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. :0.00	Fem	Min. :112.	Min. :44.0	Min. : 86.0	Min. : 30.00	No :150	Min. : 0.00	Min. :14.4	No :214	No :197	Min. : 44.00	Min. : 46.00	No :218	No :226	No : 957	Min. : 10.00	Min. : 20.0
	1st Qu.:0.1[illegible]	Male :1320	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.[illegible]	Yes: 162	Yes: 333	1st Qu.: 70.00	1st Qu.: 75.00	Yes: 117	Yes: 46	Yes:1349	1st Qu.: 38.00	1st Qu.:152.0
	Med :0.22	NA	Med :235.	Med :60.0	Med :136.	Med : 80.00	NA	Med : 0.00	Med :25.4	NA	NA	Med : 76.00	Med : 83.00	NA	NA	NA	Med : 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.:	NA	3rd Qu.:	3rd Qu.:	3rd Qu.:	3rd Qu.: 88.00	NA	3rd Qu.:	3rd Qu.:	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

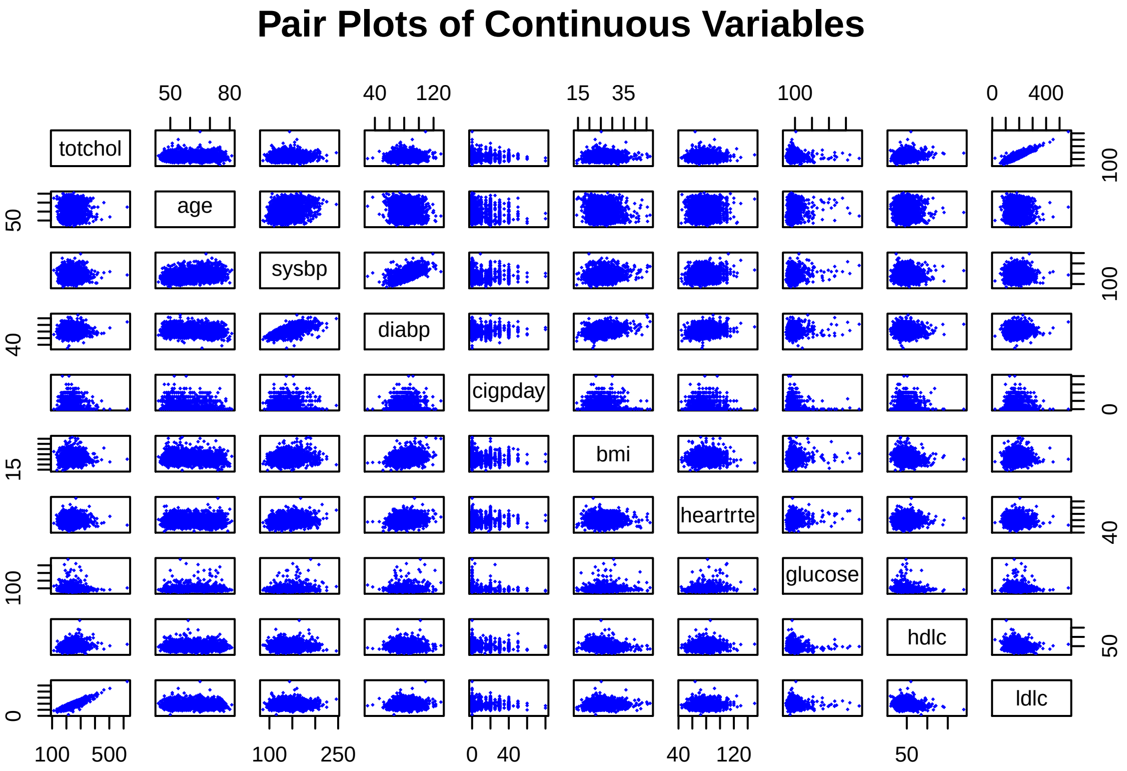
Then take a look at `chdrisk` grouped by `sex` as well as `chdrisk` grouped by `cursmoke`.

```
## 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`.



Pair Plots of Continuous Variables

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

```r
# 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"
```

```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(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
#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
```

```r
#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