# STAT 331 Final Project

Krishna Prem Pasumarthy & Islam Amin

April 11, 2020

## 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 | NA | Median :235.5 | Median :60.00 | Median :136.0 | Median : 80.00 | NA | Median : 0.00 | Median :25.40 | NA | NA | Median : 76.00 | Median : 83.00 | NA | NA | NA | Median : 47.00 | Median :180.0 |
| Mean :0.2655 | NA | Mean :237.8 | Mean :60.23 | Mean :139.2 | Mean : 81.07 | NA | Mean : 6.84 | Mean :25.78 | NA | NA | Mean : 77.61 | Mean : 89.07 | NA | NA | NA | Mean : 48.89 | Mean :183.1 |
| 3rd Qu.:0.3448 | NA | 3rd Qu.:265.0 | 3rd Qu.:67.00 | 3rd Qu.:153.0 | 3rd Qu.: 88.00 | NA | 3rd Qu.:10.00 | 3rd Qu.:27.91 | NA | NA | 3rd Qu.: 85.00 | 3rd Qu.: 95.00 | NA | NA | NA | 3rd Qu.: 57.00 | 3rd Qu.:210.0 |
| Max. :0.9770 | NA | Max. :625.0 | Max. :81.00 | Max. :246.0 | Max. :130.00 | NA | Max. :80.00 | Max. :46.52 | NA | NA | Max. :150.00 | Max. :478.00 | NA | NA | NA | Max. :189.00 | Max. :565.0 |

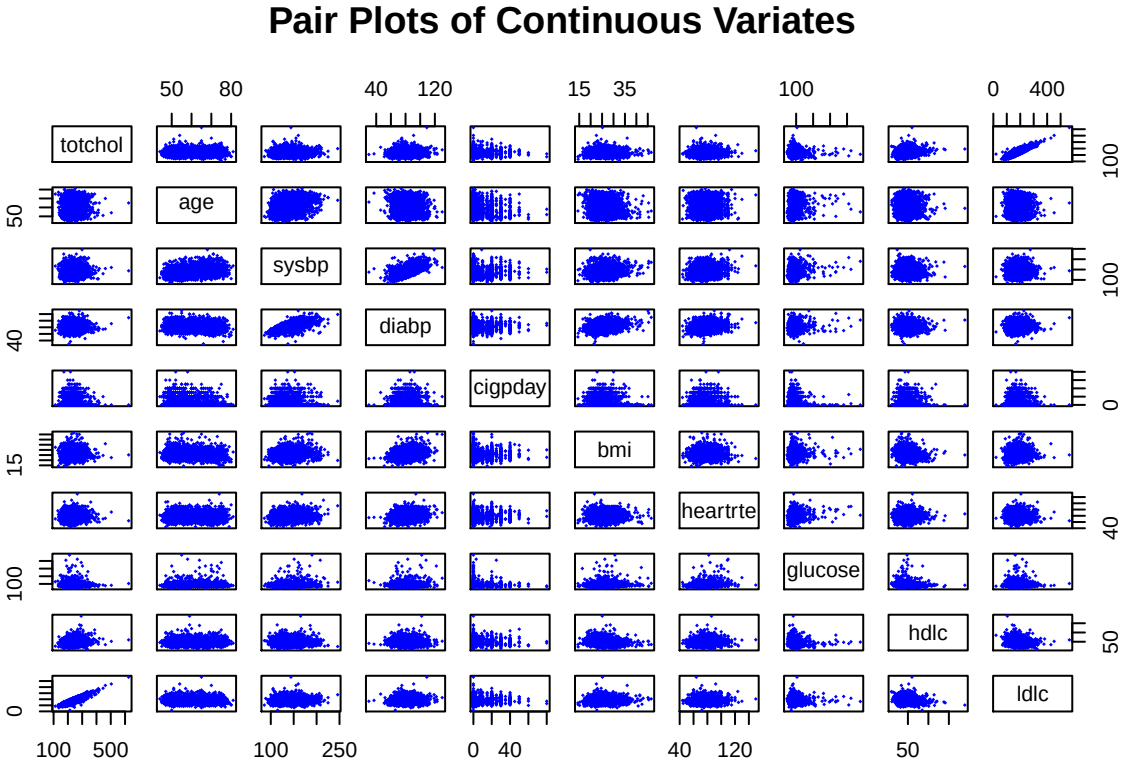
Then take a look at `chdrisk` grouped by `sex` as well as `chdrisk` grouped by `cursmoke`.

```
## 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.

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

```
##     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

```
# model with only intercept
M0 <- lm(logit(chdrisk) ~ 1, data = fhsd)
Mmax <- lm(logit(chdrisk) ~ (.)^2, data = fhsd)
# starting model for stepwise selection
Mstart <- lm(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(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
```

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

```
##    user  system elapsed
##  14.011   1.255  15.551
```

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

```
##    user  system elapsed
##  15.406   1.509  21.298
```

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

```
##    user  system elapsed
##  54.411   4.117  65.644
```

```r
# Stepwise model selection
Mstep$call
```

```
## lm(formula = 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 = 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 = 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)
```

### 3.2 Manual Model Selection

# 4 Model Diagnostics

# 5 Model Selection

# 6 Discussion