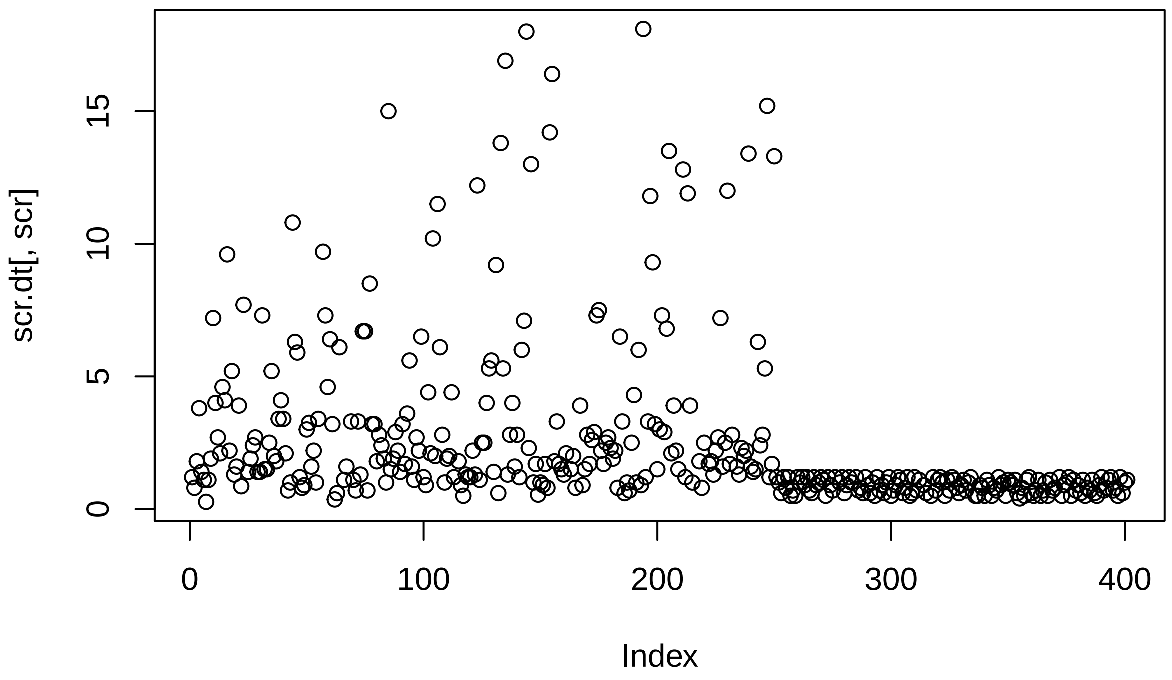
Problem 2.a (7 points)

For the scr.csv dataset available on Learn, examine a summary of the distribution of serum creatinine and report the inter-quartile range. If you suspect that some serum creatinine values may have been reported in µmol/L convert them to mg/dL by dividing by 88.42. Justify your choice of values to convert and examine the distribution of serum creatinine following any changes you have made.

```r
# Enter code here.
scr.dt = data.table(fread('./data/scr.csv'))
plot(scr.dt[,scr])
```



```r
# longegfr_nas[,missing_ind:=ifelse(V1>0,1,0)]

scr.dt[, scr:=ifelse(scr>19, scr/88.42, scr)]
plot(scr.dt[,scr])
```



```r
IQR_scr = summary(scr.dt[,scr])[5] - summary(scr.dt[,scr])[2]
IQR_scr
```

```
## 3rd Qu.
##    1.85
```

Problem 2.b (11 points)

Compute the eGFR according to the two equations. Report (rounded to the second decimal place) mean and standard deviation of the two eGFR vectors and their Pearson correlation coefficient. Also report the same quantities according to strata of MDRD4 eGFR: 0-60, 60-90 and > 90.

```r
# Enter code here.
scr.dt[,scr_est1:=175*
         scr^(-1.154)*
         age^(-0.203)*
         (fifelse(scr.dt[,sex=='Female'],0.742,1, na=1))*
         (fifelse(scr.dt[,ethnic=='Black'],1.212,1,na=1))]

scr.dt[,min_scr_1:=pmin(scr/fifelse(scr.dt[,sex=='Female'],0.7,0.9,na=1),1, na.rm=TRUE)^(fifelse(scr.dt
scr.dt[,max_scr_1:=pmax(scr/fifelse(scr.dt[,sex=='Female'],0.7,0.9,na=1),1, na.rm=TRUE)^(-1.209)]
scr.dt[,scr_est2:=141*
         min_scr_1*
         max_scr_1*
         0.993^age*
         (fifelse(scr.dt[,sex=='Female'],1.018,1, na=1))*
         (fifelse(scr.dt[,ethnic=='Black'],1.158,1,na=1))]

scr.dt
```

```
##      age scr    sex ethnic  scr_est1 min_scr_1 max_scr_1  scr_est2
##   1:  48 1.2 Female  Other  47.94848  1.000000 0.5211868  53.39791
##   2:   7 0.8   Male  Black 184.85020  1.049600 1.0000000 163.15339
##   3:  62 1.8 Female   <NA>  28.51031  1.000000 0.3192266  29.64281
##   4:  48 3.8 Female  Other  12.67885  1.000000 0.1293496  13.25244
##   5:  51 1.4   Male  Other  53.42808  1.000000 0.5861522  57.76186
##  ---
## 397:  55 0.5 Female  Other 128.09641  1.117059 1.0000000 108.95613
## 398:  42 1.2   Male  Black  80.47221  1.000000 0.7062347  85.85096
## 399:  12 0.6   Male  Other 190.53629  1.181336 1.0000000 153.10297
## 400:  17 1.0 Female  Black  88.54488  1.000000 0.6497160  95.83766
## 401:  58 1.1 Female  Other  51.01512  1.000000 0.5790016  55.29719
```

```
mean_est_1 = round(mean(scr.dt$scr_est1, na.rm=TRUE),2)
sd_est_1   = round(sd  (scr.dt$scr_est1, na.rm=TRUE),2)
mean_est_2 = round(mean(scr.dt$scr_est2, na.rm=TRUE),2)
sd_est_2   = round(sd  (scr.dt$scr_est2, na.rm=TRUE),2)

mean_est_1
```

```
## [1] 61.11
```

```
sd_est_1
```

```
## [1] 49.82
```

```
mean_est_2
```

```
## [1] 61.77
```

```
sd_est_2
```

```
## [1] 42.44
```

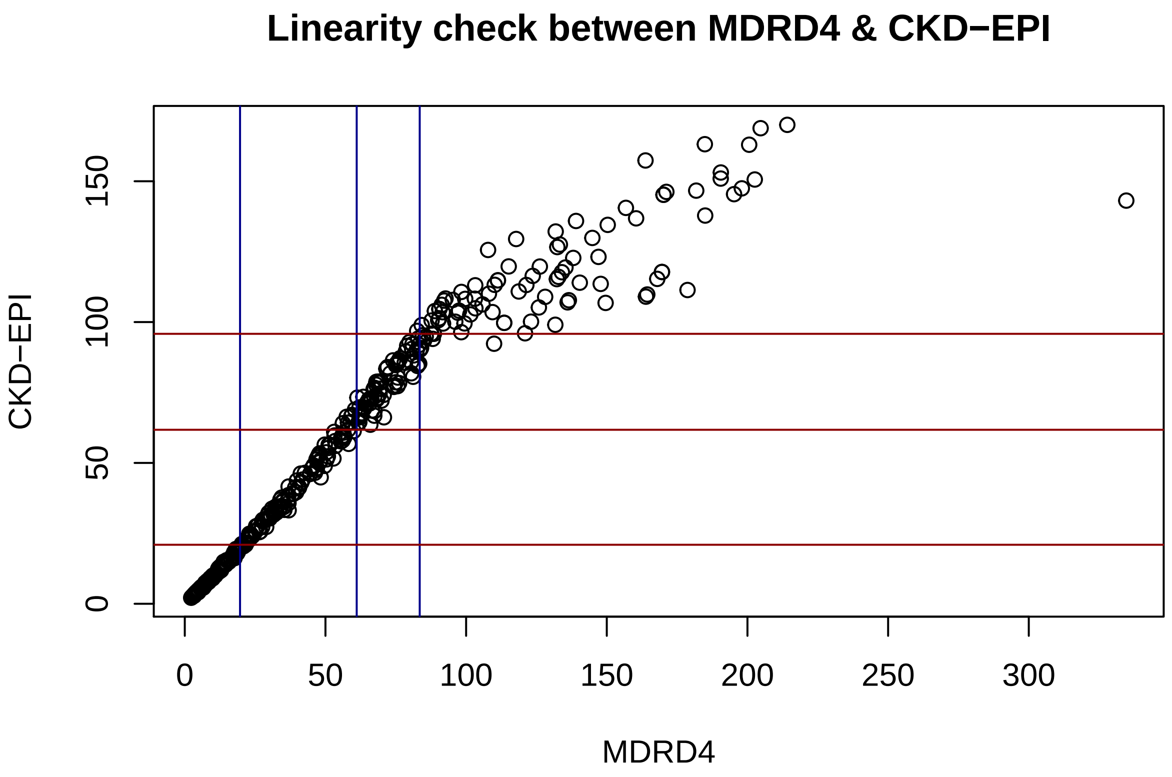
```
cor(scr.dt$scr_est1,scr.dt$scr_est2, method='pearson', use = "complete.obs")
```

```
## [1] 0.9531475
```

Problem 2.c (7 points)

Produce a scatter plot of the two eGFR vectors, and add vertical and horizontal lines (i.e.) corresponding to median, first and third quartiles. Is the relationship between the two eGFR equations linear? Justify your answer.

```
# Enter code here.
plot(scr.dt$scr_est1,scr.dt$scr_est2, xlab='MDRD4', ylab='CKD-EPI', main='Linearity check between MDRD4
abline(v=mean_est_1, col='blue4')
abline(v=quantile(scr.dt$scr_est1, na.rm=TRUE)[2], col='blue4')
abline(v=quantile(scr.dt$scr_est1, na.rm=TRUE)[4], col='blue4')
abline(h=mean_est_2, col='red4')
abline(h=quantile(scr.dt$scr_est2, na.rm=TRUE)[2], col='red4')
abline(h=quantile(scr.dt$scr_est2, na.rm=TRUE)[4], col='red4')
```



Problem 3 (31 points)

You have been provided with electronic health record data from a study cohort. Three CSV (Comma Separated Variable) files are provided on learn.

The first file is a cohort description file cohort.csv file with fields: * id = study identifier * yob = year of birth * age = age at measurement * bp = systolic blood pressure * albumin = last known albuminuric status (categorical) * diabetes = diabetes status

The second file lab1.csv is provided by a laboratory after measuring various biochemistry levels in the cohort blood samples. Notice that a separate lab identifier is used to anonymise results from the cohort. The year of birth is also provided as a check that the year of birth aligns between the two merged sets. * LABID = lab identifier * yob = year of birth * urea = blood urea * creatinine = serum creatinine * glucose = random blood glucose

To link the two data files together, a third linker file linker.csv is provided. The linker file includes a LABID identifier and the corresponding cohort id for each person in the cohort.

Problem 3.a (6 points)

Using all three files provided on learn, load and merge to create a single data table based dataset cohort.dt. This will be used in your analysis. Perform assertion checks to ensure that all identifiers in cohort.csv have been accounted for in the final table and that any validation fields are consistent between sets. After the checks are complete, drop the identifier that originated from lab dataset LABID. Ensure that a single yob field remains and rename it. Ensure that the albumin field is converted to a factor and the ordering of the factor is 1="normo",2="micro",3="macro".

```r
# Enter code here.
cohort = data.table(fread('./data/cohort.csv', stringsAsFactors = TRUE))
lab1 = data.table(fread('./data/lab1.csv'))
linker = data.table(fread('./data/linker.csv'))
tmp = merge(cohort, linker, by=c('id'), all=TRUE)
```

```r
cohort.dt = merge(tmp, lab1, by.x=c('LABID', 'yob'), by.y=c('LABID', 'yob'), all=TRUE)
cohort.dt$albumin = ordered(cohort.dt$albumin,
                            levels = c('normo','micro','macro'))
cohort.dt
```

```
##        LABID  yob      id age  bp diabetes albumin urea creatinine glucose
##   1:   LID_1 1986 PID_285  33  80        0   normo 37.0    106.104     100
##   2:  LID_10 1980 PID_153  39  70        1   normo 20.0     70.736     121
##   3: LID_100 1951  PID_13  68  70        1   micro 72.0    185.682     208
##   4: LID_101 1965 PID_110  54  70        1    <NA> 50.1    167.998     233
##   5: LID_102 1953 PID_222  66  70        1   micro 30.0    150.314     248
##  ---
## 396:  LID_95 1962 PID_254  57  80        0   normo 17.0    106.104     119
## 397:  LID_96 1978 PID_297  41  70        0   normo 38.0     53.052     125
## 398:  LID_97 1964 PID_119  55  70        0   micro 25.0    106.104      99
## 399:  LID_98 1974 PID_236  45  70        0   micro 93.0    203.366     113
## 400:  LID_99 1963 PID_100  56 180        1   normo 24.0    106.104     298
```

Problem 3.b (10 points)

Create a copy of the dataset where you will impute all missing values. Update any missing age fields using the year of birth, for all other continuous variables write a function called impute.to.mean and impute to mean, impute any categorical variable to the mode. Compare the distributions of the imputed and non-imputed variables and decide which ones to keep for further analysis. Justify your answer.

```r
# Enter code here.
cohort_complete = copy(cohort.dt)
cohort_complete[is.na(age), age:=abs(year(Sys.Date())-round(yob))]
cohort_complete
```

```
##        LABID  yob      id age  bp diabetes albumin urea creatinine glucose
##   1:   LID_1 1986 PID_285  33  80        0   normo 37.0    106.104     100
##   2:  LID_10 1980 PID_153  39  70        1   normo 20.0     70.736     121
##   3: LID_100 1951  PID_13  68  70        1   micro 72.0    185.682     208
##   4: LID_101 1965 PID_110  54  70        1    <NA> 50.1    167.998     233
##   5: LID_102 1953 PID_222  66  70        1   micro 30.0    150.314     248
##  ---
## 396:  LID_95 1962 PID_254  57  80        0   normo 17.0    106.104     119
## 397:  LID_96 1978 PID_297  41  70        0   normo 38.0     53.052     125
## 398:  LID_97 1964 PID_119  55  70        0   micro 25.0    106.104      99
## 399:  LID_98 1974 PID_236  45  70        0   micro 93.0    203.366     113
## 400:  LID_99 1963 PID_100  56 180        1   normo 24.0    106.104     298
```

```r
#' This is a function that takes as impute a column of a data.table and imputes
#' the NAs with its mean / mode if tha vector is numeric or categorical respectively.
#' @param x A vector of numeric or categorical values for which the NAs will be imputed.
impute.to.mean = function(x) {
    if (is.numeric(x)){
      if (all(na.omit(x) %in% 0:1)){
        x[is.na(x)] = unique(x)[which.max(tabulate(match(x, unique(x))))]
      } else {x[is.na(x)] = mean(x, na.rm=TRUE)}
    } else if (is.factor(x)){x[is.na(x)] = unique(x)[which.max(tabulate(match(x, unique(x))))]}
    return(x)
  }
```

```
# diab.dt.imputed2 = diab.dt %>% copy() %>%
#                          .[, (numcols) := lapply(.SD, impute.to.median),.SDcols = numcols]
# bp,diabetes,urea,creatinine,glucose, albumin
numcols = cohort_complete %>% select(bp,diabetes,urea,creatinine,glucose, albumin) %>% colnames
cohort_complete %>% .[, (numcols) := lapply(.SD, impute.to.mean), .SDcols = numcols]
unique(cohort.dt$bp)[which.max(tabulate(match(cohort.dt$bp, unique(cohort.dt$bp))))]
```

```
## [1] 80
```

```
summary(cohort_complete)
```

```
##     LABID                 yob            id                  age       
##  Length:400         Min.   :1929   Length:400         Min.   : 2.00  
##  Class :character   1st Qu.:1955   Class :character   1st Qu.:42.00  
##  Mode  :character   Median :1965   Mode  :character   Median :54.00  
##                     Mean   :1968                      Mean   :51.52  
##                     3rd Qu.:1977                      3rd Qu.:64.00  
##                     Max.   :2017                      Max.   :90.00  
##        bp            diabetes       albumin         urea       
##  Min.   : 50.00   Min.   :0.0000   normo:245   Min.   :  1.50  
##  1st Qu.: 70.00   1st Qu.:0.0000   micro:130   1st Qu.: 27.00  
##  Median : 78.23   Median :0.0000   macro: 25   Median : 44.00  
##  Mean   : 76.47   Mean   :0.3375               Mean   : 57.43  
##  3rd Qu.: 80.00   3rd Qu.:1.0000               3rd Qu.: 61.75  
##  Max.   :180.00   Max.   :1.0000               Max.   :391.00  
##    creatinine         glucose   
##  Min.   :  35.37   Min.   : 22  
##  1st Qu.:  79.58   1st Qu.:101  
##  Median : 123.79   Median :126  
##  Mean   : 271.67   Mean   :148  
##  3rd Qu.: 271.67   3rd Qu.:150  
##  Max.   :6719.92   Max.   :490
```

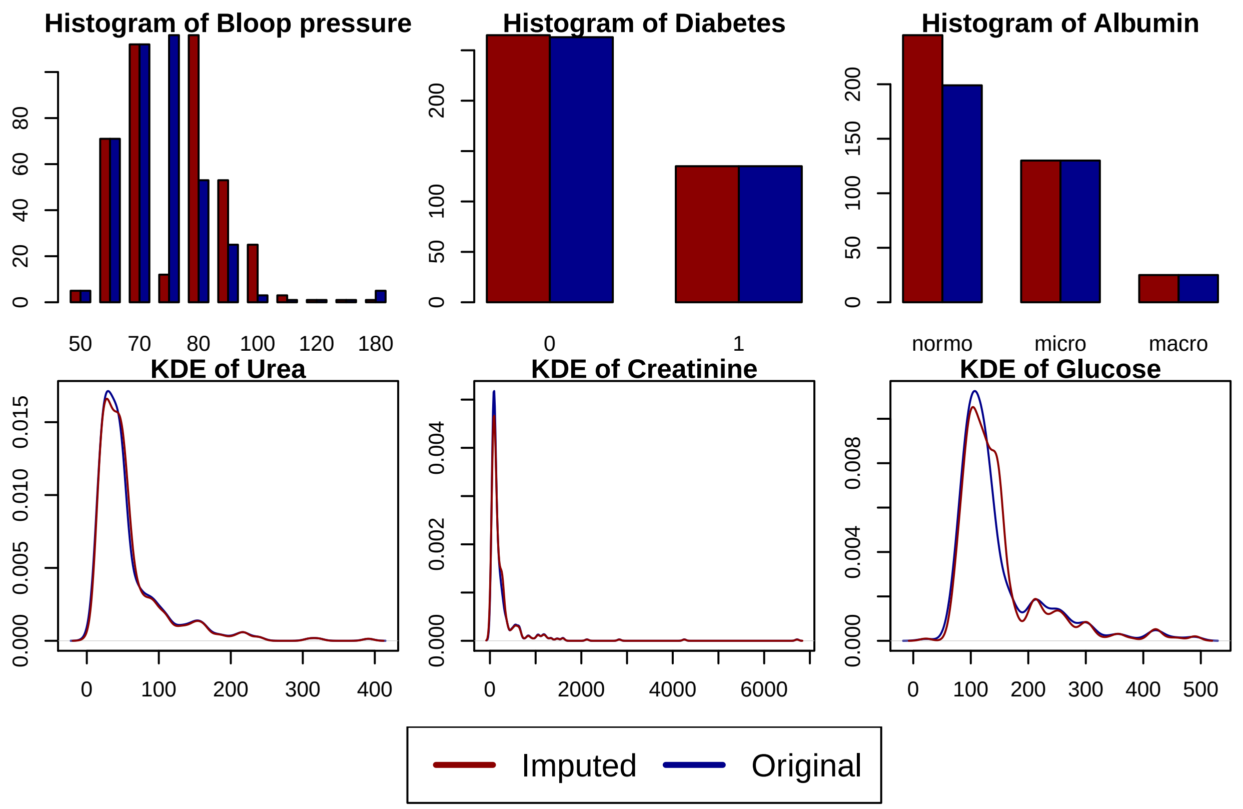
```
cohort_complete
```

```
##        LABID  yob      id age  bp diabetes albumin urea creatinine glucose
##   1:   LID_1 1986 PID_285  33  80        0   normo 37.0    106.104     100
##   2:  LID_10 1980 PID_153  39  70        1   normo 20.0     70.736     121
##   3: LID_100 1951  PID_13  68  70        1   micro 72.0    185.682     208
##   4: LID_101 1965 PID_110  54  70        1   normo 50.1    167.998     233
##   5: LID_102 1953 PID_222  66  70        1   micro 30.0    150.314     248
##  ---                                                                      
## 396:  LID_95 1962 PID_254  57  80        0   normo 17.0    106.104     119
## 397:  LID_96 1978 PID_297  41  70        0   normo 38.0     53.052     125
## 398:  LID_97 1964 PID_119  55  70        0   micro 25.0    106.104      99
## 399:  LID_98 1974 PID_236  45  70        0   micro 93.0    203.366     113
## 400:  LID_99 1963 PID_100  56 180        1   normo 24.0    106.104     298
```

```
m = matrix(c(1,2,3,4,5,6,7,7,7),nrow = 3,ncol = 3,byrow = TRUE)
layout(mat = m,heights = c(0.4,0.4,0.2))
par(mar = c(2,2,1,1))
barplot(rbind(table(cohort_complete$bp), table(cohort.dt$bp)), beside=TRUE, col=c('red4','blue4'), main
```

```
## Warning in rbind(table(cohort_complete$bp), table(cohort.dt$bp)): number of
## columns of result is not a multiple of vector length (arg 2)
```

```
barplot(rbind(table(cohort_complete$diabetes), table(cohort.dt$diabetes)), beside=TRUE, col=c('red4','bl
barplot(rbind(table(cohort_complete$albumin), table(cohort.dt$albumin)), beside=TRUE, col=c('red4','blu
plot(density(cohort.dt$urea, na.rm=TRUE), col='blue4', main='KDE of Urea')
lines(density(cohort_complete$urea), col='red4')
plot(density(cohort.dt$creatinine, na.rm=TRUE), col='blue4', main='KDE of Creatinine')
lines(density(cohort_complete$creatinine), col='red4')
plot(density(cohort.dt$glucose, na.rm=TRUE), col='blue4', main='KDE of Glucose')
lines(density(cohort_complete$glucose), col='red4')
plot(1, type = "n", axes=FALSE, xlab="", ylab="")
legend(x = "top",inset = 0,
       legend = c("Imputed", "Original"),
       col=c('red4', 'blue4'), lwd=3, cex=1.5, horiz = TRUE)
```

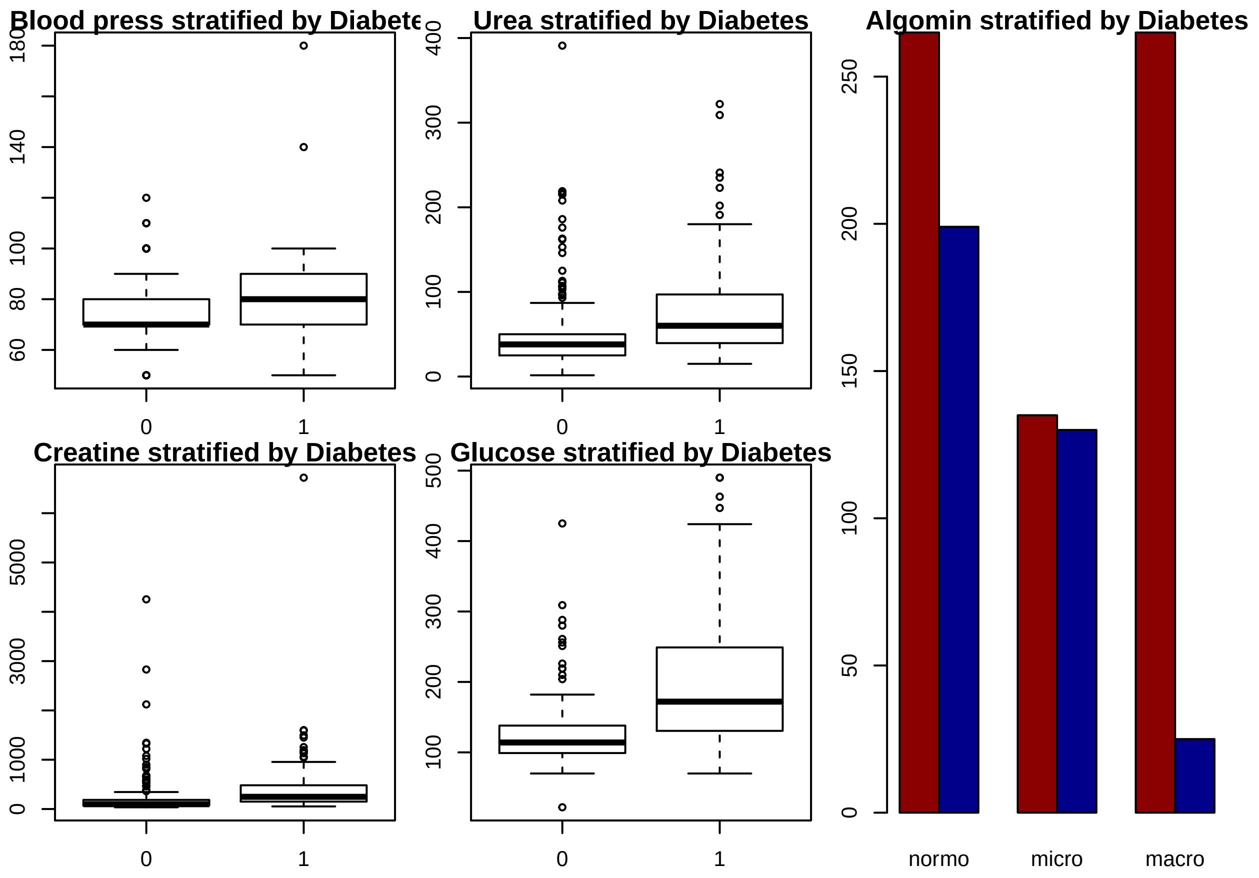


Problem 3.c (6 points)

Plot boxplots of potential predictors for diabetes grouped by cases and controls and use these to decide which predictors to keep for future analysis. For any categorical variables create a table instead. Justify your answers.

```
# Enter code here.
# bp,diabetes,urea,creatinine,glucose, albumin
bp = cohort_complete$bp
urea = cohort_complete$urea
creatinine = cohort_complete$creatinine
glucose = cohort_complete$glucose
albumin = cohort_complete$albumin
diabetes = cohort_complete$diabetes

m = matrix(c(1,2,3,4,5,3),nrow = 2,ncol = 3,byrow = TRUE)
```

```
layout(mat = m,heights = c(0.4,0.4,0.2))
par(mar = c(2,2,1,1))
boxplot(bp ~ diabetes, data=cohort_complete, main="Blood press stratified by Diabetes")
boxplot(urea ~ diabetes, data=cohort_complete, main="Urea stratified by Diabetes")
barplot(rbind(table(cohort_complete$diabetes), table(cohort.dt$albumin)), beside=TRUE, col=c('red4','blu
boxplot(creatinine ~ diabetes, data=cohort_complete, main="Creatine stratified by Diabetes")
boxplot(glucose ~ diabetes, data=cohort_complete, main="Glucose stratified by Diabetes")
```



```
albumin_table = table(albumin, diabetes)
colnames(albumin_table) = c("No Diabetes", "Diabetes")
albumin_table
```

```
##         diabetes
## albumin No Diabetes Diabetes
##   normo         192       53
##   micro          61       69
##   macro          12       13
```

Problem 3.d (9 points)

Use your findings from the previous exercise fit an appropriate model of diabetes with two predictors. Print a summary and explain the results as you would communicate it to a colleague with a medical rather than statistical background.

```
# Enter code here.
model1 = glm(diabetes ~ glucose + albumin, family='binomial')
summary(model1)
```

```
##
## Call:
## glm(formula = diabetes ~ glucose + albumin, family = "binomial")
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.0990  -0.7013  -0.5208   0.6802   2.2565
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.151621   0.416888  -7.560 4.03e-14 ***
## glucose      0.017834   0.002513   7.095 1.29e-12 ***
## albumin.L    0.534820   0.342585   1.561   0.1185
## albumin.Q   -0.448139   0.256400  -1.748   0.0805 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 511.49  on 399  degrees of freedom
## Residual deviance: 389.59  on 396  degrees of freedom
## AIC: 397.59
##
## Number of Fisher Scoring iterations: 5
```

Problem 4 (19 points)

Problem 4.a. (9 points)

Add a third predictor to the final model from problem 3, perform a likelihood ratio test to compare both models and report the p-value for the test. Is there any support for the additional term? Plot a ROC curve for both models and report the AUC, explain the results as you would communicate it to a colleague with a medical rather than statistical background.

```
# Enter code here.
model2 = glm(diabetes ~ glucose + albumin + cohort_complete$age, family='binomial')
summary(model2)
```

```
##
## Call:
## glm(formula = diabetes ~ glucose + albumin + cohort_complete$age,
##     family = "binomial")
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.7615  -0.7072  -0.4022   0.6420   2.5238
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -5.451612   0.681802  -7.996 1.29e-15 ***
## glucose              0.016281   0.002538   6.416 1.40e-10 ***
## albumin.L            0.642553   0.373277   1.721   0.0852 .
## albumin.Q           -0.247191   0.277030  -0.892   0.3722
## cohort_complete$age  0.047137   0.009543   4.940 7.83e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 511.49  on 399  degrees of freedom
## Residual deviance: 359.43  on 395  degrees of freedom
## AIC: 369.43
##
## Number of Fisher Scoring iterations: 5
```

```
pval = pchisq(model1$deviance - model2$deviance, df=1, lower.tail=FALSE)
signif(pval, 2)
```

```
## [1] 4e-08
```

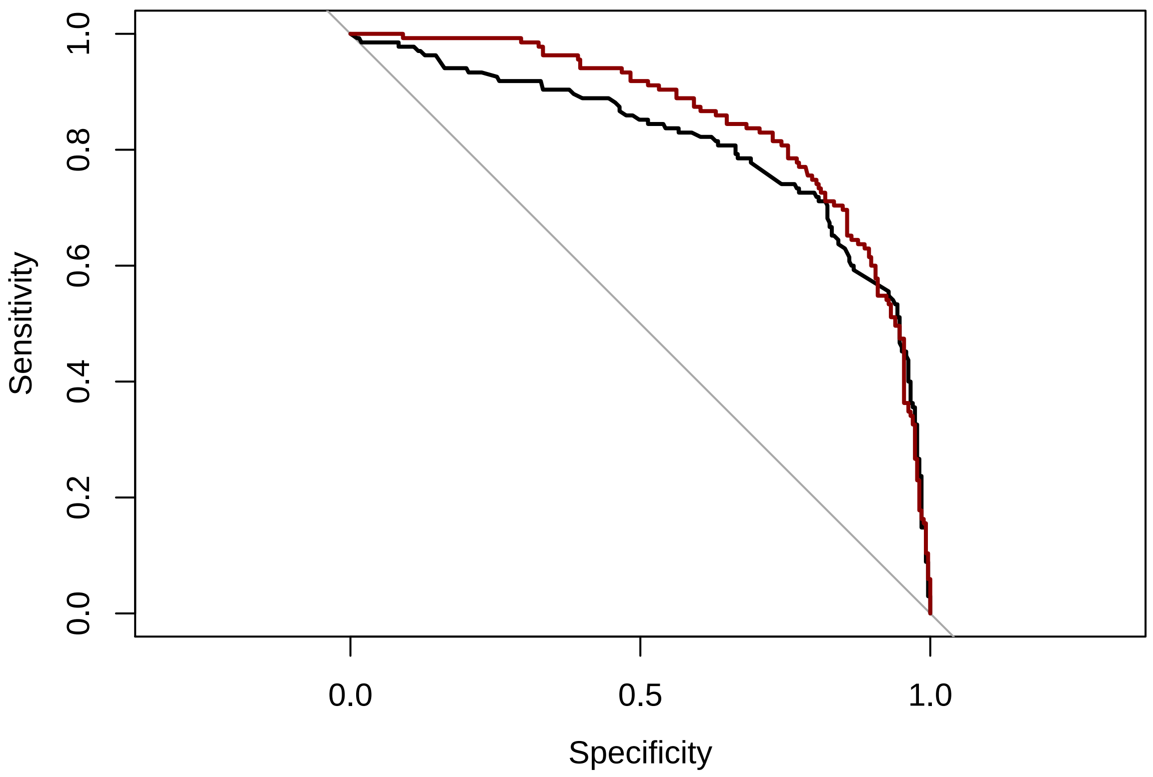
```
roc1 = roc(cohort_complete$diabetes, model1$fitted.values , plot=TRUE, xlim = c(0,1))
```

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

```
## Setting direction: controls < cases
```

```
roc2 = roc(cohort_complete$diabetes, model2$fitted.values , plot=TRUE, xlim = c(0,1), add=TRUE, col="re
```

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
```



```
roc1$auc
```

```
## Area under the curve: 0.8089
```

```
roc2$auc
```

```
## Area under the curve: 0.8522
```

Problem 4.b (10 points)

Perform 10-folds cross-validation for your chosen model and report the mean cross-validated AUCs.

```r
# Enter code here.
set.seed(1903)
k = 10
folds = createFolds(cohort_complete$diabetes, k=k)

pred.cv <- NULL
regr.cv <- NULL
auc.cv <- numeric(k)
for(f in 1:k) {
  train.idx <- setdiff(1:nrow(cohort_complete), folds[[f]])
  regr.cv[[f]] <- glm(diabetes ~ glucose + albumin + cohort_complete$age, family='binomial')
  test.idx <- folds[[f]]
  pred.cv[[f]] <- data.frame(obs = cohort_complete$diabetes[test.idx],
                             pred = predict(regr.cv[[f]], newdata = cohort_complete, type = "response")
  auc.cv[f] <- roc(obs ~ pred, data = pred.cv[[f]])$auc
}

round(mean(auc.cv), 3)
```

```
## [1] 0.843
```