STAT 331 Final Project

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1 Summary

2 Descriptive Statistics

First, take a look at summary statistics of the `fhsd` dataset.

Table 1: Summary Statistics

chdrisk	sex	totchol	age	sysbp	diabp	cursmoke	cigpday	bmi	diabetes	bpmeds	heartrte	glucose	prevmi	prevstrk	prevhyp	hdlc	ldlc
Min. :0.0050	Female:1305	Min. :112.0	Min. :44.00	Min. : 86.0	Min. : 30.00	No :1504	Min. : 0.00	Min. :14.43	No :2142	No :1973	Min. : 44.00	Min. : 46.00	No :2189	No :2260	No : 957	Min. : 10.00	Min. : 20.0
1st Qu.:0.1320	Male :1001	1st Qu.:207.0	1st Qu.:53.00	1st Qu.:122.5	1st Qu.: 73.00	Yes: 802	1st Qu.: 0.00	1st Qu.:23.22	Yes: 164	Yes: 333	1st Qu.: 70.00	1st Qu.: 75.00	Yes: 117	Yes: 46	Yes:1349	1st Qu.: 38.00	1st Qu.:152.0
Median :0.2240		Median :235.5	Median :60.00	Median :136.0	Median : 80.00		Median : 0.00	Median :25.40			Median : 76.00	Median : 83.00				Median : 47.00	Median :180.0
Mean :0.2655		Mean :237.8	Mean :60.23	Mean :139.2	Mean : 81.07		Mean : 6.84	Mean :25.78			Mean : 77.61	Mean : 89.07				Mean : 48.89	Mean :183.1
3rd Qu.:0.3448		3rd Qu.:265.0	3rd Qu.:67.00	3rd Qu.:153.0	3rd Qu.: 88.00		3rd Qu.:10.00	3rd Qu.:27.91			3rd Qu.: 85.00	3rd Qu.: 95.00				3rd Qu.: 57.00	3rd Qu.:210.0
Max. :0.9770		Max. :625.0	Max. :81.00	Max. :246.0	Max. :130.00		Max. :80.00	Max. :46.52			Max. :150.00	Max. :478.00				Max. :189.00	Max. :565.0

First observation we make from the summary is that the median and average ages are around 60, which means the survey seems to have been done on a relatively old group of people. We also have a significantly higher number of females in the study, almost 30% more than the number of males. This might affect the nature of the data to be skewed towards behaviours and physical attributes associated with females.

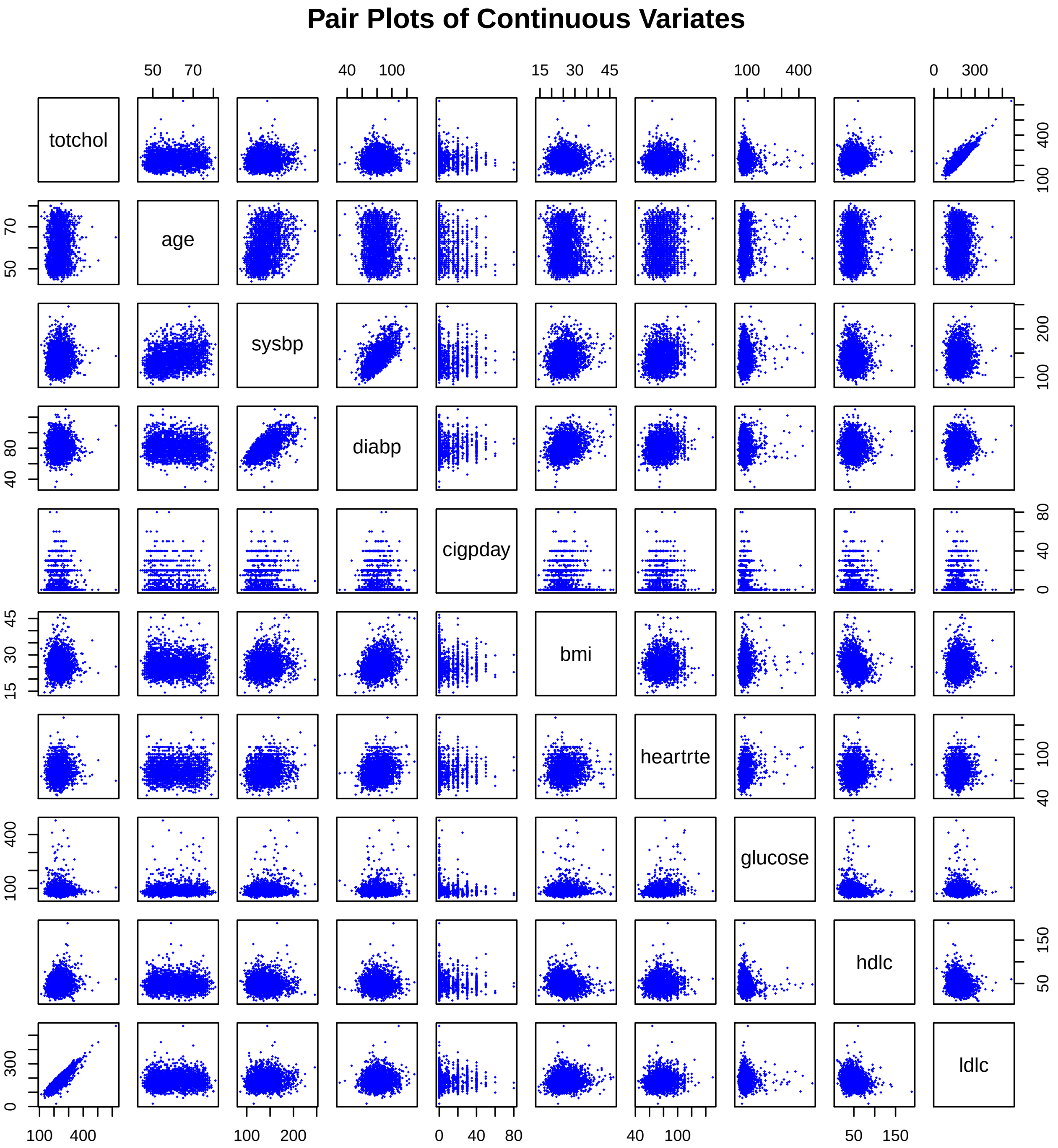
Then take a look at `chdrisk` grouped by `sex` as well as `chdrisk` grouped by `cursmoke`.

```
## fhsd$sex: Female
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.005   0.104   0.179   0.215   0.285   0.949
## ------------------------------------------------------------
## fhsd$sex: Male
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.0210  0.1860  0.2860  0.3314  0.4060  0.9770
```

```
## fhsd$cursmoke: No
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.0050  0.1390  0.2350  0.2754  0.3580  0.9770
## ------------------------------------------------------------
## fhsd$cursmoke: Yes
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##  0.0080  0.1220  0.1995  0.2471  0.3140  0.9710
```

[ADD SOME COMMENTS HERE REGARDING SUMMARY]

Now take a look at pair plots of all numeric explanatory variates i.e. variates excluding response variate `chdrisk` and logical variates such as `cursmoke`.



From the pair plots, we can observe a strong correlation between low density lipoprotein cholesterol and serum total cholestrol. This correlation could be explained by the fact that there could be a relationship between the amount [TO BE CONTINUED]

Now take a look at the VIFs of these variates.

```
##     sexMale     totchol         age       sysbp       diabp cursmokeYes
##    1.225191   10.634882    1.489926    2.918660    2.406411    2.978609
##     cigpday         bmi diabetesYes   bpmedsYes    heartrte     glucose
##    2.973594    1.181865    1.286401    1.214744    1.105902    1.308923
##   prevmiYes prevstrkYes  prevhypYes        hdlc        ldlc
##    1.067134    1.045746    1.823014    2.287571   10.367649
```

[ADD COMMENTS]

3 Candidate Models

3.1 Automated Model Selection

```
library(gtools)
```

```
## Warning: package 'gtools' was built under R version 3.6.2
```

```
load_calcs = FALSE
# model with only intercept
M0 <- lm(I(logit(chdrisk)) ~ 1, data = fhsd)
Mmax <- lm(I(logit(chdrisk)) ~ (.)^2, data = fhsd)
# starting model for stepwise selection
Mstart <- lm(I(logit(chdrisk)) ~ ., data = fhsd)
# find model coefficients which are NA
beta.max <- coef(Mmax)
names(beta.max)[is.na(beta.max)]
```

```
## [1] "cursmokeYes:cigpday"  "bpmedsYes:prevhypYes"
```

```
# find the problem with the NA coeffs
kable(table(fhsd[c("cursmoke", "cigpday")]), "latex")
```

	0	1	2	3	4	5	6	7	8	9	10	12	14	15	16	17	18	19	20	23	25	26	27
No	1504	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Yes	0	16	18	34	11	18	24	9	18	5	76	3	3	50	6	1	8	1	279	1	14	1	1

```
kable(table(fhsd[c("bpmeds", "prevhyp")]), "latex")
```

	No	Yes
No	957	1016
Yes	0	333

```
# remove the coeffs with the problem and add quadratic terms for the continuous variables
Mmax <- lm(I(logit(chdrisk)) ~ (.)^2 - cursmoke:cigpday - bpmeds:prevhyp +
             I(totchol ^ 2) + I(sysbp ^ 2) + I(diabp ^ 2)
           + I(bmi ^ 2) + I(glucose ^ 2)
           + I(hdlc ^ 2) + I(ldlc ^ 2), data = fhsd)
anyNA(coef(Mmax)) # check if there are any remaining NAs
```

```
## [1] FALSE
```

```
if(!load_calcs){
  #forward model selection
  system.time({
    Mfwd <- step(object = M0,
                 scope = list(lower = M0, upper = Mmax),
                 direction = "forward", trace = FALSE)
  })

  #backward model selection
  system.time({
    Mback <- step(object = Mmax,
                  scope = list(lower = M0, upper = Mmax),
                  direction = "backward", trace = FALSE)
  })
  #stepwise model selection
  system.time({
    Mstep <- step(object = Mstart,
                  scope = list(lower = M0, upper = Mmax),
                  direction = "both", trace = FALSE)
  })
}
```

```
##    user  system elapsed
##  50.255   3.035  53.615
```

```
# the caching/loading block
if(!load_calcs) {
  saveRDS(list(Mfwd = Mfwd, Mback = Mback, Mstep = Mstep), file = "models_automated.rds")
} else {
  # just load the calculations
  tmp <- readRDS("models_automated.rds")
  Mfwd <- tmp$Mfwd
  Mback <- tmp$Mback
  Mstep <- tmp$Mstep
  rm(tmp) # optionally remove tmp from workspace
}
# Stepwise model selection
Mstep$call
```

```
## lm(formula = I(logit(chdrisk)) ~ sex + totchol + age + sysbp +
##     diabp + cursmoke + cigpday + bmi + diabetes + bpmeds + heartrte +
##     glucose + prevmi + prevstrk + prevhyp + hdlc + ldlc + I(hdlc^2) +
##     I(bmi^2) + I(diabp^2) + I(sysbp^2) + sysbp:prevmi + totchol:prevhyp +
##     diabetes:prevmi + prevhyp:ldlc + sysbp:prevhyp + totchol:heartrte +
##     sysbp:diabetes + diabp:bmi + diabp:hdlc + prevmi:hdlc + prevmi:prevhyp +
##     sex:glucose + age:ldlc + age:heartrte + cigpday:hdlc + bmi:ldlc +
##     totchol:hdlc + totchol:prevmi + sysbp:heartrte + sysbp:bpmeds +
##     cursmoke:hdlc + prevmi:prevstrk + diabetes:hdlc + sex:sysbp +
##     cigpday:glucose + heartrte:glucose + diabp:glucose + cursmoke:ldlc +
##     age:cigpday + age:hdlc + hdlc:ldlc + age:prevhyp + diabp:prevhyp +
##     diabp:cursmoke + diabp:cigpday + bmi:bpmeds + bpmeds:glucose +
##     age:prevmi + sex:ldlc + cigpday:heartrte + cigpday:prevmi +
##     glucose:prevmi + heartrte:prevmi + bpmeds:prevstrk, data = fhsd)
```

```
# Forward model selection
Mfwd$call
```

```
## lm(formula = I(logit(chdrisk)) ~ prevmi + sysbp + sex + age +
##     ldlc + prevhyp + diabetes + hdlc + I(hdlc^2) + cigpday +
##     I(bmi^2) + bmi + totchol + I(glucose^2) + I(sysbp^2) + bpmeds +
##     heartrte + cursmoke + prevstrk + prevmi:sysbp + sysbp:age +
##     prevhyp:hdlc + prevmi:diabetes + sysbp:prevhyp + prevhyp:totchol +
##     sysbp:diabetes + prevmi:hdlc + prevmi:prevhyp + age:ldlc +
##     age:cigpday + hdlc:cigpday + prevhyp:bmi + ldlc:bmi + prevmi:totchol +
##     ldlc:prevhyp + sysbp:bpmeds + sysbp:hdlc + hdlc:totchol +
##     totchol:heartrte + age:heartrte + diabetes:hdlc + sysbp:heartrte +
##     bmi:bpmeds + sysbp:sex + ldlc:hdlc + prevmi:bmi + age:bmi +
##     prevmi:age + sysbp:cursmoke + hdlc:cursmoke + ldlc:cursmoke +
##     prevmi:cigpday + sex:diabetes + prevmi:prevstrk, data = fhsd)
```

```r
# Backward model selection
Mback$call
```

```
## lm(formula = I(logit(chdrisk)) ~ sex + totchol + age + sysbp +
##     diabp + cursmoke + cigpday + bmi + diabetes + bpmeds + heartrte +
##     glucose + prevmi + prevstrk + prevhyp + hdlc + ldlc + I(totchol^2) +
##     I(sysbp^2) + I(diabp^2) + I(bmi^2) + I(hdlc^2) + I(ldlc^2) +
##     sex:totchol + sex:sysbp + sex:glucose + sex:prevstrk + sex:prevhyp +
##     totchol:age + totchol:bpmeds + totchol:heartrte + totchol:prevmi +
##     totchol:prevstrk + totchol:prevhyp + totchol:hdlc + totchol:ldlc +
##     age:cursmoke + age:bmi + age:heartrte + age:prevmi + age:prevhyp +
##     age:hdlc + sysbp:diabetes + sysbp:bpmeds + sysbp:heartrte +
##     sysbp:prevmi + sysbp:prevhyp + diabp:cursmoke + diabp:cigpday +
##     diabp:bmi + diabp:glucose + diabp:prevhyp + diabp:hdlc +
##     cursmoke:bmi + cursmoke:hdlc + cursmoke:ldlc + cigpday:bmi +
##     cigpday:heartrte + cigpday:glucose + cigpday:prevmi + cigpday:hdlc +
##     bmi:prevmi + bmi:prevhyp + bmi:ldlc + diabetes:prevmi + diabetes:hdlc +
##     bpmeds:glucose + bpmeds:prevstrk + bpmeds:ldlc + heartrte:glucose +
##     heartrte:prevmi + glucose:prevmi + prevmi:prevhyp + prevmi:hdlc +
##     prevhyp:ldlc, data = fhsd)
```

```r
beta.fwd = coef(Mfwd)
beta.back = coef(Mback)
beta.step = coef(Mstep)
identical(names(beta.fwd)[names(beta.fwd) %in% names(beta.back)], names(beta.fwd))
```

```
## [1] FALSE
```

```r
identical(names(beta.fwd)[names(beta.fwd) %in% names(beta.step)], names(beta.fwd))
```

```
## [1] FALSE
```

```r
identical(names(beta.back)[names(beta.back) %in% names(beta.step)], names(beta.back))
```

```
## [1] FALSE
```

3.2 Manual Model Selection

```r
library(stringr) # For string operations
 table <- c() # Initialize empty vector
 names.table <- names(beta.step)                  # Obtain variate names in stepwise model
 names.table <- str_remove_all(names.table,"Yes") # Remove "Yes" from interactions
 names.table <- str_remove_all(names.table,"Male") # Remove "Male"
 # Perform F-tests with Mstep by removing one variate at a time
  for(i in names.table){
    # Obtain model without variate i
    mdl <- lm(as.formula(paste0("update(Mstep, . ~ . -", i,")")),data = fhsd)
   test <- anova(Mstep,mdl)                 # F-Test between Stepwise and reduced model
   table <- cbind(table,test$`Pr(>F)`[2]) # Add corresponding p-value to the table
  }
 table <- as.data.frame(table)
 colnames(table) <- names.table            # Add appropriate column names to the table
sort(table,decreasing = TRUE)              # Arrange variates by decreasing significance
```

```
##   cigpday:heartrte bpmeds:prevstrk bpmeds:glucose diabp:cigpday   cigpday
## 1        0.1506282       0.1492283      0.1189197     0.1155989 0.1151079
##    sex:ldlc age:prevmi cigpday:prevmi hdlc:ldlc bmi:bpmeds prevmi:prevstrk
## 1 0.1141483  0.1097987      0.1051865 0.0923568  0.0855445      0.06997763
##   heartrte:prevmi glucose:prevmi I(sysbp^2) cursmoke:hdlc age:heartrte
## 1      0.06451949     0.05883116  0.0585469    0.05660935   0.05562064
##    age:hdlc cursmoke:ldlc  sex:sysbp sysbp:bpmeds   age:ldlc cigpday:glucose
## 1 0.0510796     0.0417893 0.03623249    0.0300776 0.02915113       0.0291137
##   prevmi:prevhyp       hdlc sex:glucose diabetes:hdlc diabp:glucose    bmi:ldlc
## 1     0.02242217 0.01880445  0.01702301    0.01394662    0.01362058 0.009985489
##   totchol:hdlc    bpmeds age:cigpday heartrte:glucose    cursmoke
## 1  0.009840662 0.0077735 0.006735591      0.004772297 0.004188557
##   totchol:prevmi sysbp:heartrte diabp:prevhyp diabp:cursmoke prevhyp:ldlc
## 1    0.003609581    0.002926201   0.001409115    0.001393474   0.00066789
##            bmi  age:prevhyp sysbp:diabetes   I(hdlc^2)   diabp:hdlc
## 1 0.0006664543 0.0005753017   0.0004931994 0.000320732 0.0001422969
##   sysbp:prevhyp cigpday:hdlc  prevmi:hdlc diabetes:prevmi        diabp
## 1  0.0001292531 0.0001038006 7.056001e-05    6.226049e-05 6.021714e-05
##   totchol:heartrte    diabp:bmi sysbp:prevmi          sex     heartrte
## 1     3.512093e-05 2.940165e-05 2.305381e-05 2.396724e-06 9.478088e-07
##            age totchol:prevhyp     I(bmi^2)   I(diabp^2)       prevmi
## 1 4.238229e-07    1.203731e-09 2.735937e-11 1.257752e-19 1.595006e-22
##        prevhyp
## 1 1.119628e-27
```

```r
# Remove as many insignificant continuous variate interactions as possible
anova(Mstep, update(Mstep,. ~ . - cigpday:heartrte - diabp:cigpday))
```

```
## Analysis of Variance Table
##
## Model 1: I(logit(chdrisk)) ~ sex + totchol + age + sysbp + diabp + cursmoke +
##     cigpday + bmi + diabetes + bpmeds + heartrte + glucose +
##     prevmi + prevstrk + prevhyp + hdlc + ldlc + I(hdlc^2) + I(bmi^2) +
##     I(diabp^2) + I(sysbp^2) + sysbp:prevmi + totchol:prevhyp +
##     diabetes:prevmi + prevhyp:ldlc + sysbp:prevhyp + totchol:heartrte +
##     sysbp:diabetes + diabp:bmi + diabp:hdlc + prevmi:hdlc + prevmi:prevhyp +
##     sex:glucose + age:ldlc + age:heartrte + cigpday:hdlc + bmi:ldlc +
##     totchol:hdlc + totchol:prevmi + sysbp:heartrte + sysbp:bpmeds +
##     cursmoke:hdlc + prevmi:prevstrk + diabetes:hdlc + sex:sysbp +
##     cigpday:glucose + heartrte:glucose + diabp:glucose + cursmoke:ldlc +
##     age:cigpday + age:hdlc + hdlc:ldlc + age:prevhyp + diabp:prevhyp +
##     diabp:cursmoke + diabp:cigpday + bmi:bpmeds + bpmeds:glucose +
##     age:prevmi + sex:ldlc + cigpday:heartrte + cigpday:prevmi +
##     glucose:prevmi + heartrte:prevmi + bpmeds:prevstrk
## Model 2: I(logit(chdrisk)) ~ sex + totchol + age + sysbp + diabp + cursmoke +
##     cigpday + bmi + diabetes + bpmeds + heartrte + glucose +
##     prevmi + prevstrk + prevhyp + hdlc + ldlc + I(hdlc^2) + I(bmi^2) +
##     I(diabp^2) + I(sysbp^2) + sysbp:prevmi + totchol:prevhyp +
##     diabetes:prevmi + prevhyp:ldlc + sysbp:prevhyp + totchol:heartrte +
##     sysbp:diabetes + diabp:bmi + diabp:hdlc + prevmi:hdlc + prevmi:prevhyp +
##     sex:glucose + age:ldlc + age:heartrte + cigpday:hdlc + bmi:ldlc +
##     totchol:hdlc + totchol:prevmi + sysbp:heartrte + sysbp:bpmeds +
##     cursmoke:hdlc + prevmi:prevstrk + diabetes:hdlc + sex:sysbp +
##     cigpday:glucose + heartrte:glucose + diabp:glucose + cursmoke:ldlc +
##     age:cigpday + age:hdlc + hdlc:ldlc + age:prevhyp + diabp:prevhyp +
##     diabp:cursmoke + bmi:bpmeds + bpmeds:glucose + age:prevmi +
##     sex:ldlc + cigpday:prevmi + glucose:prevmi + heartrte:prevmi +
##     bpmeds:prevstrk
##   Res.Df    RSS Df Sum of Sq      F  Pr(>F)
## 1   2240 489.70
## 2   2242 490.84 -2   -1.1458 2.6205 0.07299 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#anova(Mstep, update(Mstep,. ~ . - cigpday:heartrte - diabp:cigpday -age:heartrte))
# Now remove less insignificant interactions
anova(Mstep, update(Mstep,. ~ . - cigpday:heartrte - diabp:cigpday - cigpday:heartrte
                    - bpmeds:prevstrk))
```

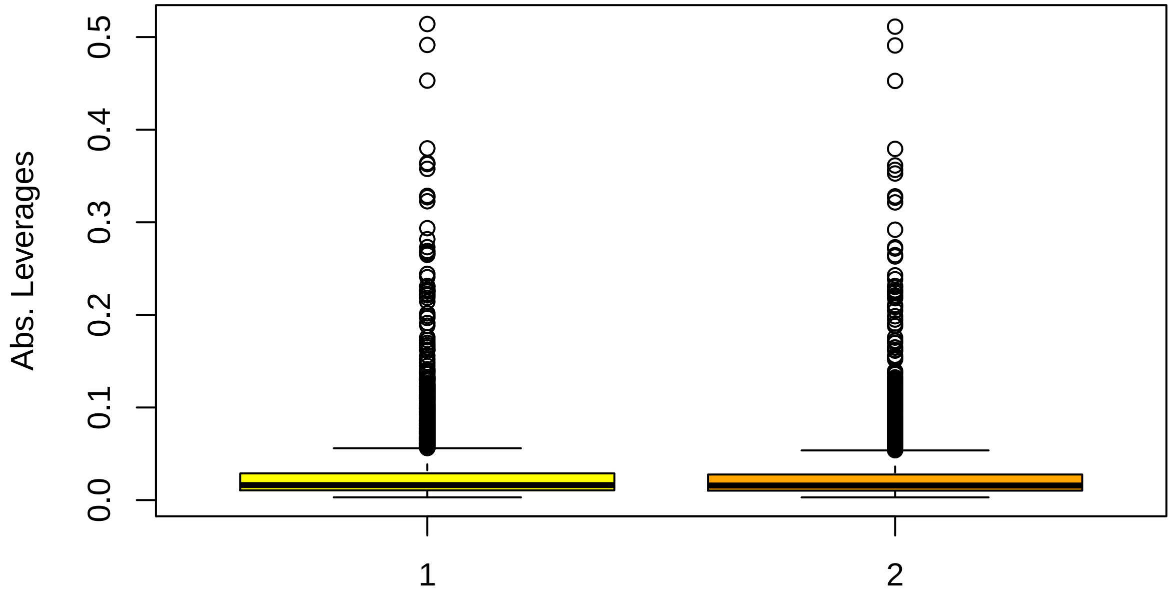
```
## Analysis of Variance Table
##
## Model 1: I(logit(chdrisk)) ~ sex + totchol + age + sysbp + diabp + cursmoke +
##     cigpday + bmi + diabetes + bpmeds + heartrte + glucose +
##     prevmi + prevstrk + prevhyp + hdlc + ldlc + I(hdlc^2) + I(bmi^2) +
##     I(diabp^2) + I(sysbp^2) + sysbp:prevmi + totchol:prevhyp +
##     diabetes:prevmi + prevhyp:ldlc + sysbp:prevhyp + totchol:heartrte +
##     sysbp:diabetes + diabp:bmi + diabp:hdlc + prevmi:hdlc + prevmi:prevhyp +
##     sex:glucose + age:ldlc + age:heartrte + cigpday:hdlc + bmi:ldlc +
##     totchol:hdlc + totchol:prevmi + sysbp:heartrte + sysbp:bpmeds +
##     cursmoke:hdlc + prevmi:prevstrk + diabetes:hdlc + sex:sysbp +
##     cigpday:glucose + heartrte:glucose + diabp:glucose + cursmoke:ldlc +
##     age:cigpday + age:hdlc + hdlc:ldlc + age:prevhyp + diabp:prevhyp +
##     diabp:cursmoke + diabp:cigpday + bmi:bpmeds + bpmeds:glucose +
##     age:prevmi + sex:ldlc + cigpday:heartrte + cigpday:prevmi +
##     glucose:prevmi + heartrte:prevmi + bpmeds:prevstrk
## Model 2: I(logit(chdrisk)) ~ sex + totchol + age + sysbp + diabp + cursmoke +
##     cigpday + bmi + diabetes + bpmeds + heartrte + glucose +
##     prevmi + prevstrk + prevhyp + hdlc + ldlc + I(hdlc^2) + I(bmi^2) +
##     I(diabp^2) + I(sysbp^2) + sysbp:prevmi + totchol:prevhyp +
##     diabetes:prevmi + prevhyp:ldlc + sysbp:prevhyp + totchol:heartrte +
##     sysbp:diabetes + diabp:bmi + diabp:hdlc + prevmi:hdlc + prevmi:prevhyp +
##     sex:glucose + age:ldlc + age:heartrte + cigpday:hdlc + bmi:ldlc +
##     totchol:hdlc + totchol:prevmi + sysbp:heartrte + sysbp:bpmeds +
##     cursmoke:hdlc + prevmi:prevstrk + diabetes:hdlc + sex:sysbp +
##     cigpday:glucose + heartrte:glucose + diabp:glucose + cursmoke:ldlc +
##     age:cigpday + age:hdlc + hdlc:ldlc + age:prevhyp + diabp:prevhyp +
##     diabp:cursmoke + bmi:bpmeds + bpmeds:glucose + age:prevmi +
##     sex:ldlc + cigpday:prevmi + glucose:prevmi + heartrte:prevmi
##   Res.Df    RSS Df Sum of Sq      F  Pr(>F)
## 1   2240 489.70
## 2   2243 491.35 -3   -1.6506 2.5168 0.05656 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Mmanual <- update(Mstep,. ~ . - cigpday:heartrte - diabp:cigpday - cigpday:heartrte
                    - bpmeds:prevstrk)     # Denotes manually constructed model
```

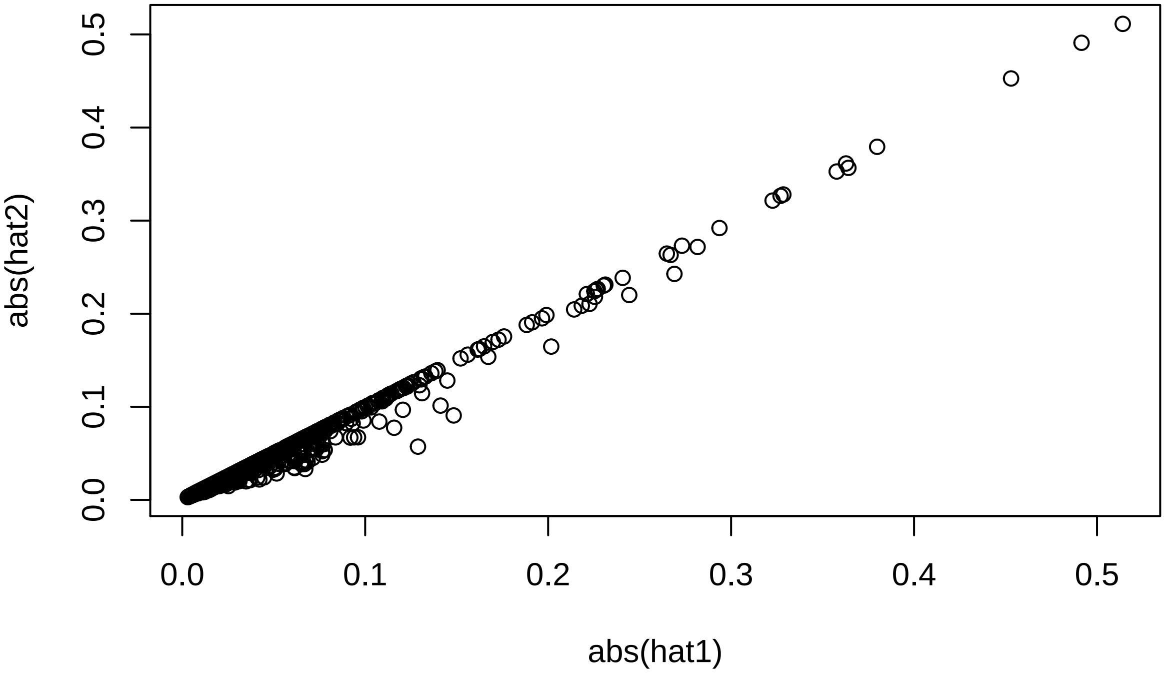
4 Model Diagnostics

4.1 Leverage and Influence Measures

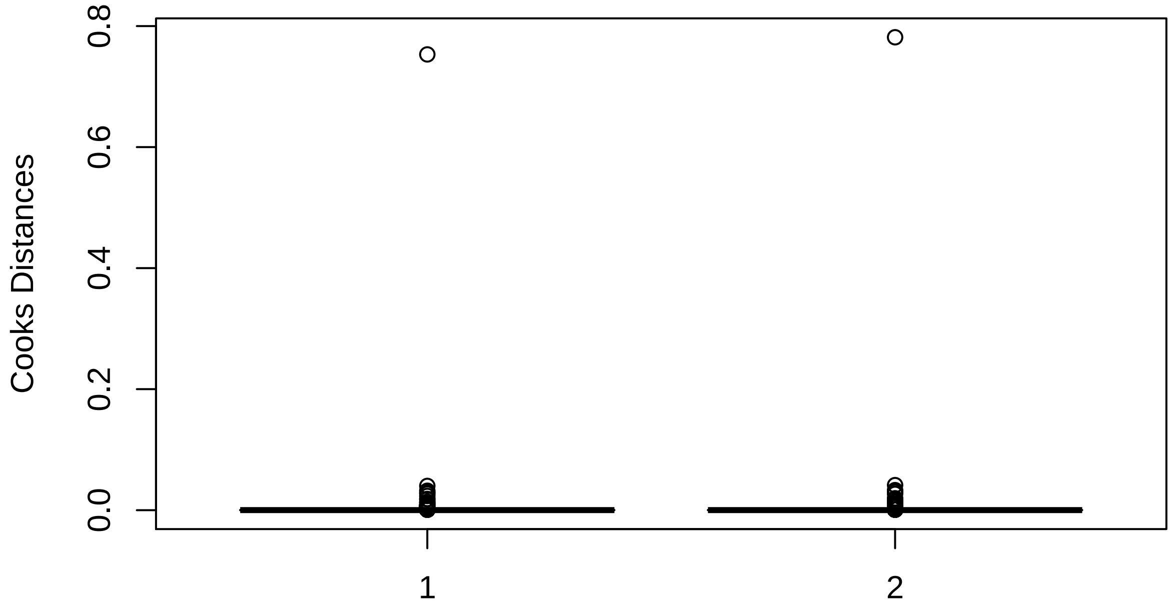
```
hat1 <- hatvalues(Mstep) # Leverages of stepwise model
hat2 <- hatvalues(Mmanual)

# Should be ideally close to 1 (as in course notes)
boxplot(x = list(abs(hat1), abs(hat2)),
        ylab = "Abs. Leverages", col = c("yellow", "orange"))
```



```
plot(abs(hat1),abs(hat2)) # Nearly linear
```



```r
cook1 <- cooks.distance(Mstep)
cook2 <- cooks.distance(Mmanual)

 # Values should ideally be close to zero
boxplot(x = list(abs(cook1), abs(cook2)),
        ylab = "Cooks Distances", col = c("yellow", "orange"))
```



```r
# Should this even be done since cooks is already done?
# dffits1 <- dffits(Mstep)
# dffits2 <- dffits(Mmanual)
#
# boxplot(x = list(abs(dffits1), abs(dffits2)),
#         ylab = "Abs. Leverages", col = c("yellow", "orange"))
#
# cooks.distance(Mstep)
```

5 Model Selection

5.1 Cross Validation

This is the written function

```r
library(statmod) # Load this package for using gauss.quad.prob() function
library(gtools) # Load this package for using the logit function

#' Following function calculates the mean of logit-normal distribution
#'
#' @param mu Mean of underlying normal distribution
#' @param sigma Standard deviation of underlying normal distribution
#'
#' @return A single number representing mean of the logit-normal distribution
#'
#' @details The calculation of w's and g(x)'s is vectorized
```

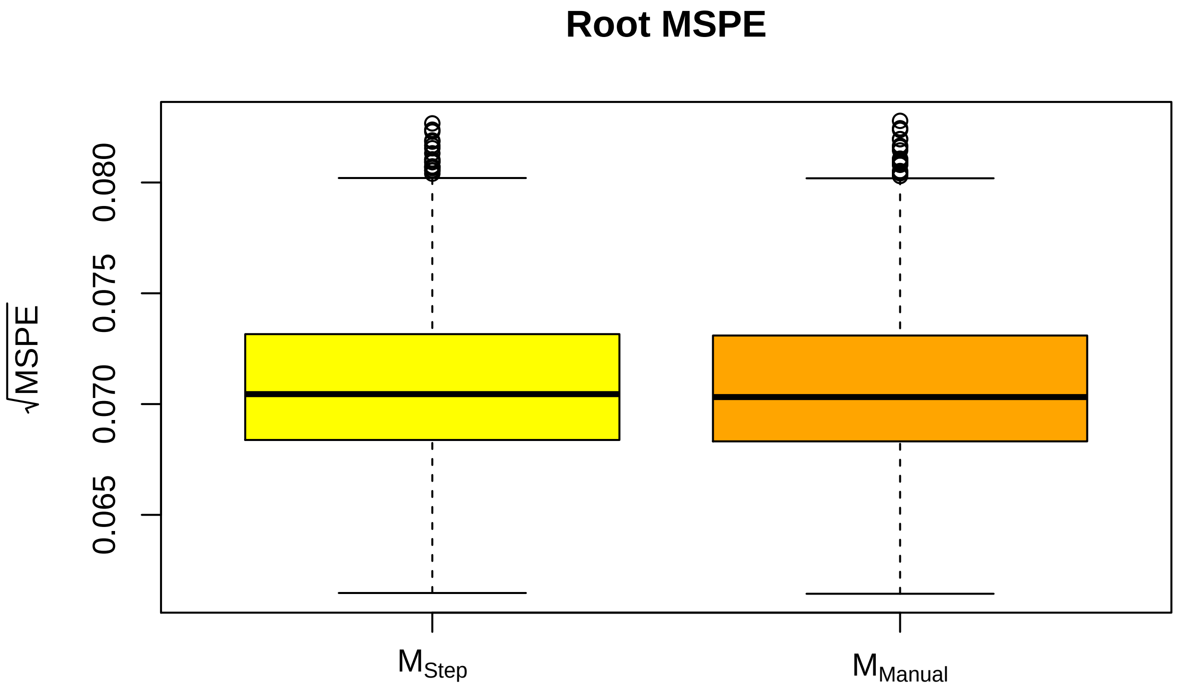
```r
logitnorm_mean <- function(mu,sigma){
  v = 1/(1+ exp(-mu))           # Value passed into both shape parameters
  alpha_1 = 1/(sigma^2 * (1-v)) # Shape parameter 1
  alpha_2 = 1/(v * sigma^2) # Shape parameter 2
  # Calculate nodes and weights for Gaussian quadrature
  gqp <- gauss.quad.prob(n = 10,dist = "beta",alpha = alpha_1,beta = alpha_2)
  x <- gqp$nodes   # Extract the nodes into a vector
  w <- gqp$weights # Similarly the weights
  # Apply the function g (defined in the project description) onto the above x's
  g <- dnorm(logit(x),mean = mu,sd = sigma,log = TRUE) - log(1-x) -
      dbeta(x,shape1 = alpha_1,shape2 = alpha_2,log = TRUE)
  # Calculate and return the mean
  answer <- sum(w*exp(g))
  return(answer)
}

# For testing
mu <- c(0.7,3.2,-1.1)
sigma <- c(0.8,0.1,2.3)
sapply(1:3, function(i) logitnorm_mean(mu[i],sigma[i]))
```

```
## [1] 0.6491002 0.9606606 0.3530580
```

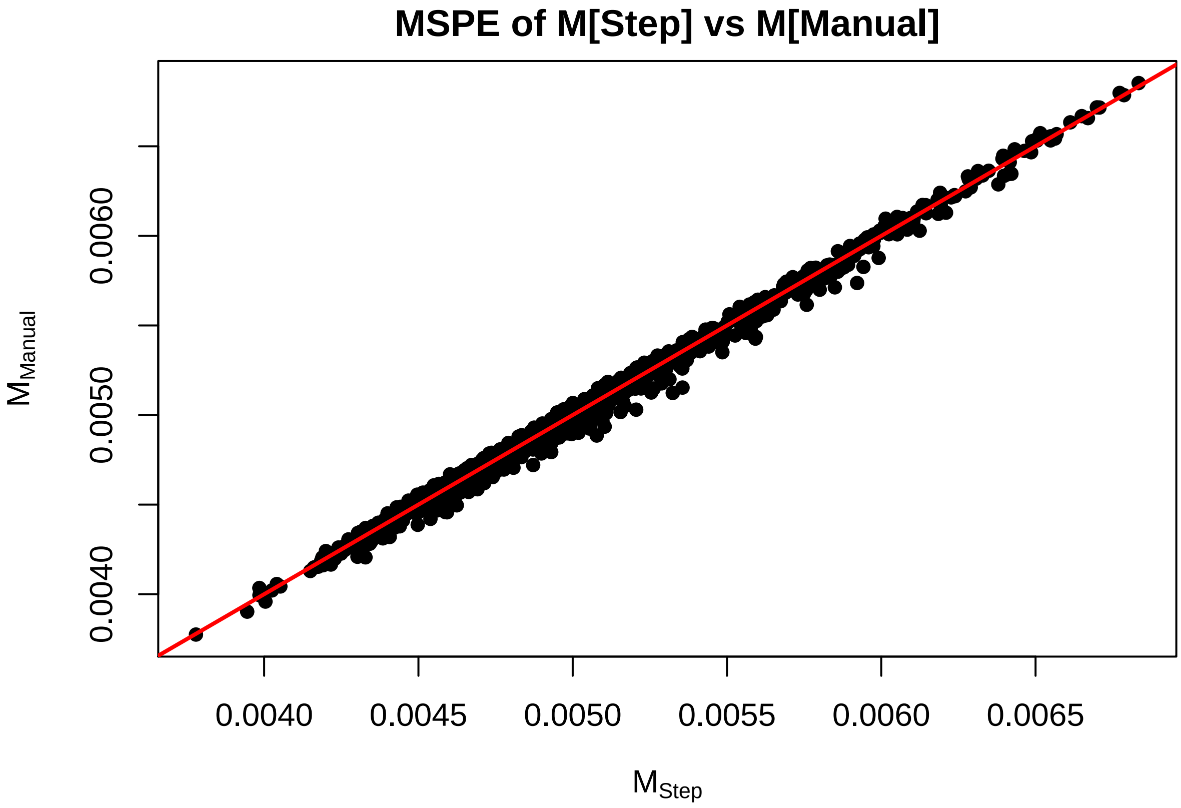
```r
load_calcs = FALSE

# compare Mstep to Mmanual
M1 <- Mstep
M2 <- Mmanual
Mnames <- expression(M[Step], M[Manual])

# number of cross-validation replications
nreps <- 1e3

ntot <- nrow(fhsd)   # total number of observations
ntrain <- 1800       # for fitting MLE's, roughly 80% of total
ntest <- ntot-ntrain # for out-of-sample prediction

# storage space
mspe1 <- rep(NA, nreps) # mspe for M1
mspe2 <- rep(NA, nreps) # mspe for M2

if (!load_calcs){
system.time({
  for(ii in 1:nreps) {
    train.ind <- sample(ntot, ntrain) # training observations

    # Update the models for this training set
    M1.cv <- update(M1, subset = train.ind)
    M2.cv <- update(M2, subset = train.ind)

    # MLE of sigma
    M1.sigma <- sqrt(sum(resid(M1.cv)^2)/ntrain)
    M2.sigma <- sqrt(sum(resid(M2.cv)^2)/ntrain)
    # predictions of logit(chdrisk) for test set
    predictions.M1 <- predict(M1.cv,newdata = fhsd[-train.ind,])
    predictions.M2 <- predict(M2.cv,newdata = fhsd[-train.ind,])

   # predictions of chdrisk for the test set
   values.M1 <- sapply(predictions.M1, function(i) logitnorm_mean(i,M1.sigma))
   values.M2 <- sapply(predictions.M2, function(i) logitnorm_mean(i,M2.sigma))

    M1.res <- fhsd$chdrisk[-train.ind] -   # test observations
              values.M1                    # prediction using training data
    M2.res <- fhsd$chdrisk[-train.ind] - values.M2

    # mspe for each model
    mspe1[ii] <- mean(M1.res^2)
    mspe2[ii] <- mean(M2.res^2)

  }
})
}
```

```
##    user  system elapsed
##  79.925   1.217  83.539
```

```
# the caching/loading block
if(!load_calcs) {
  saveRDS(list(mspe1 = mspe1,mspe2 = mspe2), file = "cross_validation_automated.rds")
} else {
  # just load the calculations
  tmp <- readRDS("cross_validation_automated.rds")
  mspe1 <- tmp$mspe1
  mspe2 <- tmp$mspe2
  rm(tmp) # optionally remove tmp from workspace
}

# compare Root MSPEs of both the models through boxplots
boxplot(x = list(sqrt(mspe1), sqrt(mspe2)), names = Mnames,
        main = "Root MSPE",
        ylab = expression(sqrt(MSPE)),
        col = c("yellow", "orange"))
```



```r
# compare predictions by training set
par(mar = c(5, 5, 2, 1))
plot(mspe1, mspe2, pch = 16,
     xlab = Mnames[1], ylab = Mnames[2],
     main = paste0("MSPE of ", Mnames[1]," vs ", Mnames[2])) # Fix this
abline(a = 0, b = 1, col= "red", lwd = 2)
```



6 Discussion