

## Lab 4: Simple Linear Regression in R

STAT 310, Spring 2023

In this lab we will go over how to fit a simple linear regression model in R. We will again use the NHANES data set, which was introduced in Lab 2.

```
# read in data set  
nhanes = readRDS(url("https://ericwfox.github.io/data/nhanes.rds"))
```

```
# check dimension (number of rows and columns)  
dim(nhanes)
```

```
## [1] 1500  11
```

```
# get columns names  
names(nhanes)
```

```
## [1] "Gender"      "Age"          "Education"    "HHIncome"    "Weight"  
## [6] "Height"      "BPSysAve"     "BPDiaAve"     "HealthGen"    "PhysActive"  
## [11] "Smoke100"
```

Type the following command to look at a scrollable, spreadsheet display of the data set:

```
View(nhanes)
```

## Simple Linear Regression Model

We can use the `lm()` function in R to fit a simple linear regression model. Here we'll fit a model with systolic blood pressure (`BPSysAve`) as the response variable, and diastolic blood pressure (`BPDiaAve`) as the explanatory variable.<sup>1</sup>

```
lm1 = lm(BPSysAve ~ BPDiaAve, data = nhanes)
```

The function uses the formula notation  $y \sim x$ , where  $y$  is the response variable, and  $x$  is the explanatory variable.

Use the `summary()` function to print out important information about the linear regression model we just fit.

```
summary(lm1)
```

```
##
## Call:
## lm(formula = BPSysAve ~ BPDiaAve, data = nhanes)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -33.666 -10.047  -2.328   7.451  99.100
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  89.65230    2.32651   38.53  <2e-16 ***
## BPDiaAve      0.44137    0.03267   13.51  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15.28 on 1498 degrees of freedom
## Multiple R-squared:  0.1086, Adjusted R-squared:  0.108
## F-statistic: 182.5 on 1 and 1498 DF,  p-value: < 2.2e-16
```

The least squares estimates of the slope and intercept are given in the **Coefficients** table of the summary output. The equation of the least squares regression line can therefore be written as

$$\hat{y} = 89.6523 + 0.44137x$$

The summary output also gives an  $R^2 = 0.1086$ . This means that about 11% of the variability in systolic blood pressure ( $y$ ) can be explained by diastolic blood pressure ( $x$ ).

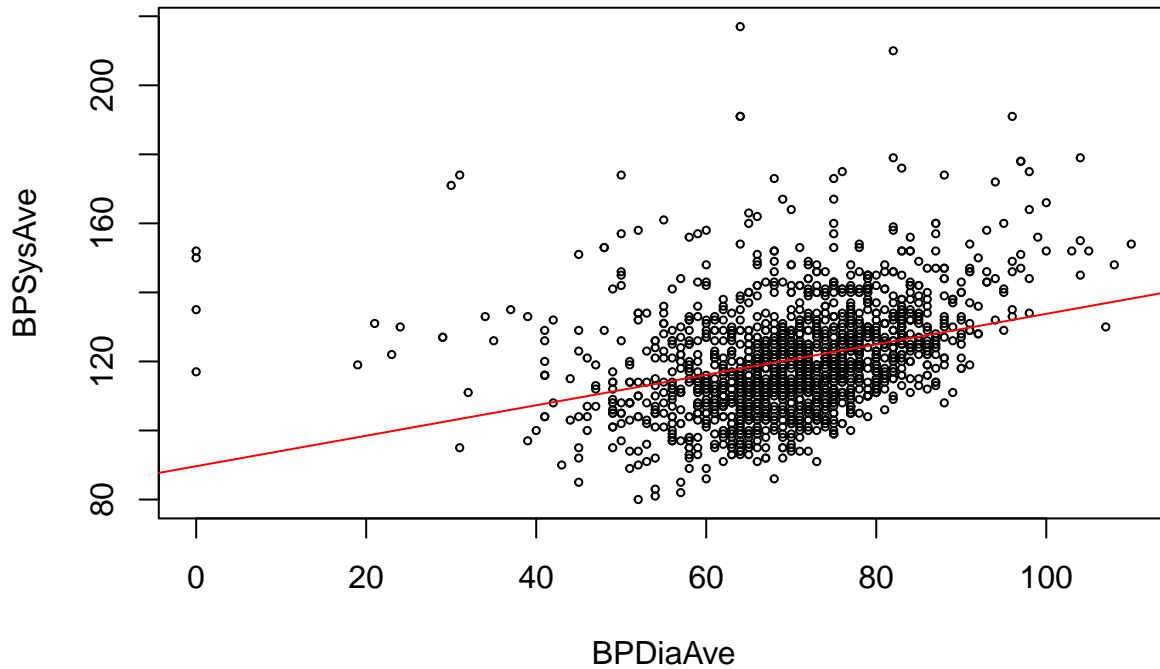
---

<sup>1</sup>Some background info about blood pressure: <https://www.cdc.gov/bloodpressure/about.htm>

## Plot Least Squares Line

Next we make a scatter plot of the data, and add the least squares line:

```
plot(BPSysAve ~ BPDiaAve, data = nhanes, cex = 0.5)
abline(lm1, col = "red") # add least squares line
```



The scatter plot shows a positive linear association between diastolic and systolic blood pressure. However, there are some outliers – four individuals with a diastolic blood pressure reading of zero.

Note that `cex` controls the size of the points (magnification relative to 1); since there are 1500 points, I reduced the point size.

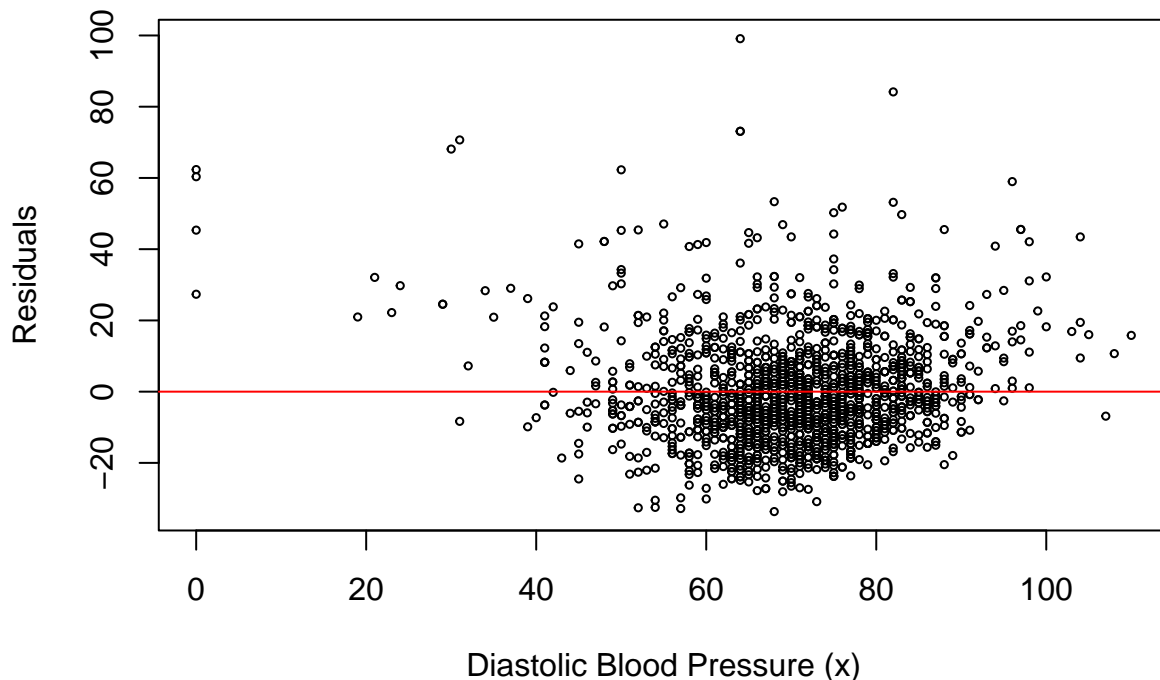
## Check Conditions

Recall the conditions for simple linear regression:

- Linearity: The data should follow a linear trend.
- Constant Variability: The variability of the points around the least squares line remains roughly constant.
- Normality: The residuals should have an approximate normal distribution with mean 0.
- Independence: Values of the response variable are independent of each other.

Based on the scatter plot the linearity condition seems satisfied. One useful plot for checking the constant variability condition is a plot of the residuals ( $\hat{e}_i = y_i - \hat{y}_i$ ) versus the values of the explanatory variable ( $x_i$ ):

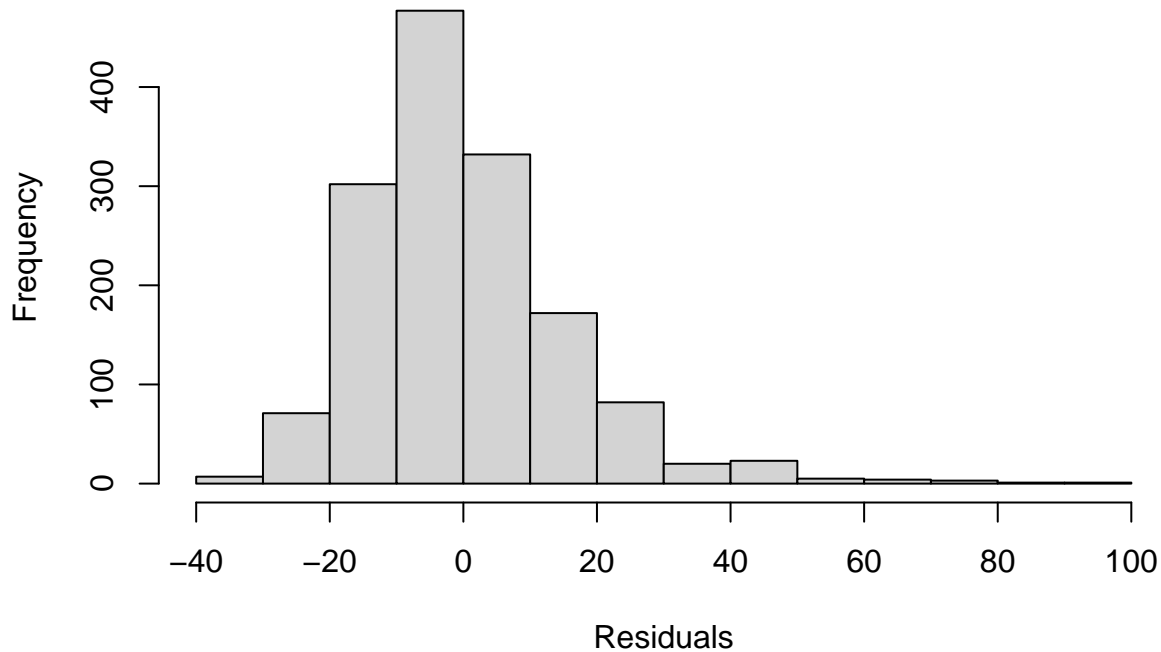
```
# residual plot  
plot(nhanes$BPDiaAve, resid(lm1), cex = 0.5,  
      xlab = "Diastolic Blood Pressure (x)", ylab = "Residuals")  
abline(h = 0, col = "red") # horizontal line at 0
```



The points look randomly scattered in the residual plot, so the constant variability condition is satisfied.

Next, to check the normality condition, make a histogram of the residuals:

```
hist(resid(lm1), xlab = "Residuals", main = "")
```



The distribution has a bell-curve shape. Although, the histogram looks a little right skewed, which indicates that there are some outliers.

Last, note that the data come from a random sample of people, so the independence condition is satisfied.

Overall, the conditions for simple linear regression appear mostly satisfied with this data set. The only concern is that there are some outliers.