# STAT 331 Final Project

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## 1 Summary

## 2 Descriptive Statistics

First, take a look at summary statistics of the Framingham Heart Study dataset.

Table 1: Summary Statistics

| chdrisk | sex | totchol | age | sysbp | diabp | cursmoke | cigpday | bmi |
|---|---|---|---|---|---|---|---|---|
| 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 |
| 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 |
| Median :0.2240 | | Median :235.5 | Median :60.00 | Median :136.0 | Median : 80.00 | | Median : 0.00 | Median :25.40 |
| Mean :0.2655 | | Mean :237.8 | Mean :60.23 | Mean :139.2 | Mean : 81.07 | | Mean : 6.84 | Mean :25.78 |
| 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 |
| Max. :0.9770 | | Max. :625.0 | Max. :81.00 | Max. :246.0 | Max. :130.00 | | Max. :80.00 | Max. :46.52 |

| diabetes | bpmeds | heartrte | glucose | prevmi | prevstrk | prevhyp | hdlc | ldlc |
|---|---|---|---|---|---|---|---|---|
| No :2142 | No :1973 | Min. : 44.00 | Min. : 46.00 | No :2189 | No :2260 | No : 957 | Min. : 10.00 | Min. : 20.0 |
| 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 : 76.00 | Median : 83.00 | | | | Median : 47.00 | Median :180.0 |
| | | Mean : 77.61 | Mean : 89.07 | | | | Mean : 48.89 | Mean :183.1 |
| | | 3rd Qu.: 85.00 | 3rd Qu.: 95.00 | | | | 3rd Qu.: 57.00 | 3rd Qu.:210.0 |
| | | 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.

A further inspection of the expected coronary heart disease (CHD) risk against certain categorical variates, gives more insights.

For instance, if we take a look at expected CHD risk against whether or not an individual has hypertension, we get the following result:

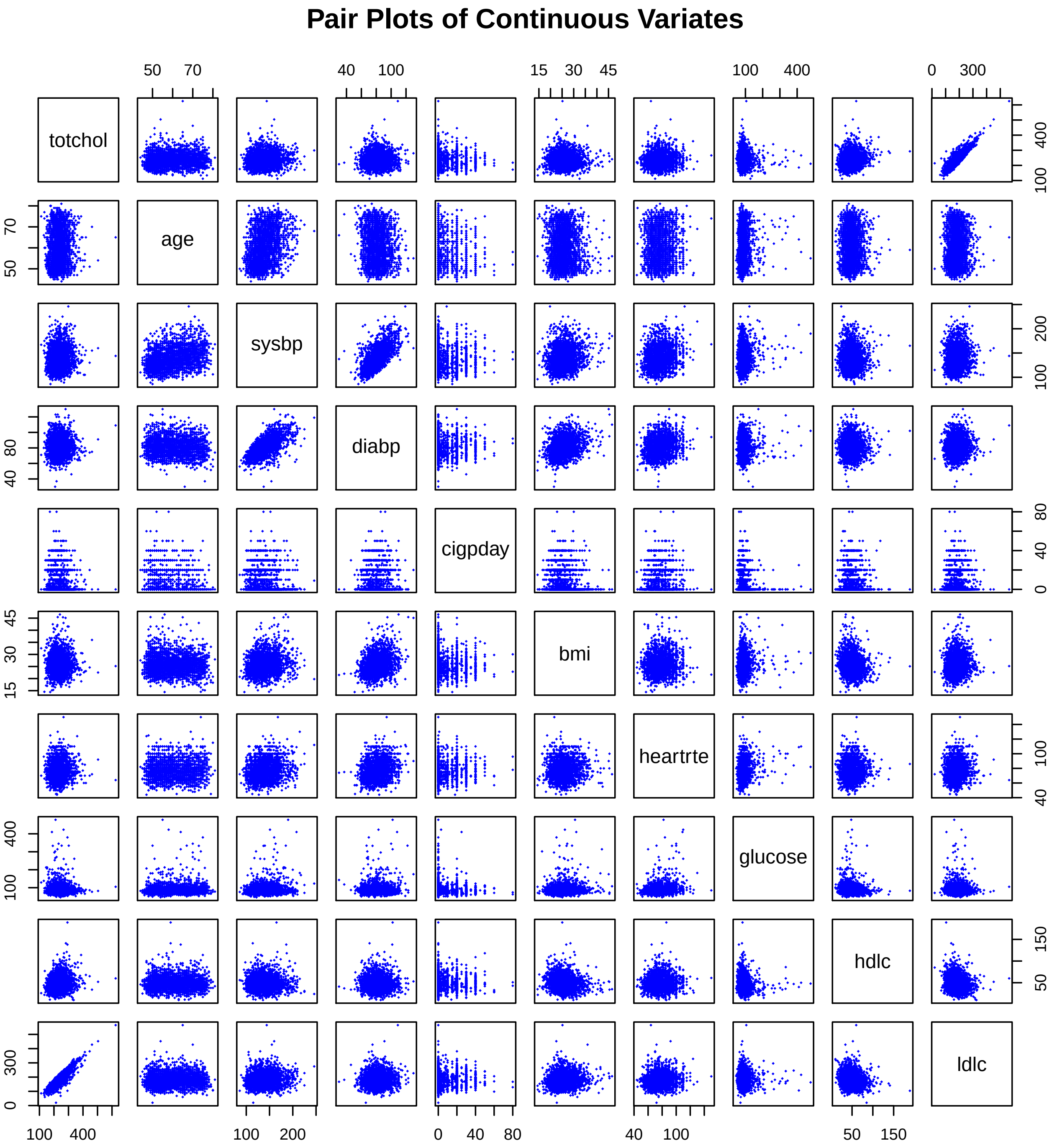
```
## fhsd$prevhyp: No
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.005   0.077   0.140   0.176   0.216   0.944
## ------------------------------------------------------------
## fhsd$prevhyp: Yes
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.0320  0.1980  0.2890  0.3291  0.4010  0.9770
```

Indeed, we have that mean CHD risk given that a person has hypertension is significantly higher than the mean for people who did not have hypertension.

```
## fhsd$prevstrk: No
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##  0.0050  0.1300  0.2200  0.2611  0.3392  0.9770 
## ------------------------------------------------------------ 
## fhsd$prevstrk: Yes
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##  0.2020  0.3412  0.4410  0.4820  0.5060  0.9660
```

Again, we see the same results with people who had a stroke before the study, with even a higher difference between the two groups.

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`.


Pair Plots of Continuous Variates

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

```r
suppressWarnings(library(gtools))
load_calcs = TRUE
# 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"
```

```r
# 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 |

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

| | No | Yes |
|---|---|---|
| No | 957 | 1016 |
| Yes | 0 | 333 |

```r
# 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
```

```r
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)
  })
}
# 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)
```

```
# 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

The following table lists terms in the stepwise model that result in insignifance when F-test is perfomed by removing them solely from the stepwise model along with corresponding p-values in a sorted order.

Table 2: Variates/Interactions with significant p-values from F-test

| cigpday:heartrte | bpmeds:prevstrk | bpmeds:glucose | diabp:cigpday | cigpday | sex:ldlc | age:prevmi | cigpday:prevmi | hdlc:ldlc | bmi:bpmeds | prevmi:prevstrk | heartrte:prevmi | glucose:prevmi | I(sysbp^2) | cursmoke:hdlc | age:heartrte | age:hdlc |
|---:|---:|---:|---:|---:|---:|---:|---:|---:|---:|---:|---:|---:|---:|---:|---:|---:|
| 0.1506282 | 0.1492283 | 0.1189197 | 0.1155989 | 0.1151079 | 0.1141483 | 0.1097987 | 0.1051865 | 0.0923568 | 0.0855445 | 0.0699776 | 0.0645195 | 0.0588312 | 0.0585469 | 0.0566094 | 0.0556206 | 0.0510796 |

Looking at the above table, removing highly insignificant continuous variate interactions `cigpday:heartrte` and `diabp:cigpday`, we have the following p-value from F-test.

```r
# Remove as many insignificant continuous variate interactions as possible
anova(Mstep, update(Mstep,. ~ . - cigpday:heartrte - diabp:cigpday))$`Pr(>F)`[2]
```

```
## [1] 0.0729871
```

Assuming the insignificance threshold of 0.05, removing categorical/continuous variate interaction `bpmeds:prevstrk` esults in the following p-value.

```r
# Now remove insignificant interactions from categroical variates
anova(Mstep, update(Mstep,. ~ . - cigpday:heartrte - diabp:cigpday- bpmeds:prevstrk))$`Pr(>F)`[2]
```

```
## [1] 0.05655719
```

Since above p-value is just slightly greater than 0.05, removing the above interactions from stepwise model is insiginificant. Therefore a reduced model can be obtained from stepwise in the followng way.

```r
# Thus we have the following manually constructed model
Mmanual <- update(Mstep,. ~ . - cigpday:heartrte - diabp:cigpday - bpmeds:prevstrk)
```

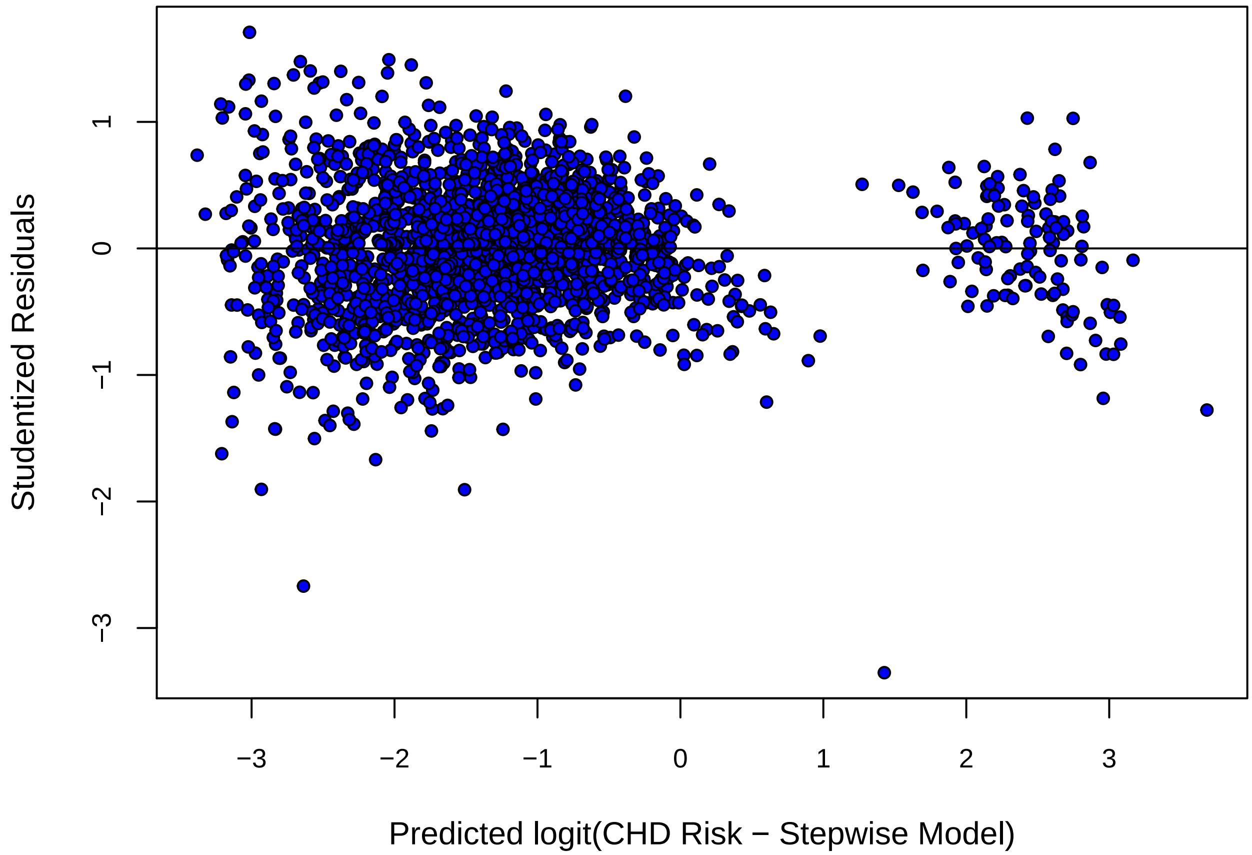
# 4 Model Diagnostics

## 4.1 Residual Plots

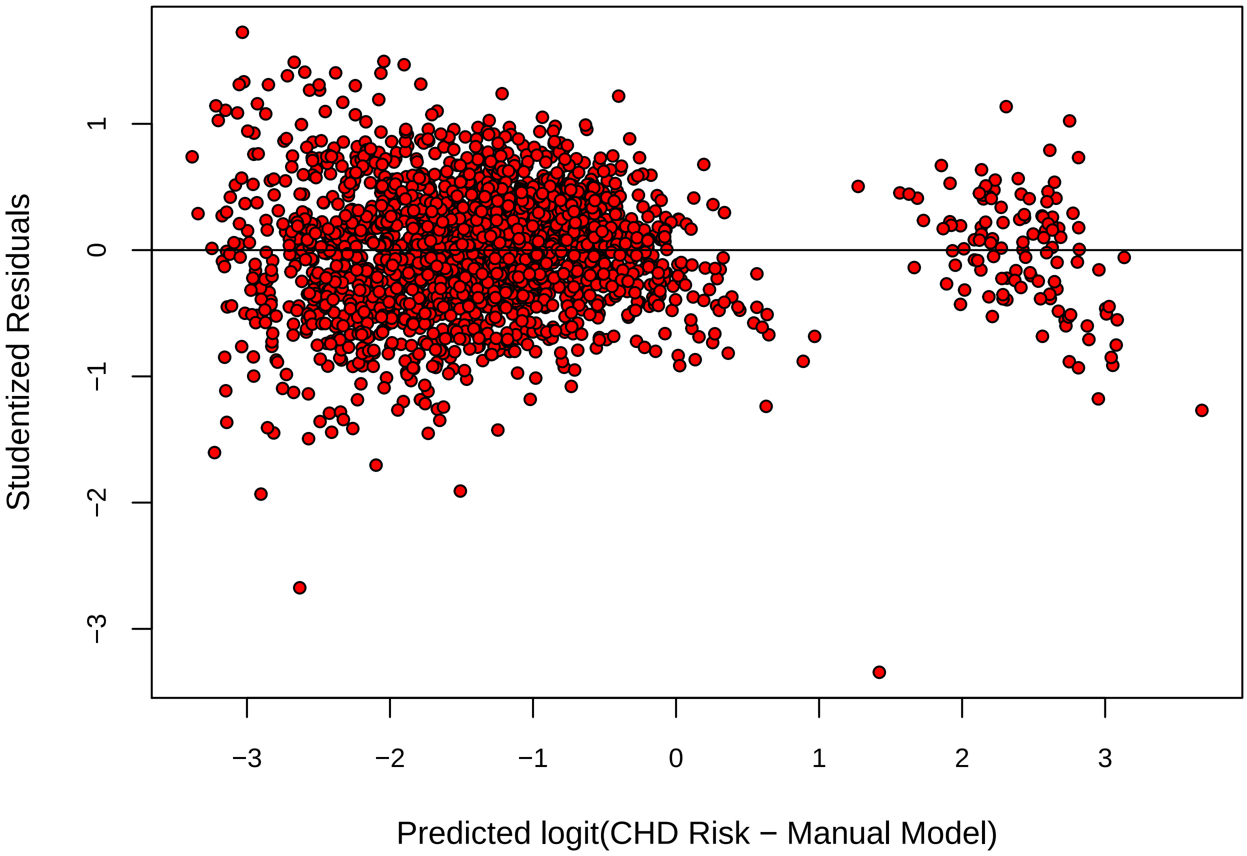
In this section we analyse the assumption that our residuals follow a normal distribution and check the homoscedasity assumption.

First, we have that the most normal looking residuals assuming that the model is true, would be the studentized residuals, so to check the homoscedasity we plot those values against the predicted values, as shown below:

```r
# First we analyze Mstep
# get the hat values
h <- hatvalues(Mstep)
res.step <- resid(Mstep)/sqrt(1-h) # studentized residuals, but on the data scale
cex <- .8 # controls the size of the points and labels
par(mar = c(4,4,.5,.1))
plot(predict(Mstep), res.step, pch = 21, bg = "blue", cex = cex, cex.axis = cex,xlab = "Predicted logit
abline(h = 0, lty = 1, col = "black") # add horizontal line at 0
```



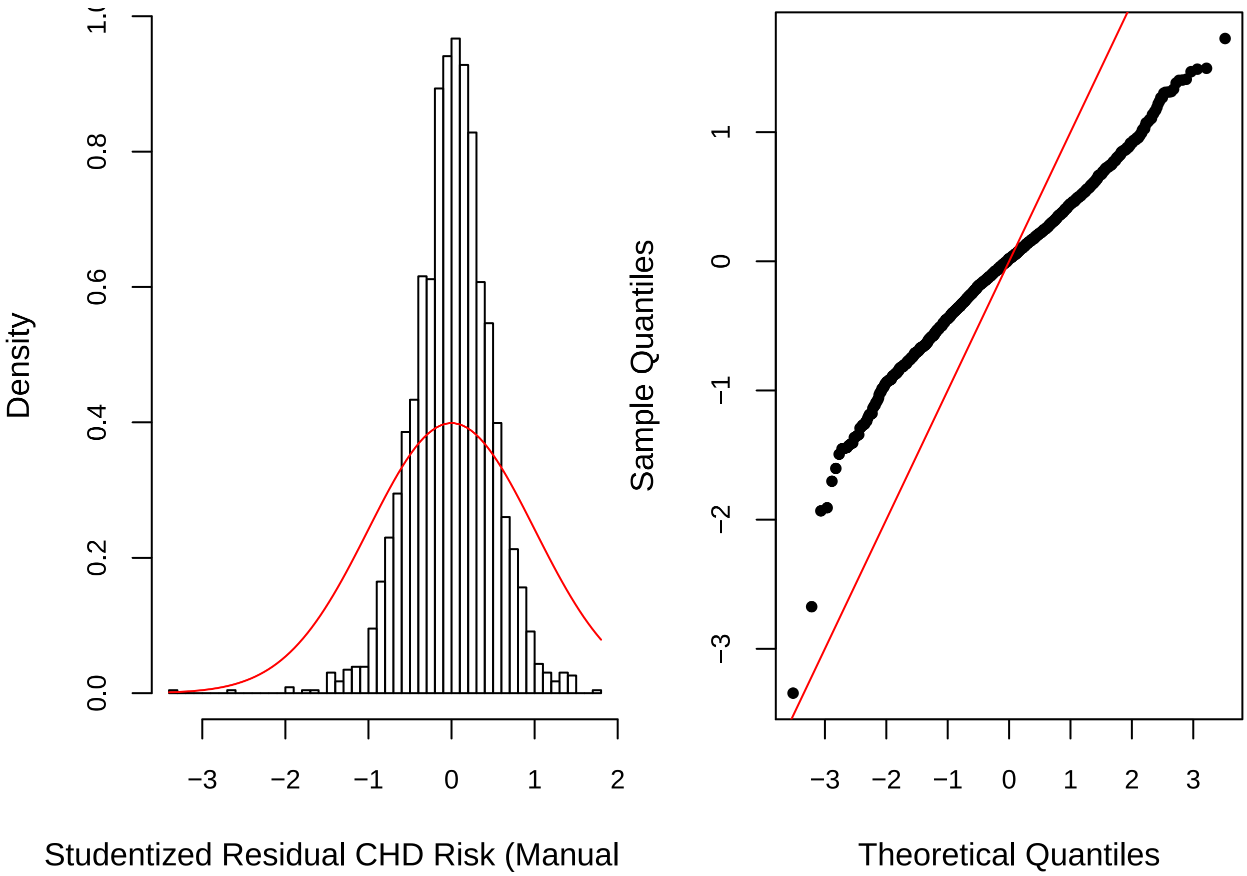
```
# Then we analyze Mdl_manual
# get the hat values
h <- hatvalues(Mmanual)
res.manual <- resid(Mmanual)/sqrt(1-h) # studentized residuals, but on the data scale
cex <- .8 # controls the size of the points and labels
par(mar = c(4,4,.5,.1))
plot(predict(Mmanual), res.manual, pch = 21, bg = "red", cex = cex, cex.axis = cex,xlab = "Predicted log
abline(h = 0, lty = 1, col = "black") # add horizontal line at 0
```



Then to check our assumption of normality of residuals we plot the residuals on a QQPlot and a histogram:

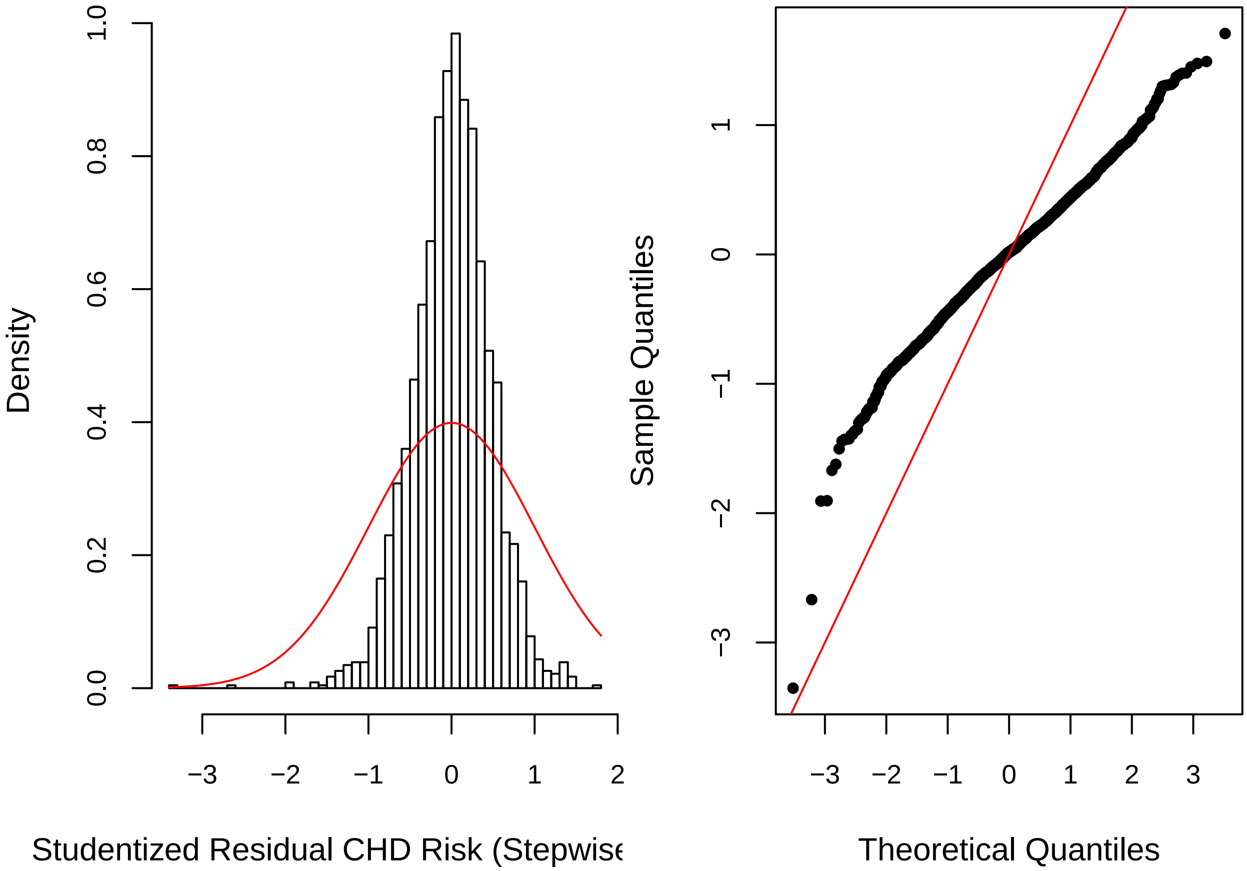
```
# plot standardized residuals
sigma.hat <- sigma(Mmanual)
cex <- .8
par(mfrow = c(1,2), mar = c(4,4,.1,.1))
# histogram
hist(res.manual, breaks = 50, freq = FALSE, cex.axis = cex,xlab = "Studentized Residual CHD Risk (Manua

curve(dnorm(x), col = "red", add = TRUE)
# theoretical normal curve
#qq-plot
qqnorm(res.manual, main = "", pch = 16, cex = cex, cex.axis = cex)
abline(a = 0, b = 1, col = "red") # add 45 degree line
```



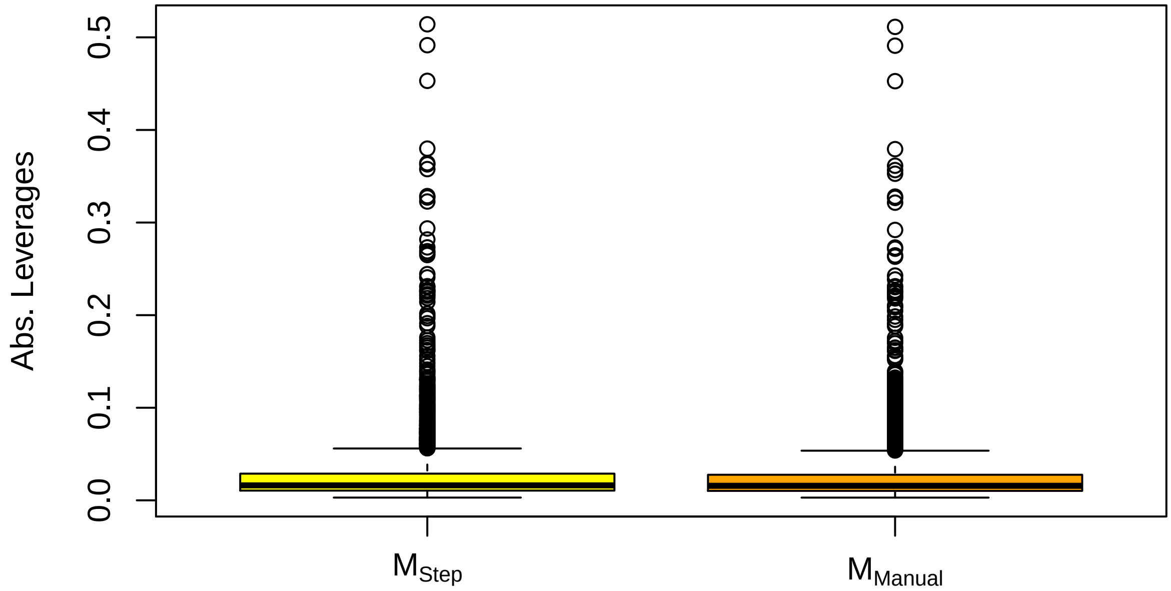
```
# plot standardized residuals
sigma.hat <- sigma(Mstep)
cex <- .8
par(mfrow = c(1,2), mar = c(4,4,.1,.1))
# histogram
hist(res.step, breaks = 50, freq = FALSE, cex.axis = cex,xlab = "Studentized Residual CHD Risk (Stepwis

curve(dnorm(x), col = "red", add = TRUE)
# theoretical normal curve
#qq-plot
qqnorm(res.step, main = "", pch = 16, cex = cex, cex.axis = cex)
abline(a = 0, b = 1, col = "red") # add 45 degree line
```

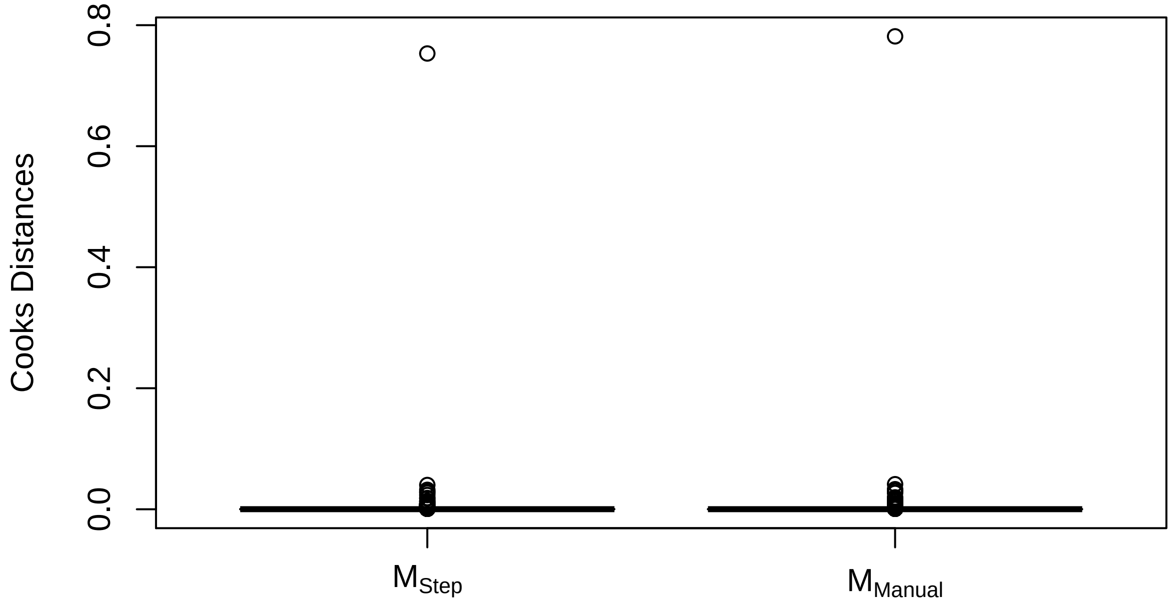


## 4.2 Leverage and Influence Measures

We have the following boxplot of absolute values of leverages of both the step-wise and manual models.



Similarly, we have the following boxplot of cook's distances of both the models.



# 5 Model Selection

## 5.1 Cross Validation

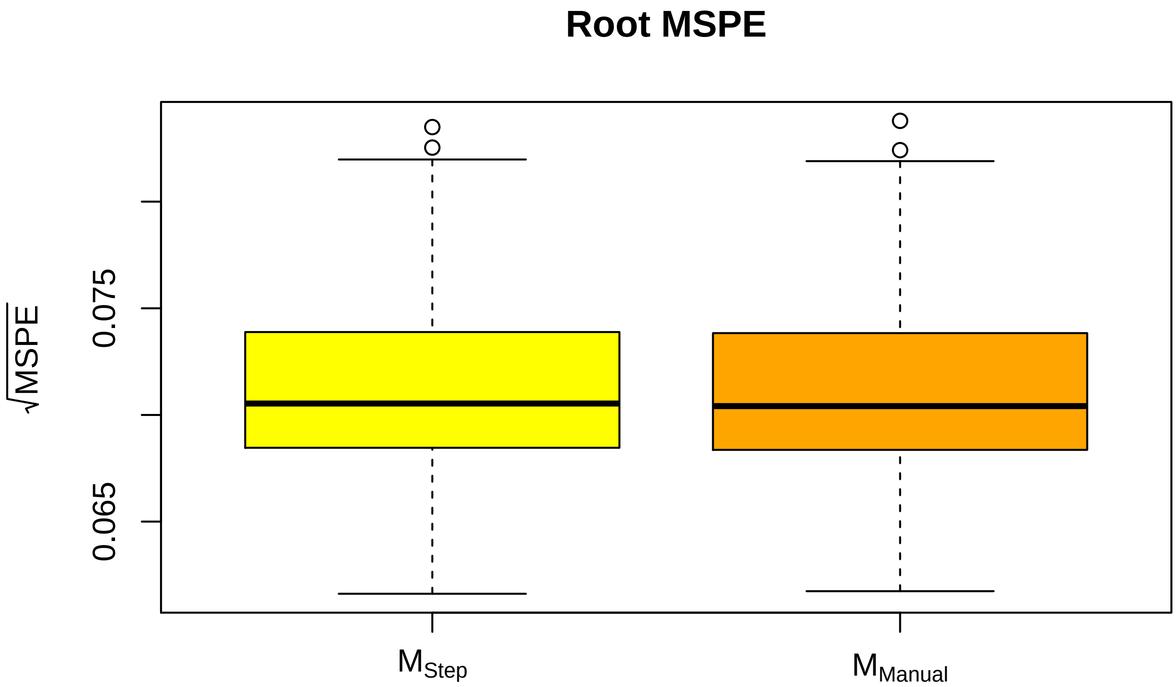
Before performing cross-valiation analysis, function `logitnorm_mean` is created to approximate the conditional mean `E[chdrisk|x]` based on the regression model logit(`chdrisk`)|x $\sim N(x'\beta, \sigma^2)$ (look into the Appendix for code). The following output is produced when tested.

```
# Test the function
mu <- c(0.7,3.2,-1.1)
sigma <- c(0.8,0.1,2.3)
# Returns results expected in the project desciption
sapply(1:3, function(i) logitnorm_mean(mu[i],sigma[i]))
```

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

The above function is then used to perform cross-validation analysis and the following boxplot that shows MSPE of the both the models is produced.

```
##    user  system elapsed
##  84.832   1.616  94.841
```



Model chosen will be the manual one [ADD MORE] These are the parameter estimates, std.errors and p-values of the manually constructed model.

Table 3: Summary of chosen manually constructed model

| | (Intercept) | sexMale | totchol | age | sysbp | diabp | cursmokeYes | cigpday | bmi |
|---|---|---|---|---|---|---|---|---|---|
| Estimate | -6.841121 | 0.7509308 | 0.0086801 | 0.0562327 | 0.0125123 | -0.0426462 | 0.4903809 | 0.0463907 | -0.0843445 |
| Std. Error | 1.017652 | 0.1622031 | 0.0029290 | 0.0101841 | 0.0061648 | 0.0106013 | 0.2180640 | 0.0087763 | 0.0244266 |
| Pr(>\|t\|) | 0.000000 | 0.0000039 | 0.0030739 | 0.0000000 | 0.0425109 | 0.0000594 | 0.0246223 | 0.0000001 | 0.0005647 |

| | diabetesYes | bpmedsYes | heartrte | glucose | prevmiYes | prevstrkYes | prevhypYes | hdlc | ldlc |
|---|---|---|---|---|---|---|---|---|---|
| Estimate | 1.0311734 | 0.8595578 | 0.0440175 | 0.0023589 | 5.6983941 | 0.1404944 | 3.9567705 | -0.0201085 | -0.0063626 |
| Std. Error | 0.2918380 | 0.3038036 | 0.0078437 | 0.0026598 | 0.5685983 | 0.0792694 | 0.3583848 | 0.0084351 | 0.0035374 |
| Pr(>\|t\|) | 0.0004186 | 0.0047062 | 0.0000000 | 0.3752314 | 0.0000000 | 0.0764694 | 0.0000000 | 0.0172127 | 0.0722106 |

| | I(hdlc^2) | I(bmi^2) | I(diabp^2) | I(sysbp^2) | sysbp:prevmiYes | totchol:prevhypYes | diabetesYes:prevmiYes | prevhypYes:ldlc | sysbp:prevhypYes |
|---|---|---|---|---|---|---|---|---|---|
| Estimate | 0.0001820 | 0.0028956 | 5.97e-04 | 0.0000426 | -0.0109765 | -0.0070567 | -0.6245291 | 0.0038926 | -0.0087679 |
| Std. Error | 0.0000508 | 0.0004308 | 6.57e-05 | 0.0000219 | 0.0025360 | 0.0011582 | 0.1511829 | 0.0011277 | 0.0023122 |
| Pr(>\|t\|) | 0.0003497 | 0.0000000 | 0.00e+00 | 0.0520383 | 0.0000157 | 0.0000000 | 0.0000375 | 0.0005671 | 0.0001534 |

| | totchol:heartrte | sysbp:diabetesYes | diabp:bmi | diabp:hdlc | prevmiYes:hdlc | prevmiYes:prevhypYes | sexMale:glucose | age:ldlc | age:heartrte |
|---|---|---|---|---|---|---|---|---|---|
| Estimate | -7.64e-05 | -0.0061063 | -0.0010390 | -0.0002321 | 0.0149580 | -0.2985780 | -0.0018741 | 0.0000606 | -0.0002377 |
| Std. Error | 1.86e-05 | 0.0017038 | 0.0002507 | 0.0000625 | 0.0038971 | 0.1305121 | 0.0007338 | 0.0000285 | 0.0000989 |
| Pr(>\|t\|) | 4.09e-05 | 0.0003457 | 0.0000353 | 0.0002120 | 0.0001274 | 0.0222452 | 0.0107144 | 0.0337545 | 0.0163262 |

| | cigpday:hdlc | bmi:ldlc | totchol:hdlc | totchol:prevmiYes | sysbp:heartrte | sysbp:bpmedsYes | cursmokeYes:hdlc | prevmiYes:prevstrkYes | diabetesYes:hdlc |
|---|---|---|---|---|---|---|---|---|---|
| Estimate | -0.0003505 | 0.0001499 | 0.0001294 | -0.0026466 | -0.0001125 | -0.0035185 | 0.0043414 | -0.3881888 | 0.0058461 |
| Std. Error | 0.0000943 | 0.0000589 | 0.0000504 | 0.0009274 | 0.0000375 | 0.0015038 | 0.0023248 | 0.1951360 | 0.0024167 |
| Pr(>\|t\|) | 0.0002059 | 0.0110647 | 0.0102686 | 0.0043574 | 0.0027333 | 0.0193871 | 0.0619759 | 0.0467867 | 0.0156403 |

# 6 Discussion

|  | sexMale:sysbp | cigpday:glucose | heartrte:glucose | diabp:glucose | cursmokeYes:ldlc | age:cigpday | age:hdlc | hdlc:ldlc | age:prevhypYes |
|---|---:|---:|---:|---:|---:|---:|---:|---:|---:|
| Estimate | -0.0018228 | -0.0000755 | 0.0000695 | -0.0000682 | -0.0010001 | -0.0003358 | -0.0001725 | -0.0000803 | -0.0103638 |
| Std. Error | 0.0009765 | 0.0000385 | 0.0000260 | 0.0000281 | 0.0004913 | 0.0001248 | 0.0000888 | 0.0000478 | 0.0029473 |
| Pr(>\|t\|) | 0.0620856 | 0.0500605 | 0.0075675 | 0.0154340 | 0.0418854 | 0.0071905 | 0.0522339 | 0.0927933 | 0.0004462 |

|  | diabp:prevhypYes | diabp:cursmokeYes | bmi:bpmedsYes | bpmedsYes:glucose | age:prevmiYes | sexMale:ldlc | cigpday:prevmiYes | glucose:prevmiYes | heartrte:prevmiYes |
|---|---:|---:|---:|---:|---:|---:|---:|---:|---:|
| Estimate | -0.0110683 | -0.0057752 | -0.0128143 | 0.0014572 | -0.0105250 | 0.0007191 | -0.0087788 | -0.0027211 | 0.0058756 |
| Std. Error | 0.0034311 | 0.0019148 | 0.0072263 | 0.0009960 | 0.0063892 | 0.0004619 | 0.0049761 | 0.0015063 | 0.0033641 |
| Pr(>\|t\|) | 0.0012740 | 0.0025893 | 0.0763179 | 0.1436117 | 0.0996373 | 0.1196056 | 0.0778372 | 0.0709783 | 0.0808493 |