

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 | cigday | bmi | diabetes | lpmeds | hearttte | 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`.

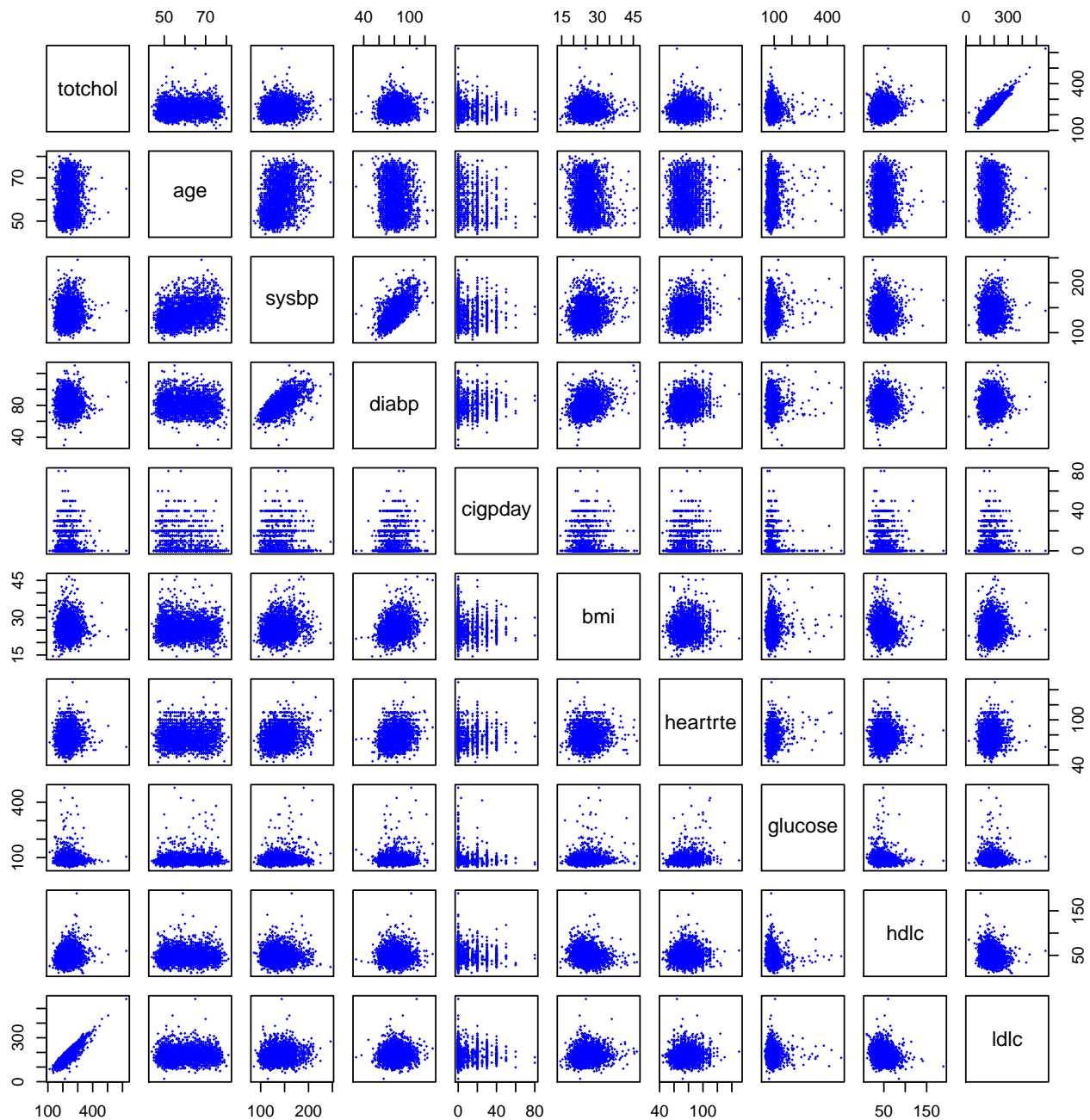
```
## fhsd$sex: Female
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.
##      0.005   0.104   0.179   0.215   0.285   0.949
## -----
## fhsd$sex: Male
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.
##      0.0210  0.1860  0.2860  0.3314  0.4060  0.9770

## 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 cholesterol. 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   hearttrte    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 = fhds)
```

```
Mmax <- lm(I(logit(chdrisk)) ~ (.)^2, data = fhds)
```

```
# starting model for stepwise selection
```

```
Mstart <- lm(I(logit(chdrisk)) ~ ., data = fhds)
```

```
# 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(fhds[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(fhds[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 = fhds)
```

```
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 = 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 + heart rte +
##     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:heart rte +
##     sysbp:diabetes + diabp:bmi + diabp:hdlc + prevmi:hdlc + prevmi:prevhyp +
##     sex:glucose + age:ldlc + age:heart rte + cigpday:hdlc + bmi:ldlc +
##     totchol:hdlc + totchol:prevmi + sysbp:heart rte + sysbp:bpmeds +
##     cursmoke:hdlc + prevmi:prevstrk + diabetes:hdlc + sex:sysbp +
##     cigpday:glucose + heart rte: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:heart rte + cigpday:prevmi +
##     glucose:prevmi + heart rte:prevmi + bpmeds:prevstrk, data = fhds)

# 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 +
##     heart rte + 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:heartрте + age:heartрте + diabetes:hdlc + sysbp:heartрте +
##      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 = fhds)

# Backward model selection
Mback$call

## lm(formula = I(logit(chdrisk)) ~ sex + totchol + age + sysbp +
##      diabp + cursmoke + cigpday + bmi + diabetes + bpmeds + heartрте +
##      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:heartрте + totchol:prevmi +
##      totchol:prevstrk + totchol:prevhyp + totchol:hdlc + totchol:ldlc +
##      age:cursmoke + age:bmi + age:heartрте + age:prevmi + age:prevhyp +
##      age:hdlc + sysbp:diabetes + sysbp:bpmeds + sysbp:heartрте +
##      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:heartрте + cigpday:glucose + cigpday:prevmi + cigpday:hdlc +
##      bmi:prevmi + bmi:prevhyp + bmi:ldlc + diabetes:prevmi + diabetes:hdlc +
##      bpmeds:glucose + bpmeds:prevstrk + bpmeds:ldlc + heartрте:glucose +
##      heartрте:prevmi + glucose:prevmi + prevmi:prevhyp + prevmi:hdlc +
##      prevhyp:ldlc, data = fhds)

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

identical(names(beta.fwd)[names(beta.fwd) %in% names(beta.step)], names(beta.fwd))

## [1] FALSE

identical(names(beta.back)[names(beta.back) %in% names(beta.step)], names(beta.back))

## [1] FALSE
```

3.2 Manual Model Selection

```
library(stringr) # For string operations

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 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 = fhds)
```

```

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) # Look at the variates that show least significance

```

```

## cigpday:heartрте 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
## heartрте:prevmi glucose:prevmi I(sysbp^2) cursmoke:hdlc age:heartрте
## 1 0.06451949 0.05883116 0.0585469 0.05660935 0.05562064
## age:hdlc cursmoke:ldlc sex:sysbp sysbp:bpmeds age:ldlc cigpday:glucose
## 1 0.0510796 0.0417893 0.03623249 0.0300776 0.02915113 0.0291137
## prevmi:prevhyp hdlc sex:glucose diabetes:hdlc diabp:glucose bmi:ldlc
## 1 0.02242217 0.01880445 0.01702301 0.01394662 0.01362058 0.009985489
## totchol:hdlc bpmeds age:cigpday heartрте:glucose cursmoke
## 1 0.009840662 0.0077735 0.006735591 0.004772297 0.004188557
## totchol:prevmi sysbp:heartрте diabp:prevhyp diabp:cursmoke prevhyp:ldlc
## 1 0.003609581 0.002926201 0.001409115 0.001393474 0.00066789
## bmi age:prevhyp sysbp:diabetes I(hdlc^2) diabp:hdlc
## 1 0.0006664543 0.0005753017 0.0004931994 0.000320732 0.0001422969
## sysbp:prevhyp cigpday:hdlc prevmi:hdlc diabetes:prevmi diabp
## 1 0.0001292531 0.0001038006 7.056001e-05 6.226049e-05 6.021714e-05
## totchol:heartрте diabp:bmi sysbp:prevmi sex heartрте
## 1 3.512093e-05 2.940165e-05 2.305381e-05 2.396724e-06 9.478088e-07
## age totchol:prevhyp I(bmi^2) I(diabp^2) prevmi
## 1 4.238229e-07 1.203731e-09 2.735937e-11 1.257752e-19 1.595006e-22
## prevhyp
## 1 1.119628e-27

```

```

# Remove first three variates from table since starting the 4th variate, reduction becomes significant
anova(Mstep, update(Mstep,. ~ . - cigpday:heartрте - bpmeds:prevstrk - bpmeds:glucose - sex:ldlc -age:p

```

```
## Analysis of Variance Table
```

```

##
## Model 1: I(logit(chdrisk)) ~ sex + totchol + age + sysbp + diabp + cursmoke +
## cigpday + bmi + diabetes + bpmeds + heartрте + 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:heartрте +
## sysbp:diabetes + diabp:bmi + diabp:hdlc + prevmi:hdlc + prevmi:prevhyp +
## sex:glucose + age:ldlc + age:heartрте + cigpday:hdlc + bmi:ldlc +
## totchol:hdlc + totchol:prevmi + sysbp:heartрте + sysbp:bpmeds +
## cursmoke:hdlc + prevmi:prevstrk + diabetes:hdlc + sex:sysbp +
## cigpday:glucose + heartрте: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:heartрте + cigpday:prevmi +
## glucose:prevmi + heartрте:prevmi + bpmeds:prevstrk
## Model 2: I(logit(chdrisk)) ~ sex + totchol + age + sysbp + diabp + cursmoke +
## cigpday + bmi + diabetes + bpmeds + heartрте + 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:hearttrte +
##      sysbp:diabetes + diabp:bmi + diabp:hdlc + prevmi:hdlc + prevmi:prevhyp +
##      sex:glucose + age:ldlc + age:hearttrte + cigpday:hdlc + bmi:ldlc +
##      totchol:hdlc + totchol:prevmi + sysbp:hearttrte + sysbp:bpmeds +
##      cursmoke:hdlc + prevmi:prevstrk + diabetes:hdlc + sex:sysbp +
##      cigpday:glucose + hearttrte:glucose + diabp:glucose + cursmoke:ldlc +
##      age:cigpday + age:hdlc + hdlc:ldlc + age:prevhyp + diabp:prevhyp +
##      diabp:cursmoke + diabp:cigpday + bmi:bpmeds + cigpday:prevmi +
##      glucose:prevmi + hearttrte:prevmi
##      Res.Df      RSS Df Sum of Sq      F Pr(>F)
## 1      2240 489.70
## 2      2245 492.27 -5      -2.5718 2.3528 0.03851 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4 Model Diagnostics

4.1 Leverage and Influence Measures

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

5 Model Selection

6 Discussion