# 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	diabetes	bpmeds	heartrte	glucose	prevmi	prevstrk	prevhyp	hdle	ldlc
Min. :0.0050	Female:1305										Min.: 44.00					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

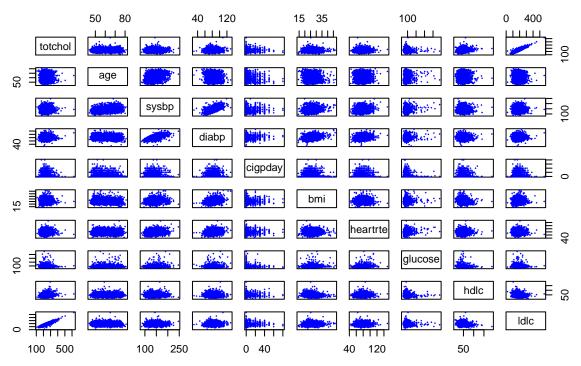
Then take a look at chdrisk grouped by sex as well as chdrisk grouped by cursmoke.

```
## fhsd$sex: Female
##
     Min. 1st Qu. Median
                         Mean 3rd Qu.
                                      Max.
                        0.215 0.285
    0.005
         0.104 0.179
                                     0.949
  _____
## fhsd$sex: Male
     Min. 1st Qu. Median
                        Mean 3rd Qu.
   0.0210 0.1860 0.2860 0.3314 0.4060 0.9770
## fhsd$cursmoke: No
    Min. 1st Qu. Median
                       Mean 3rd Qu.
  0.0050 0.1390 0.2350 0.2754 0.3580 0.9770
## fhsd$cursmoke: Yes
     Min. 1st Qu. Median
                         Mean 3rd Qu.
   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	${\tt cursmokeYes}$
##	1.225191	10.634882	1.489926	2.918660	2.406411	2.978609
##	cigpday	bmi	${\tt diabetesYes}$	bpmedsYes	heartrte	glucose
##	2.973594	1.181865	1.286401	1.214744	1.105902	1.308923
##	prevmiYes	${\tt prevstrkYes}$	prevhypYes	hdlc	ldlc	
##	1.067134	1.045746	1.823014	2.287571	10.367649	

[ADD COMMENTS]

## 3 Candidate Models

#### 3.1 Automated Model Selection

```
load_calcs = TRUE
# model with only intercept
MO <- 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)]</pre>
```

### ## [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
N	lo.	1504	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	(
7	Zes	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

### ## [1] FALSE

```
system.time({
    Mstep <- step(object = Mstart,</pre>
                  scope = list(lower = MO, 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")</pre>
  Mfwd <- tmp$Mfwd
  Mback <- tmp$Mback</pre>
  Mstep <- tmp$Mstep</pre>
  rm(tmp) # optionally remove tmp from workspace
}
# Stepwise model selection
Mstep$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