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

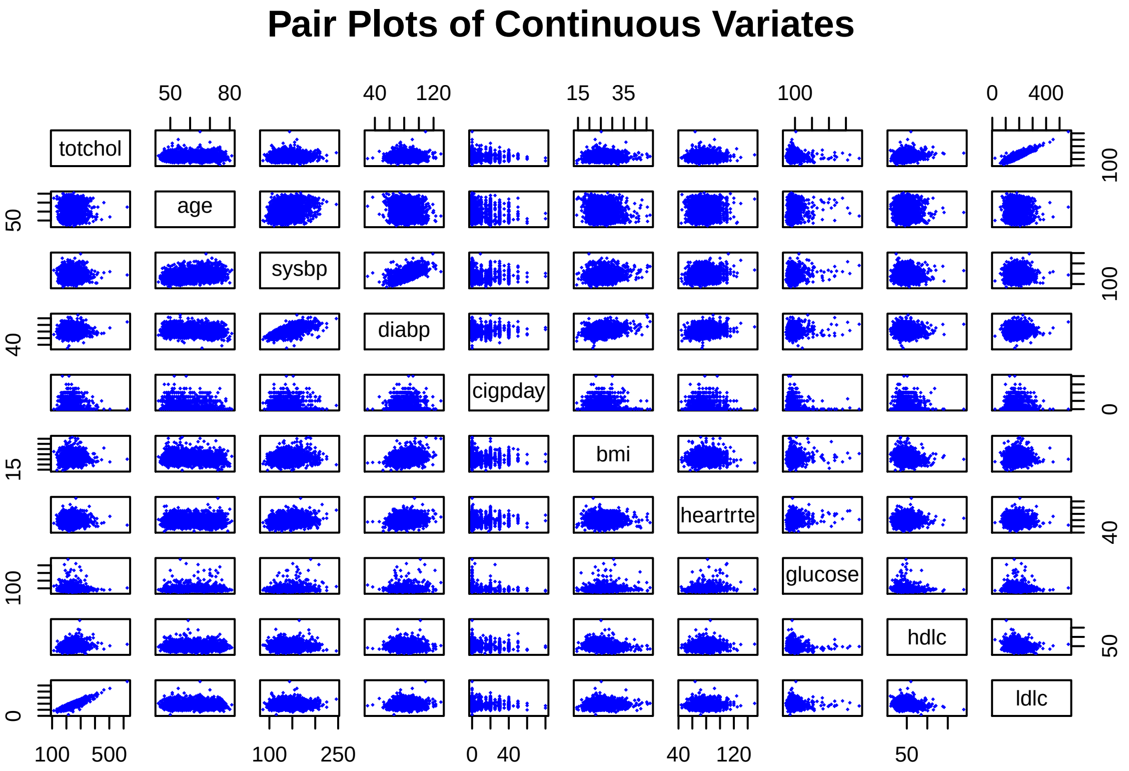
Then take a look at `chdrisk` grouped by `sex` as well as `chdrisk` grouped by `cursmoke`.

```
## 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`.



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

```
library(gtools)
```

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

```
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"
```

```
# 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 = M0,
                 scope = list(lower = M0, upper = Mmax),
                  direction = "forward", 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)) ~ 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