MLR: Regression Diagnostics

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Regression Diagnostics in R

After we fit a multiple linear regression model, we must evaluate the assumptions we have made to fit the model. We will evaluate linearity, outliers, and multicollinearity.

In this exercise we will continue the previous exercise with the birthweight data. Begin by reading in the birthweight data and fit the multiple linear regression model.

```
## Load the sas7bdat package to read in a SAS dataset
library(sas7bdat)

## Set working directory
setwd("~/OneDrive - Emory University/Documents/Work/Bios 591P 2022/R Materials/3 MLR/Data")

## Read in the data
bwt <- read.sas7bdat("birthweight.sas7bdat")

## Fit MLR model
bwt.lm <- lm(BWT ~ AGE + WT + SMOKE + HT,data=bwt)</pre>
```

We are going to load two packages which contain useful functions for regression diagnostics: car and MASS. These packages are automatically installed when you install R, but you must load them with the *library()* function before using them.

```
## Load packages for regression diagnostics
library(car)

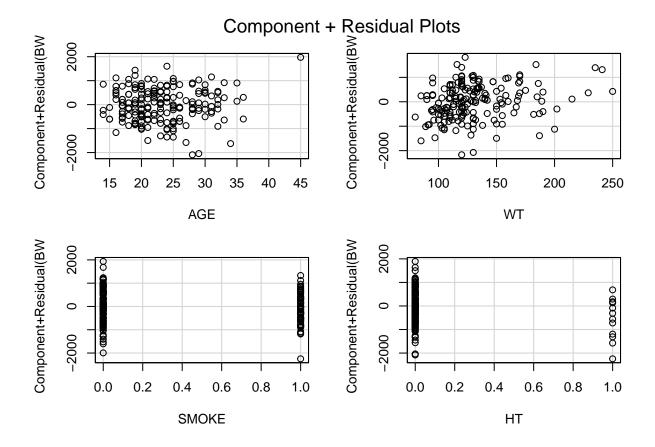
## Loading required package: carData
library(MASS)
```

Linearity

Partial Plots

We use the crPlots() function, from the car package, in order to fit partial plots. We give two additional arguments, line=FALSE and smooth=FALSE, to tell crPlots() not to fit lines over the residuals or add smoothing lines (see what happens when you remove line=FALSE and smooth=FALSE)

```
## Partial plots: crPlots()
crPlots(bwt.lm,line=FALSE,smooth=FALSE)
```



Influential Points and Outliers

Leverage

We use the function hatvalues() in order to calculate the leverage values in R. It is called "hatvalues" because the leverage values are calculated from the hat matrix (used to fit the linear model).

The *hatvalues()* function takes our linear model object as its argument. Calculate and save the leverage values.

```
## Leverage: hatvalues()
lev.vals <- hatvalues(bwt.lm)</pre>
```

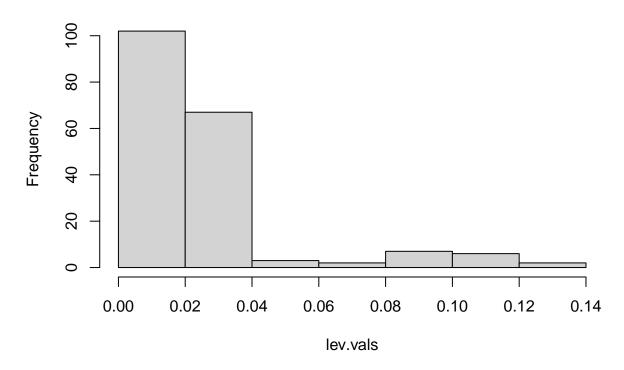
The threshold for concerning leverage values is $\frac{2(k+1)}{n}$, where we have k explanatory variables. In this case, we have 4 explanatory variables. Calculate and save the leverage threshold.

We calculate n using the length() function, which will tell us how many leverage values we have, and thus how many subjects we have in our model.

```
lev.threshold <- 2*(4+1)/length(lev.vals)</pre>
```

We can see a histogram of the leverage values with the *hist()* function.

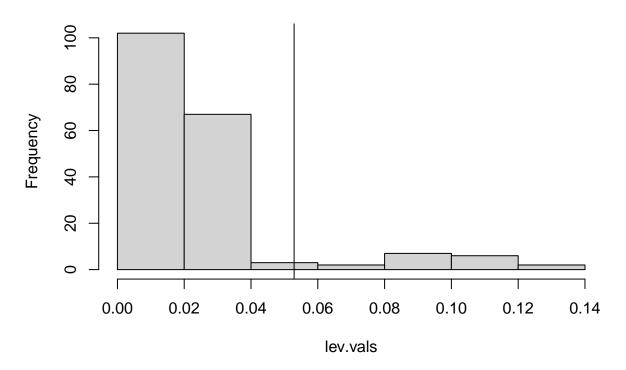
Histogram of lev.vals



To more easily see the values of concern, we add a vertical line to our plot with the abline() function. This is a very flexible function which can add lines to a plot. We'll see it again, but for now we add a vertical line with the "v=" argument in abline, and we draw the line at the leverage threshold.

hist(lev.vals)
abline(v=lev.threshold)

Histogram of lev.vals



To see which values are above the threshold, we give R a logical (true/false) statement with the > operator.

lev.vals > lev.threshold

FALSE FALSE TRUE TRUE FALSE FALSE FALSE TRUE TRUE FALSE FALSE FALSE ## FALSE ## FALSE ## FALSE ## FALSE FALSE ## FALSE TRUE FALSE ## ## FALSE FALSE FALSE FALSE TRUE TRUE FALSE FALSE FALSE FALSE FALSE ## ## FALSE FALSE FALSE FALSE FALSE TRUE FALSE FALSE FALSE FALSE FALSE ## FALSE FALSE FALSE TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE ## ## ## FALSE FALSE FALSE FALSE FALSE TRUE FALSE FALSE FALSE FALSE FALSE ## ## FALSE FALSE FALSE FALSE TRUE FALSE FALSE FALSE FALSE FALSE FALSE ## FALSE ## FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE TRUE FALSE FALSE ## ## FALSE FALSE FALSE TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE ##

```
## FALSE FALSE FALSE FALSE FALSE FALSE
                                                  TRUE FALSE FALSE FALSE
    157
          158
                                        163
##
                159
                      160
                            161
                                  162
                                             164
                                                   165
                                                         166
                                                               167
                                                                     168
                                                                           169
                           TRUE FALSE FALSE FALSE
                                                  TRUE FALSE FALSE FALSE
  FALSE FALSE FALSE
    170
                                                               180
                                                                     181
##
          171
                172
                      173
                            174
                                  175
                                        176
                                             177
                                                   178
                                                         179
                                                                           182
## FALSE FALSE
##
    183
          184
                185
                      186
                                  188
                                        189
                            187
## FALSE FALSE FALSE FALSE FALSE
                                      TRUE
```

This just gives us a list of true/false values telling us which observations have a leverage value higher than the threshold.

The list of true/false values is actually stored as 1s and 0s, so if we take the sum of the true and false values, we will see how many leverage values are higher than the threshold.

```
sum(lev.vals > lev.threshold)
```

```
## [1] 17
```

There are 17 observations with a leverage value higher than the threshold.

In order to see which leverage values are high, we use the which() function to tell us the location where "lev.vals > lev.threshold" is true.

```
which(lev.vals > lev.threshold)
```

```
## 3 4 9 10 51 58 59 72 82 98 110 127 135 152 161 165 189
## 3 4 9 10 51 58 59 72 82 98 110 127 135 152 161 165 189
```

Now, if we want to see the data for the observations with a high leverage value, we use the brackets [,] to select the specific rows of the birthweight dataset.

```
bwt[which(lev.vals > lev.threshold),]
```

```
##
             BWT AGE
                        WT SMOKE HT RACE
## 3
         11 1135
                   34 187
                                0
                                         1
                                   1
##
         13
            1330
                   25 105
                                0
                                    1
                                         2
##
   9
         19 1729
                   24 132
                                0
                                    1
                                         1
##
   10
         20
            1790
                   21 165
                                         1
##
   51
            2442
                                         2
         75
                   26 154
                                0
                                         2
##
   58
         83
            2495
                   17
                      142
                                0
                                    1
  59
         84 2495
                                         1
##
                   21 130
                                1
                                    1
   72
         98 2750
                   22
                        95
                                0
                                         2
## 82
        108 2836
                                0
                                    0
                                         3
                   36 202
        126 3005
                   31 215
                                         1
##
  98
                                1
   110 138 3100
                   22 120
                                0
                                    1
                                         1
   127 159 3303
                   28 250
                   18 229
   135 168 3402
                                0
                                    0
                                         1
   152
       187
            3629
                   19 235
                                         1
   161 197
                                         2
            3756
                   19 184
                                    1
                                         3
## 165 202 3790
                   25 241
                                0
                                   1
## 189 226 5001
                   45 123
                                0
                                   0
                                         1
```

Cook's Distance

We follow a similar process with Cook's distance, but the threshold of concern is now $\frac{4}{n}$. We calculate Cook's distance with the cooks.distance() function, which takes our linear model object as its argument.

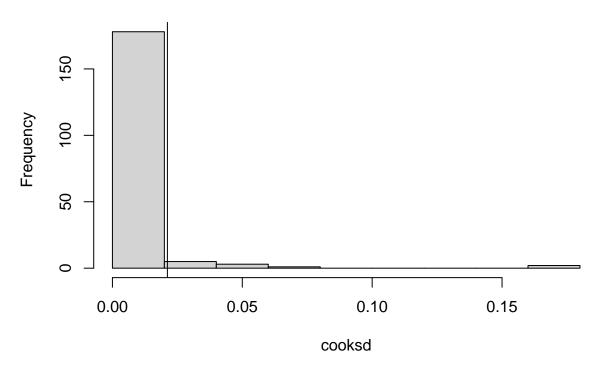
```
## Cook's distance: cooks.distance()
```

```
cooksd <- cooks.distance(bwt.lm)

# Threshold: 4/n
cooks.threshold <- 4/length(cooksd)

hist(cooksd)
abline(v=cooks.threshold)</pre>
```

Histogram of cooksd



```
cooksd > cooks.threshold
which(cooksd > cooks.threshold)
                 4
                     9 17 110 152 161 165 189
##
             3
             3
                     9 17 110 152 161 165 189
##
                 4
bwt[which(cooksd > cooks.threshold),]
##
        ID
           BWT AGE WT SMOKE HT RACE
## 1
           709
                28 120
## 2
        10 1021
                 29 130
                            0
                               0
                                    2
        11 1135
                 34 187
                                    1
        13 1330
                 25 105
                                    2
## 4
        19 1729
                 24 132
                                    1
        28 1928
                                    2
## 17
                 21 200
## 110 138 3100
                 22 120
                                    1
                 19 235
## 152 187 3629
                            1 1
                                    1
## 161 197 3756 19 184
                            1 1
                                    2
## 165 202 3790 25 241
                                    3
```

```
## 189 226 5001 45 123 0 0 1
sum(cooksd > cooks.threshold)
## [1] 11
```

Jackknife Residuals

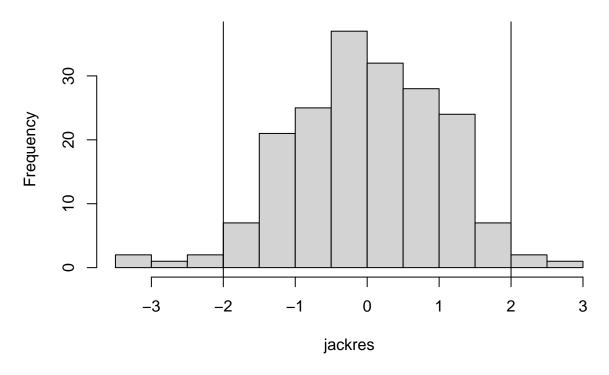
The jackknife residuals are calculated with the studres() function from the MASS package, because another name for the jackknife residuals is "studentized residuals".

```
## Jackknife Residuals: studres()
jackres <- studres(bwt.lm)</pre>
```

The threshold for the jackknife residuals is 2, but remember that the residuals can be negative—so we are looking for jackknife residuals with an absolute value greater than 2.

```
# Threshold: absolute value > 2
hist(jackres)
abline(v=2)
abline(v=-2)
```

Histogram of jackres



```
abs(jackres) > 2
which(abs(jackres) > 2)

## 1 2 3 6 17 187 188 189

## 1 2 3 6 17 187 188 189
```

bwt[which(abs(jackres) > 2),]

```
##
            BWT AGE WT SMOKE HT RACE
        ID
                             1 0
                 28 120
## 1
            709
## 2
        10 1021
                 29 130
                             0
                                0
                                      2
## 3
        11 1135
                 34 187
                             0
                                1
                                      1
## 6
        16 1588
                 27 150
                             0
                                0
                                     2
                                     2
                                0
## 17
        28 1928
                 21 200
## 187 224 4238
                                0
                                     1
                 19 120
## 188 225 4593
                 24 116
                                0
                                      1
## 189 226 5001 45 123
                             0 0
                                      1
```

Multicollinearity

Correlation

We test the correlation between explanatory variables with the cor.test() function. Here, we calculate the correlation between age and weight, which are our two continuous explanatory variables.

```
cor.test(bwt$AGE,bwt$WT)
```

```
##
## Pearson's product-moment correlation
##
## data: bwt$AGE and bwt$WT
## t = 2.5034, df = 187, p-value = 0.01316
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.03832798 0.31471467
## sample estimates:
## cor
## 0.1800732
```

Variance Inflation Factors

1.040064 1.100864 1.006497 1.063364

We can also evaluate multicollinearity by calculating the Variance Inflation Factors. The vif() function from the car package will do this for us.

```
vif(bwt.lm)
## AGE WT SMOKE HT
```

Recall that the threshold for concerning VIFs is around 10, so we do not see any VIFs of concern.