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
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.

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

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:

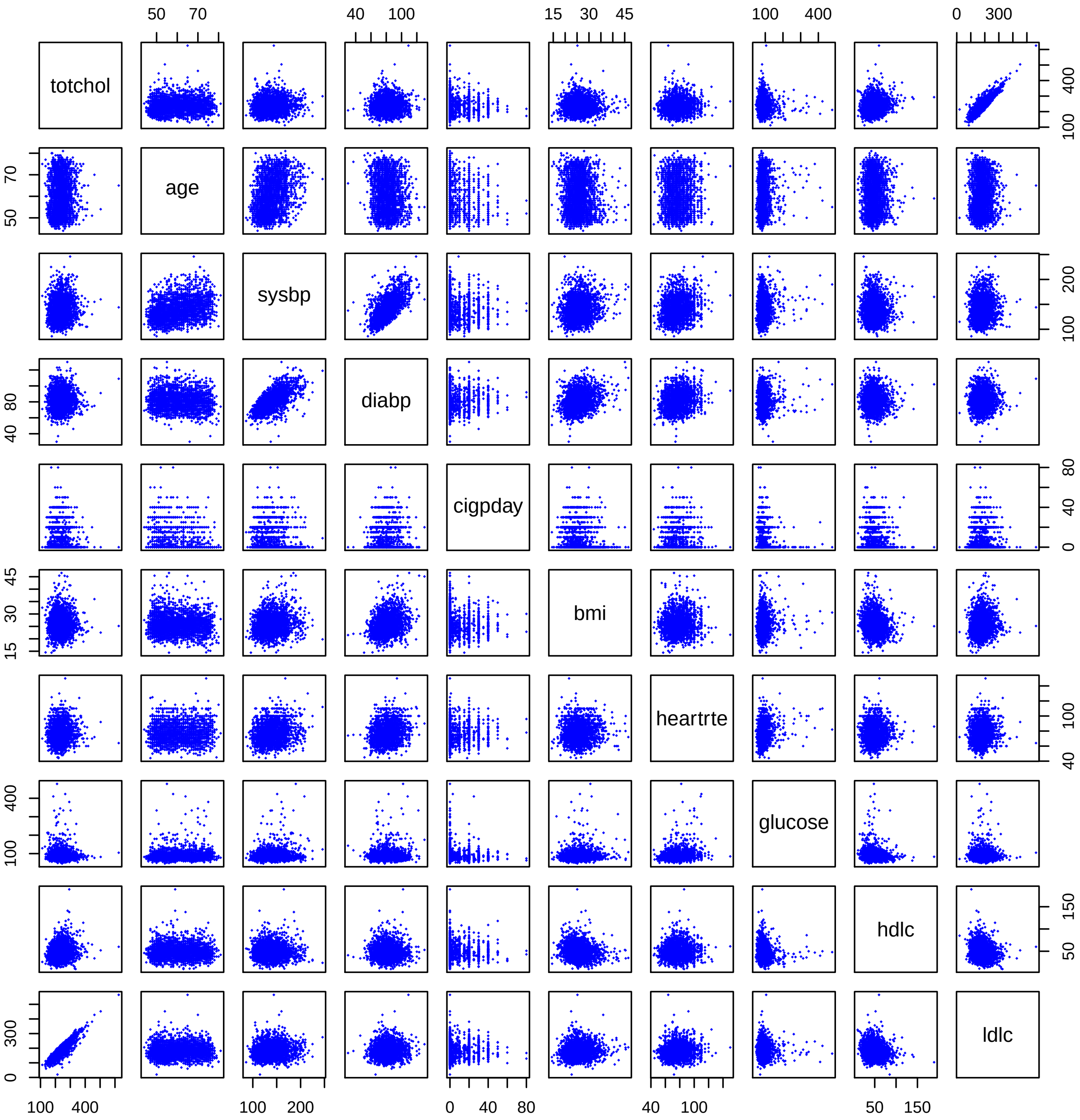
```
## fhsd$prevhyp: No
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.005   0.077   0.140   0.176   0.216   0.944
## --------------------------------------------------------
## fhsd$prevhyp: Yes
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.0320  0.1980  0.2890  0.3291  0.4010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

```r
# 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
```

```
## Warning: package 'stringr' was built under R version 3.5.2
```

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

```
# 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
```

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

4 Model Diagnostics

4.1 Leverage and Influence Measures

```
# hatvalues(Mstep) # Leverages of stepwise model
#
# cooks.distance(Mstep)
```

5 Model Selection

6 Discussion