Correlation and Simple Regression

Advanced Psychological Research Methods

Dr Christopher Wilson

Questions from last week's session?

Submit your attendance

Attendance code: 78012

http://bit.ly/APRM22

By the end of this section, you will be able to:

Correlation

- The relationship between 2 variables
- Question: Is treatment duration related to aggression levels?

How is correlation calculated?

$$\mathrm{r}_{xy} = \frac{\sum_{i=1}^{n}(x - \bar{x})(y - \bar{y})}{\sum_{i=1}^{n}(x_i - \bar{x})^2 \sum_{i=1}^{n}(y_i - \bar{y})^2}$$

How is correlation calculated?

2 *Subtract Mean*

3 *Calculate ab, a² and b²*

Temp °C	Sales	"a"	"b"	a×b	a²	b²
14.2	$215	-4.5	-$187	842	20.3	34,969
16.4	$325	-2.3	-$77	177	5.3	5,929
11.9	$185	-6.8	-$217	1,476	46.2	47,089
15.2	$332	-3.5	-$70	245	12.3	4,900
18.5	$406	-0.2	$4	-1	0.0	16
22.1	$522	3.4	$120	408	11.6	14,400
19.4	$412	0.7	$10	7	0.5	100
25.1	$614	6.4	$212	1,357	41.0	44,944
23.4	$544	4.7	$142	667	22.1	20,164
18.1	$421	-0.6	$19	-11	0.4	361
22.6	$445	3.9	$43	168	15.2	1,849
17.2	$408	-1.5	$6	-9	2.3	36
18.7	**$402**			**5,325**	**177.0**	**174,757**

1 *Calculate Means*

4 *Sum Up*

5
$$\frac{5,325}{\sqrt{177.0 \times 174,757}} = 0.9575$$

Running correlation in R

- Step 1: Check assumptions
  - Data,distribution,linearity
- Step 2: Run correlation
- Step 3: Check R value
- Step 4: Check significance

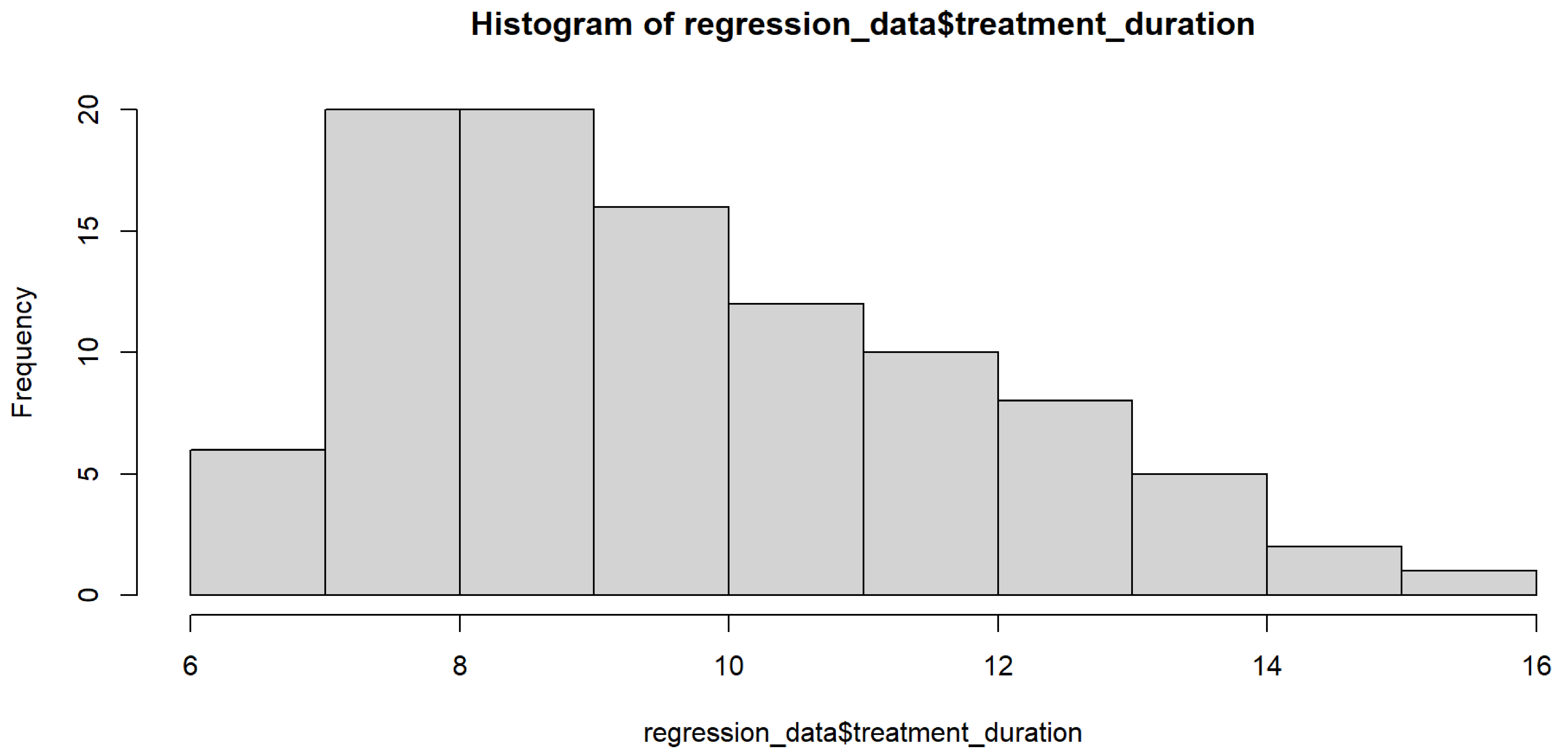
Check assumptions: data

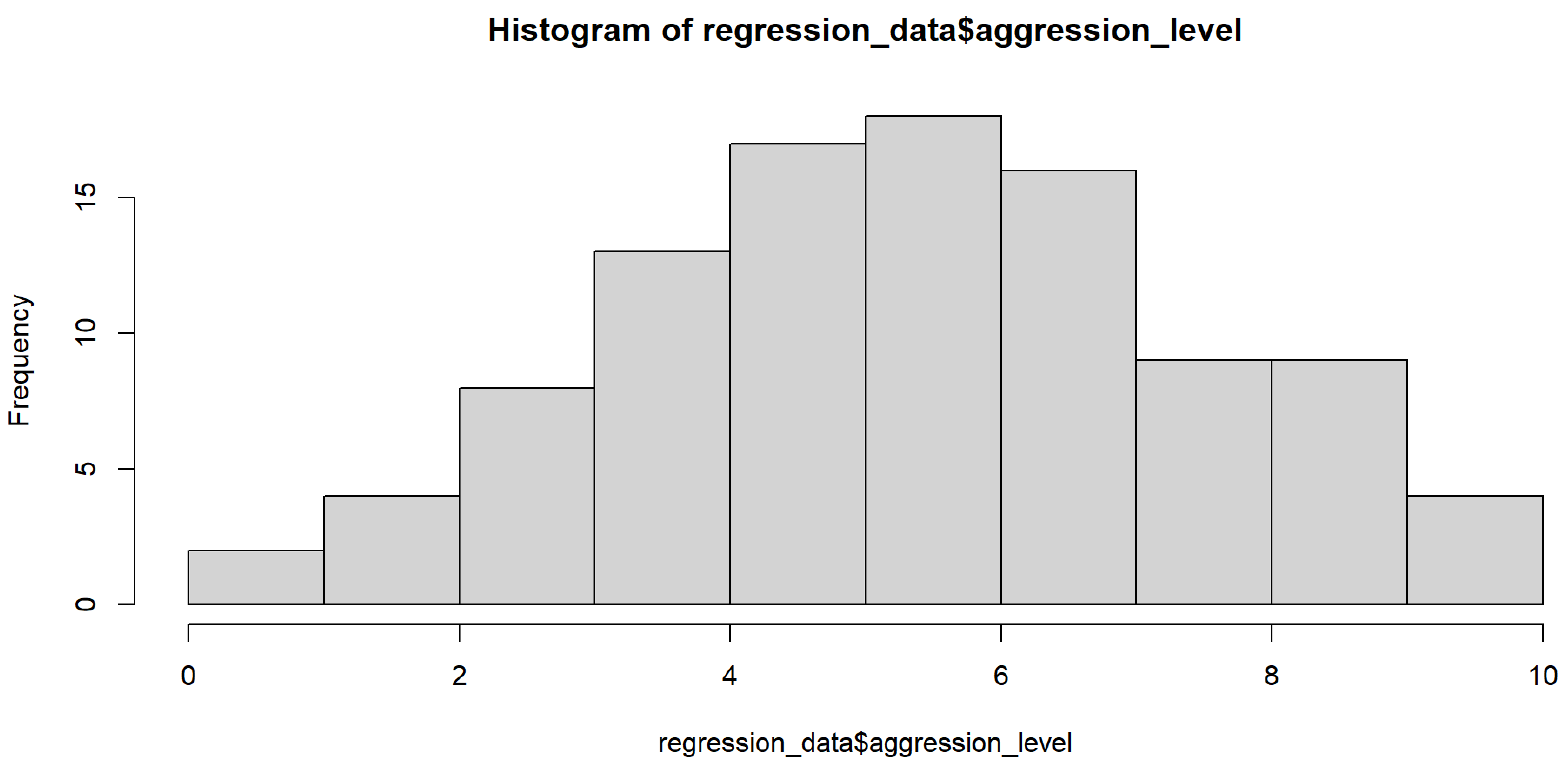
- Parametric tests require interval or ratio data
- If the data are ordinal then a non-parametric correlation is used

What type of data are treatment duration and aggression level?

Check assumptions: distribution #1

- Parametric tests require normally distributed data





Histogram of regression_data$aggression_level
Frequency
0
5
10
15
0
2
4
6
8
10
regression_data$aggression_level

Check assumptions: distribution #2

- Parametric tests require normally distributed data

```r
shapiro.test(regression_data$treatment_duration)
```

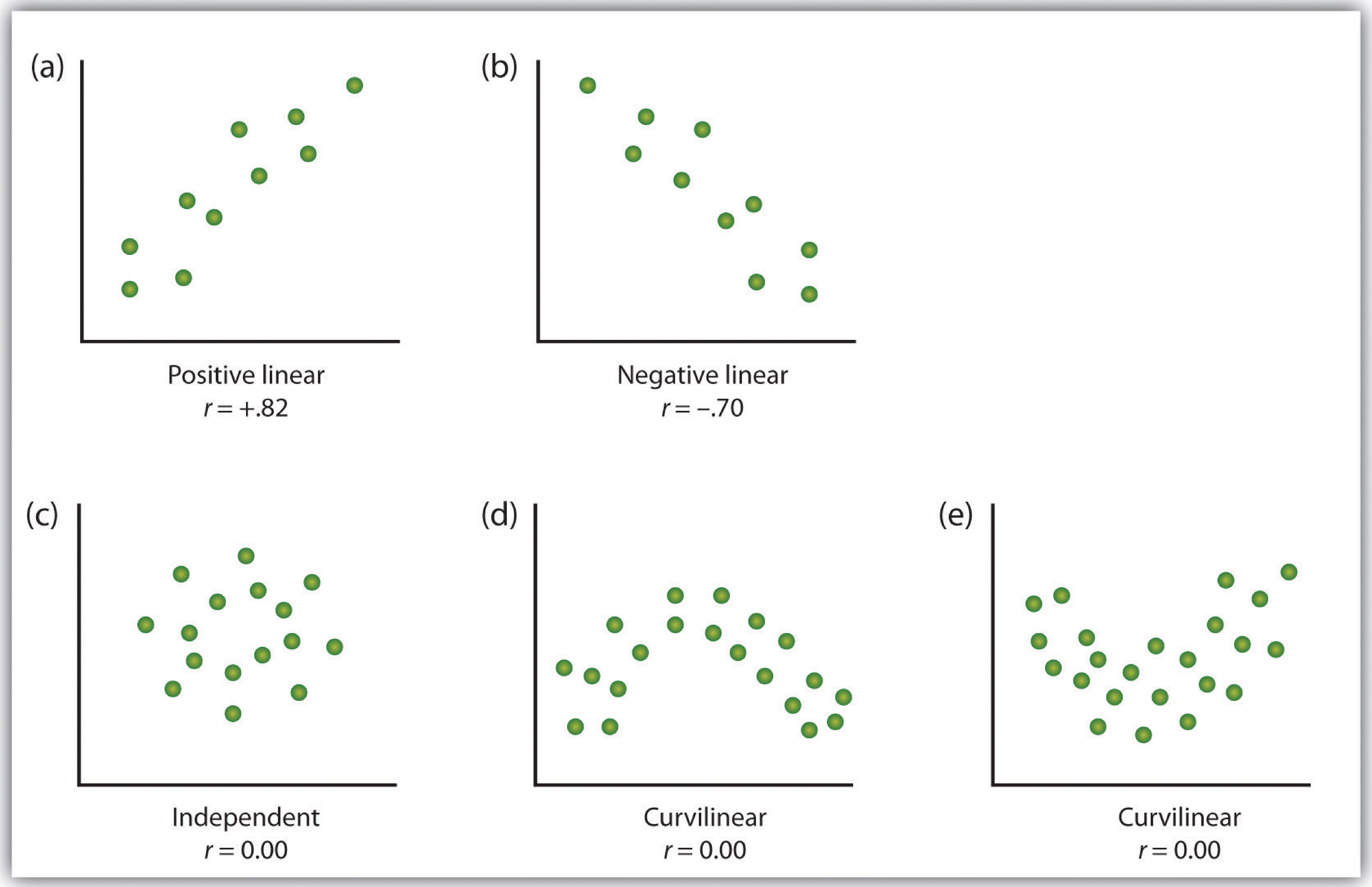
```
	Shapiro-Wilk normality test

data:  regression_data$treatment_duration
W = 0.94971, p-value = 0.0007939
```

```r
shapiro.test(regression_data$aggression_level)
```

```
	Shapiro-Wilk normality test

data:  regression_data$aggression_level
W = 0.9928, p-value = 0.8756
```

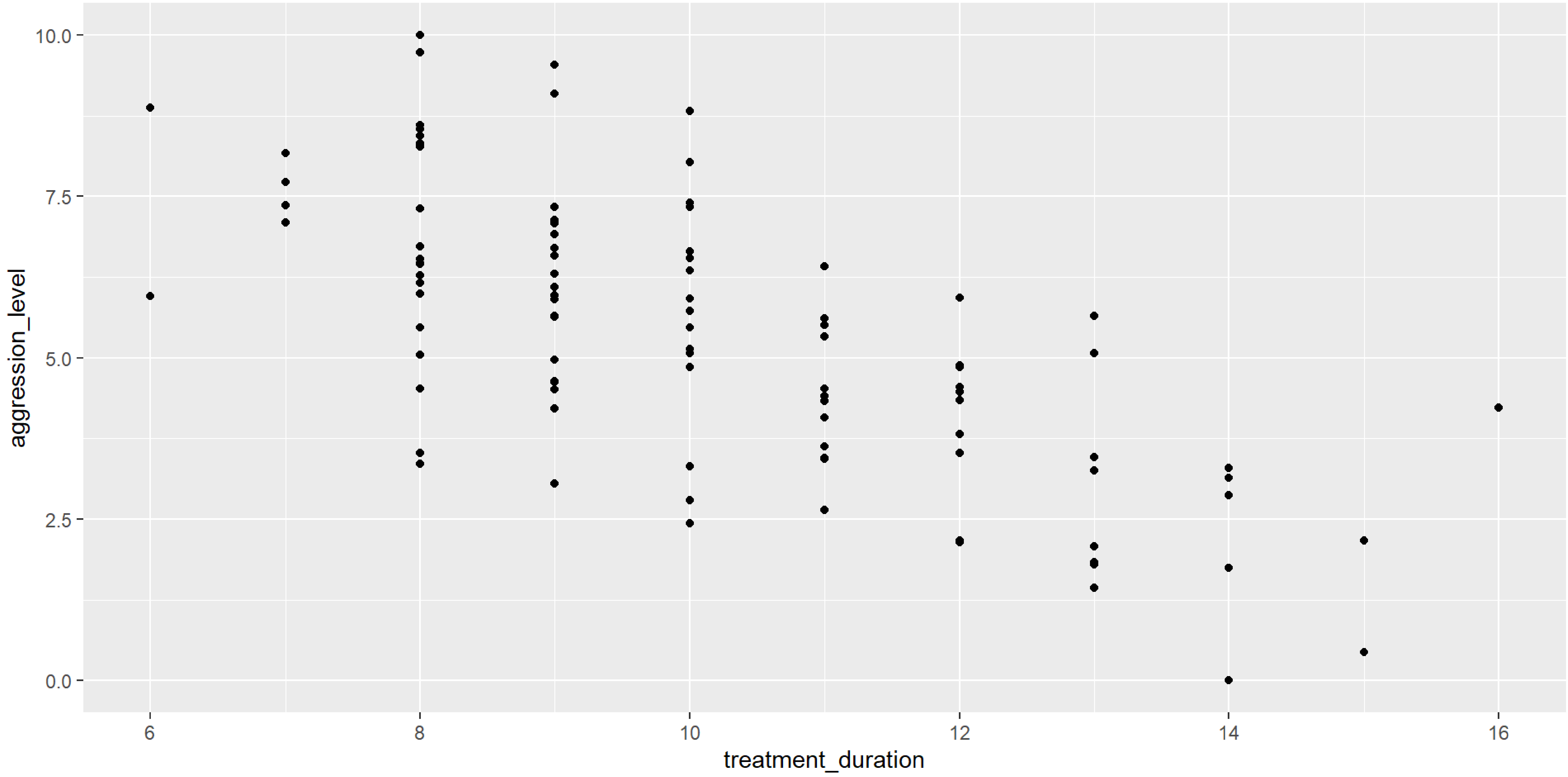
- The normality assumption is less of an issue when sample size is > 30

Checking assumptions: linearity



Checking assumptions: linearity

```
regression_data %>% ggplot(aes(x=treatment_duration,y=aggression_level)) +
  geom_point()
```



- Here we are looking to see if the relationship is linear

Run correlation

- R can run correlations using the *cor.test()* command

```
cor.test(regression_data$treatment_duration,regression_data$aggression_level)
```

```
    Pearson's product-moment correlation

data:  regression_data$treatment_duration and regression_data$aggression_level
t = -9.5503, df = 98, p-value = 1.146e-15
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.7838251 -0.5765006
sample estimates:
       cor
-0.6942996
```

Check r Value (correlation value)

- The r value tells us the strength and direction of the relationship
- In the output it is labelled as “cor” (short for correlation)

```
cor.test(regression_data$treatment_duration,regression_data$aggression_level)
```

```
	Pearson's product-moment correlation

data:  regression_data$treatment_duration and regression_data$aggression_level
t = -9.5503, df = 98, p-value = 1.146e-15
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.7838251 -0.5765006
sample estimates:
       cor
-0.6942996
```

Check the significance of the correlation

- We can see that the significance by looking at the p value
  - The significance is 1.146^-15
  - This means: 0.000000000000001146
- Therefore p value < 0.05

```r
cor.test(regression_data$treatment_duration,regression_data$aggression_level)
```

```
	Pearson's product-moment correlation

data:  regression_data$treatment_duration and regression_data$aggression_level
t = -9.5503, df = 98, p-value = 1.146e-15
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.7838251 -0.5765006
sample estimates:
       cor
-0.6942996
```

Regression

What is regression?

- Testing to see if we can make predictions based on data that are correlated

> We found a strong correlation between treatment duration and agression levels. Can we use this data to predict aggression levels of other clients, based on their treatment duration?

- When we carry out regression, we get a information about:
  - How much variance in the **outcome** is explained by the **predictor**
  - How confident we can be about these results generalising (i.e. **significance**)
  - How much error we can expect from anu predictions that we make (i.e. **standard error of the estimate**)
  - The figures we need to calculate a predicted outcome value (i.e. **coefficient values**)

How is regression calculated?

- When we run a regression analysis, a calculation is done to select the “line of best fit”
- This is a “prediction line” that minimises the overall amount of error
  - Error = difference between the data points and the line

The regression equation #1

- Once the line of best fit is calculated, predictions are based on this line
- To make predictions we need the **intercept** and **slope** of the line
  - **Intercept** or **constant**= where the line crosses the y axis
  - **Slope** or **beta** = the angle of the line

The regression equation #2

- Predictions are made using the calculation for a line:

Y = bX + c

- You can think of the equation like this:

predicted outcome value = beta coefficient * value of predictor + constant

Running regression in R

- Step 1: Run regression
- Step 2: Check assumptions
  - Data
  - Distribution
  - Linearity
  - Homogeneity of variance
  - Uncorrelated predictors
  - Independence of residuals
  - No influential cases / outliers
- Step 3: Check R^2 value
- Step 4: Check model significance
- Step 5: Check coefficient values

Run regression

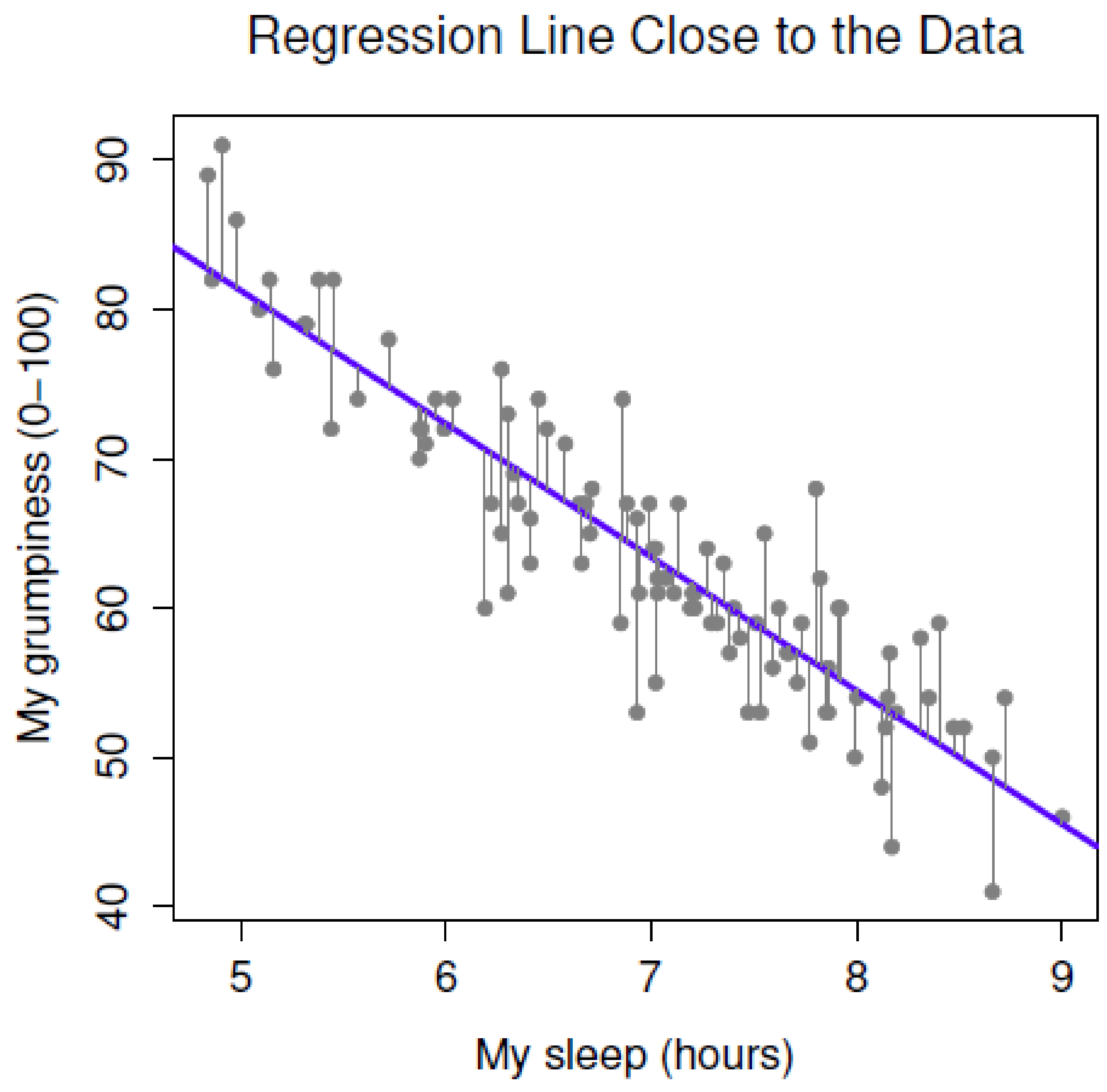
- We use the *lm()* command to run regression while saving the results
- We then use the *summary()* function to check the results

```r
model1 <- lm(formula= aggression_level ~ treatment_duration ,data=regression_data)

summary(model1)
```

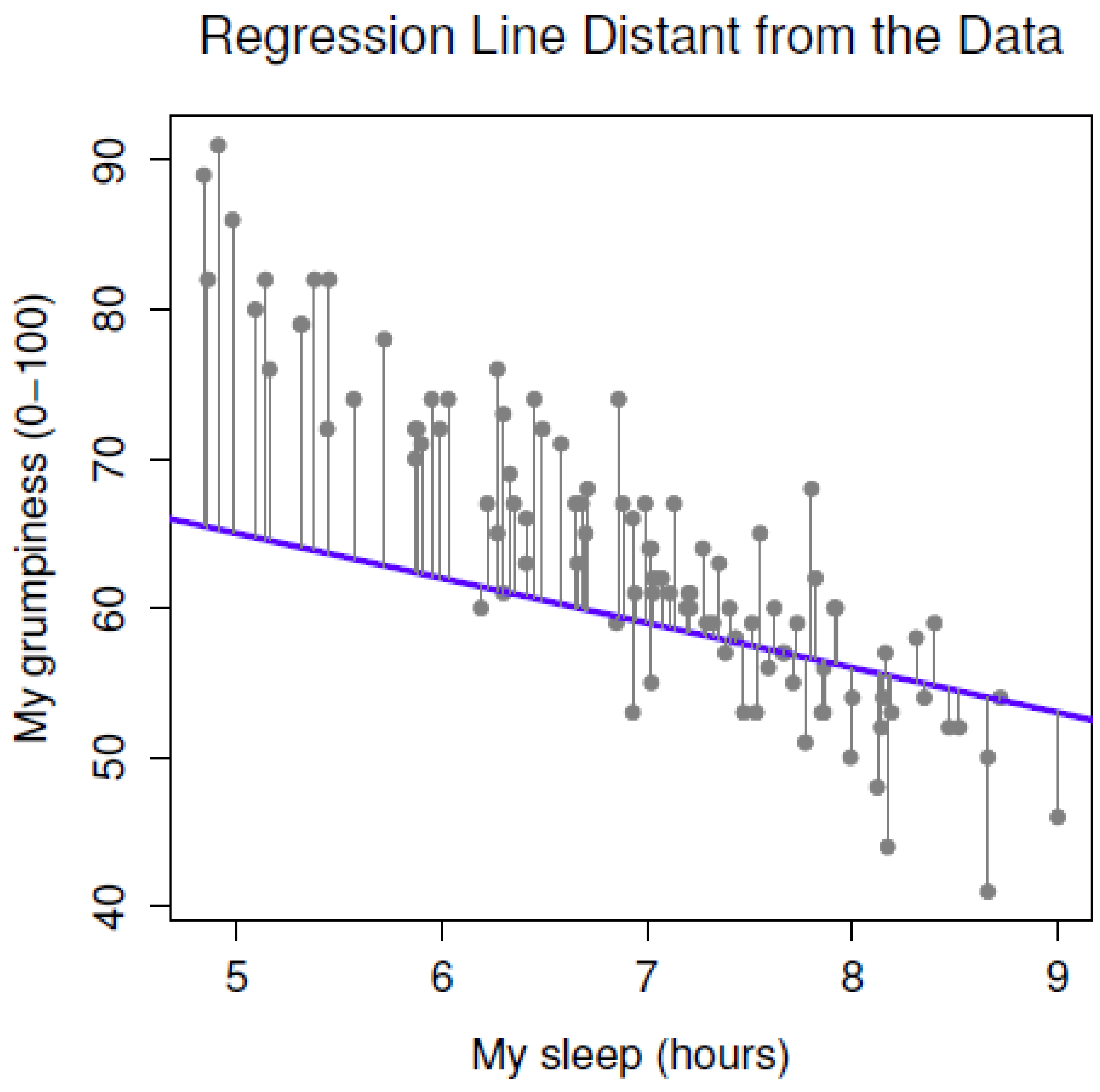
```
Call:
lm(formula = aggression_level ~ treatment_duration, data = regression_data)

Residuals:
    Min      1Q  Median      3Q     Max 
-3.4251 -1.1493 -0.0593  0.8814  3.4542 

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)    
(Intercept)         12.3300     0.7509   16.42  < 2e-16 ***
treatment_duration  -0.6933     0.0726   -9.55 1.15e-15 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.551 on 98 degrees of freedom
```

What are residuals?

- In regression, the assumptions apply to the residuals, not the data themselves
- Residual just means the difference between the data point and the regression line



(a)

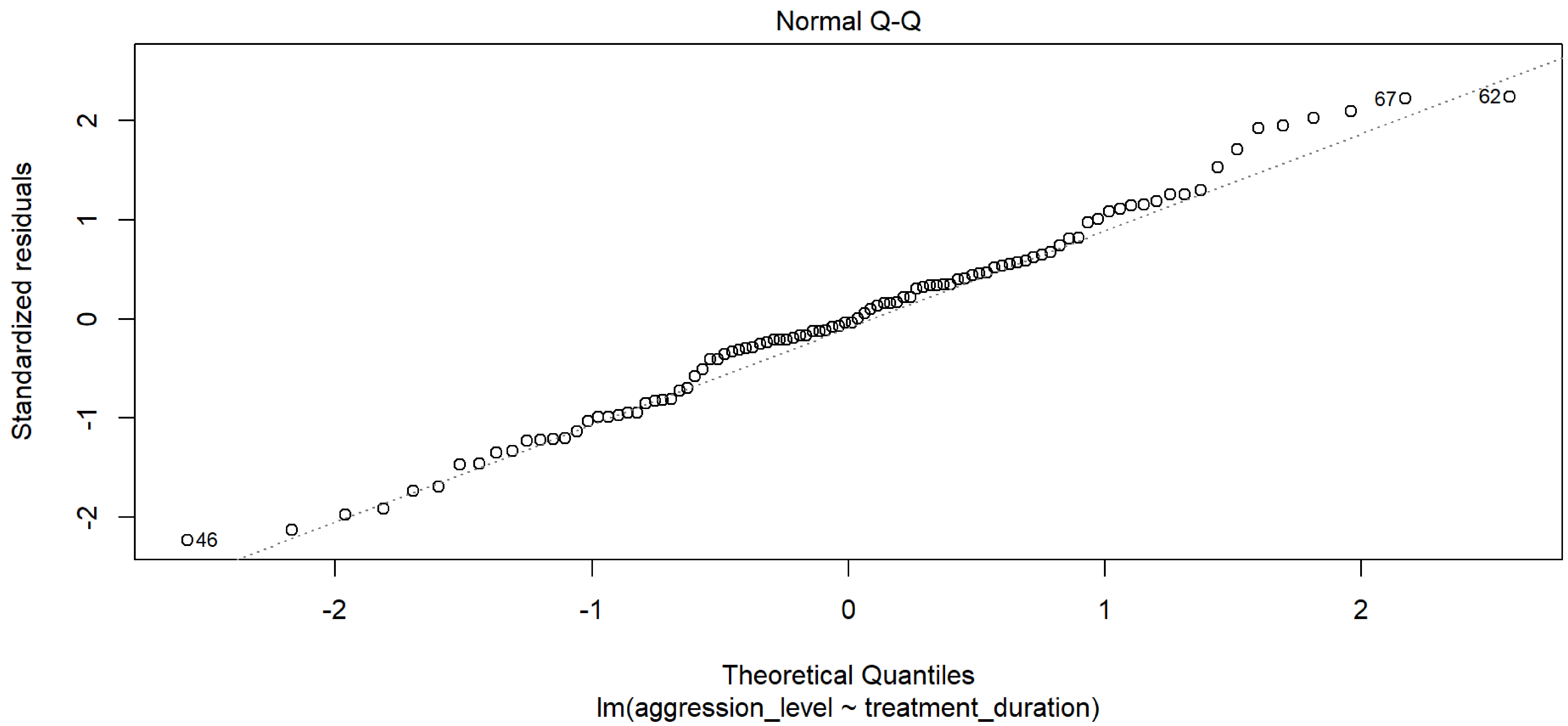


(b)

Check assumptions: distribution

- Using the *plot()* command on our regression model will give us some useful diagnostic plots
- The second plot that it outputs shows the normality

```
plot(model1, which=2)
```



Check assumptions: distribution

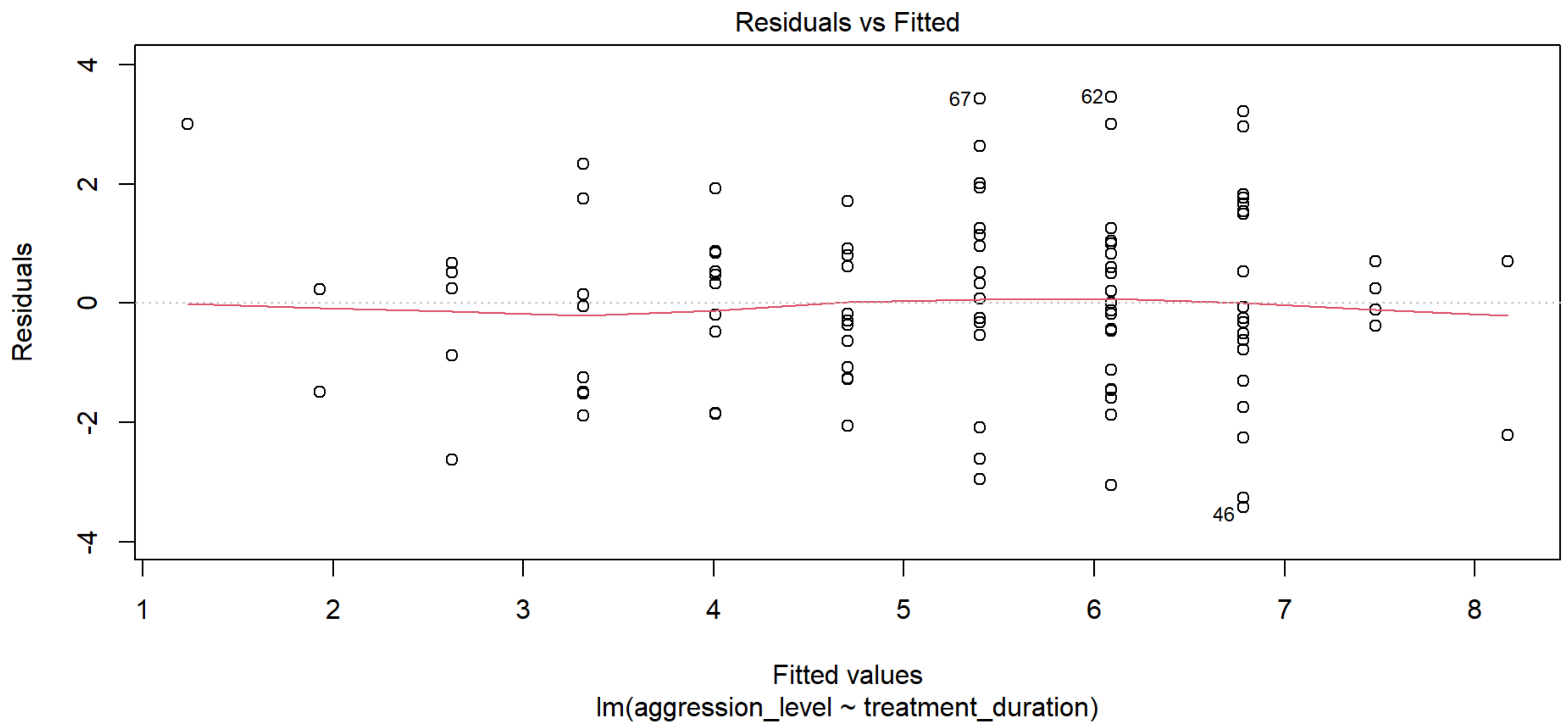
- We could also use a histogram to check the distribution
- Notice how we can use the $ sign to get the residuals from the model

```r
hist(model1$residuals)
```

Check assumptions: linearity

- Using the *plot()* command on our regression model will give us some useful diagnostic plots
- The first plot that it outputs shows the residuals vs the fitted values
- Here, we want to see them spread out, with the line being horizontal and straight

```r
plot(model1, which=1)
```

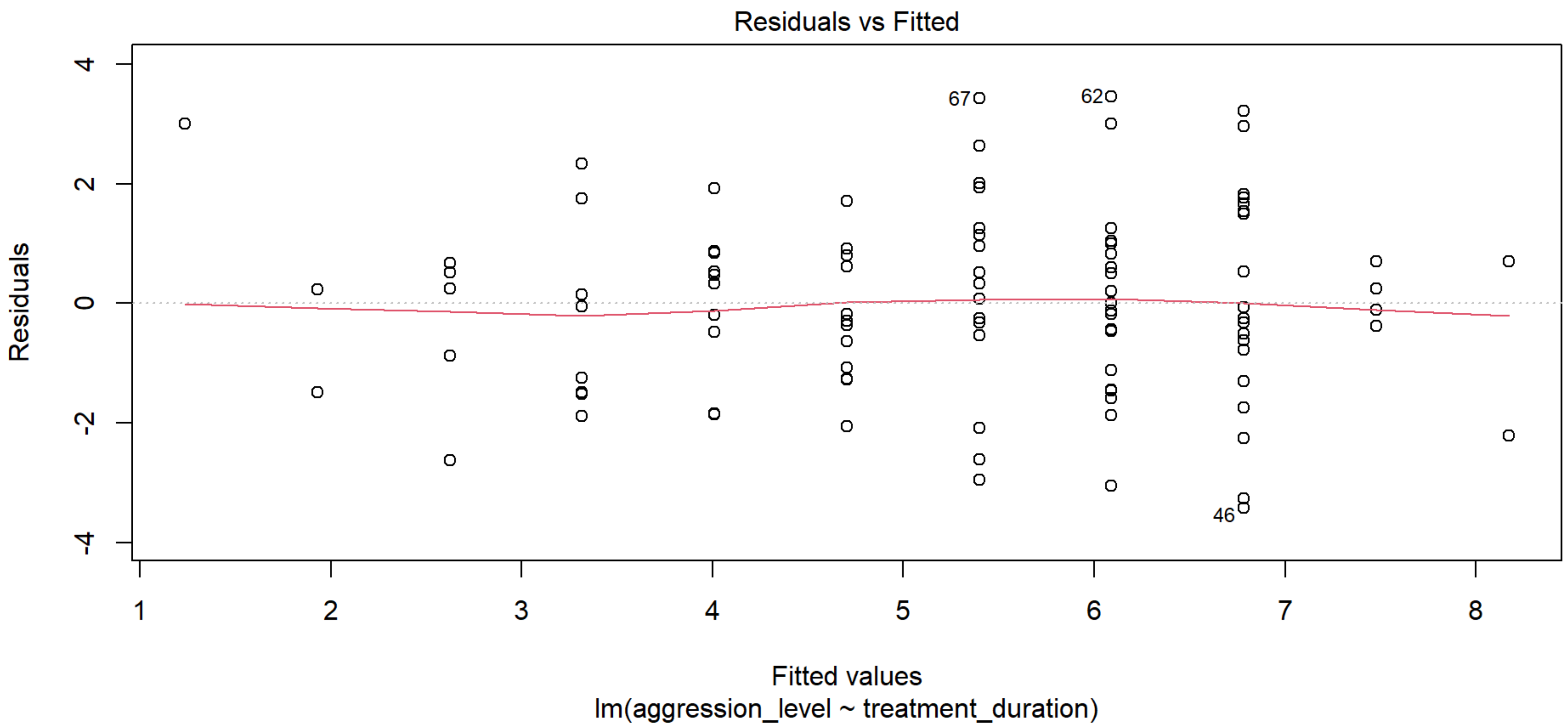


- There is a slight amount of curvilinearity here but nothing to be worried about

Check assumptions: Homogeneity of Variance #1

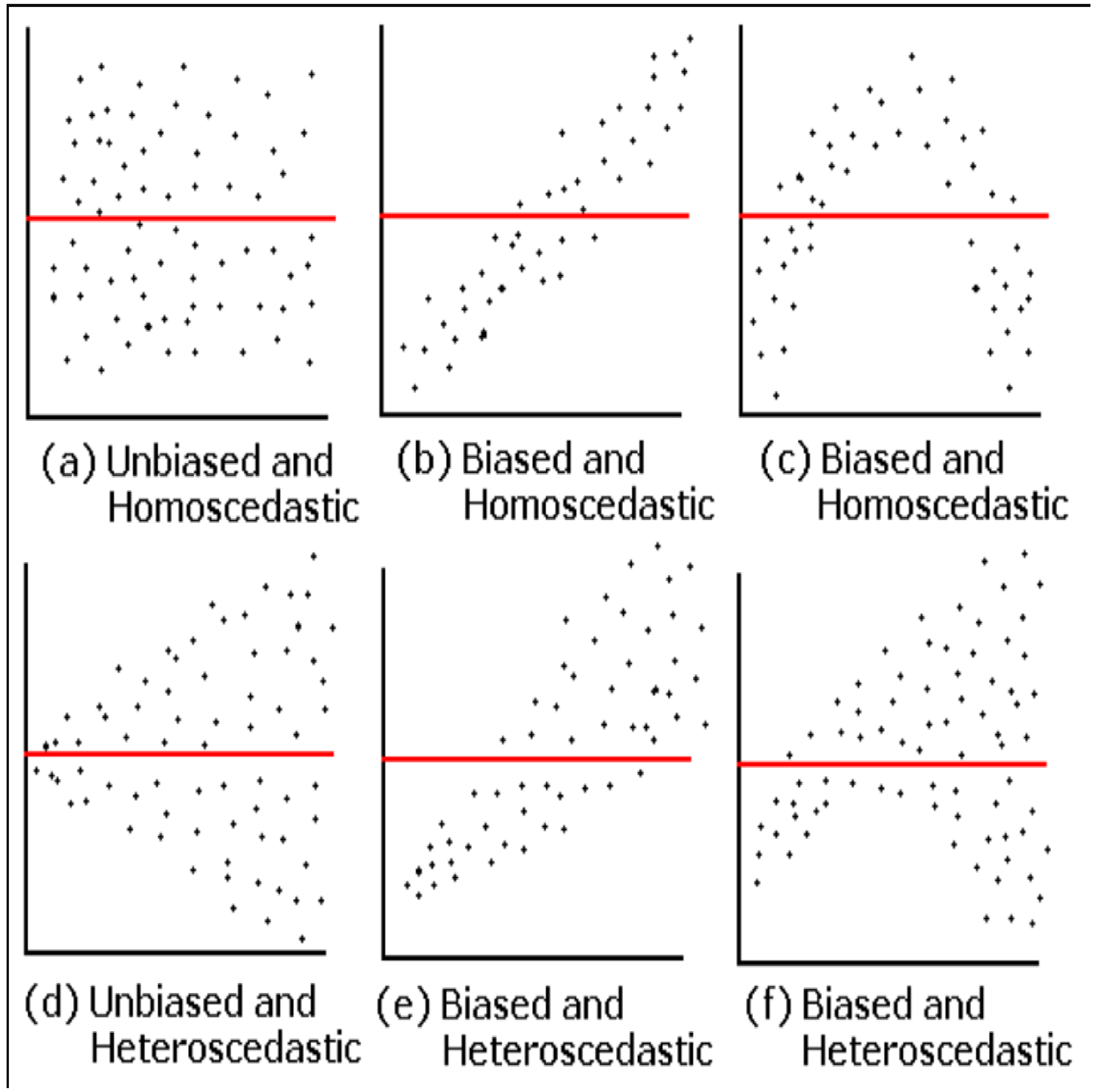
- We can use the sample plot to check Homogeneity of Variance
- We want the variance to be constant across the data set. We do not want the variance to change at different points in the data

```
plot(model1, which=1)
```



Check assumptions: Homogeneity of Variance #2

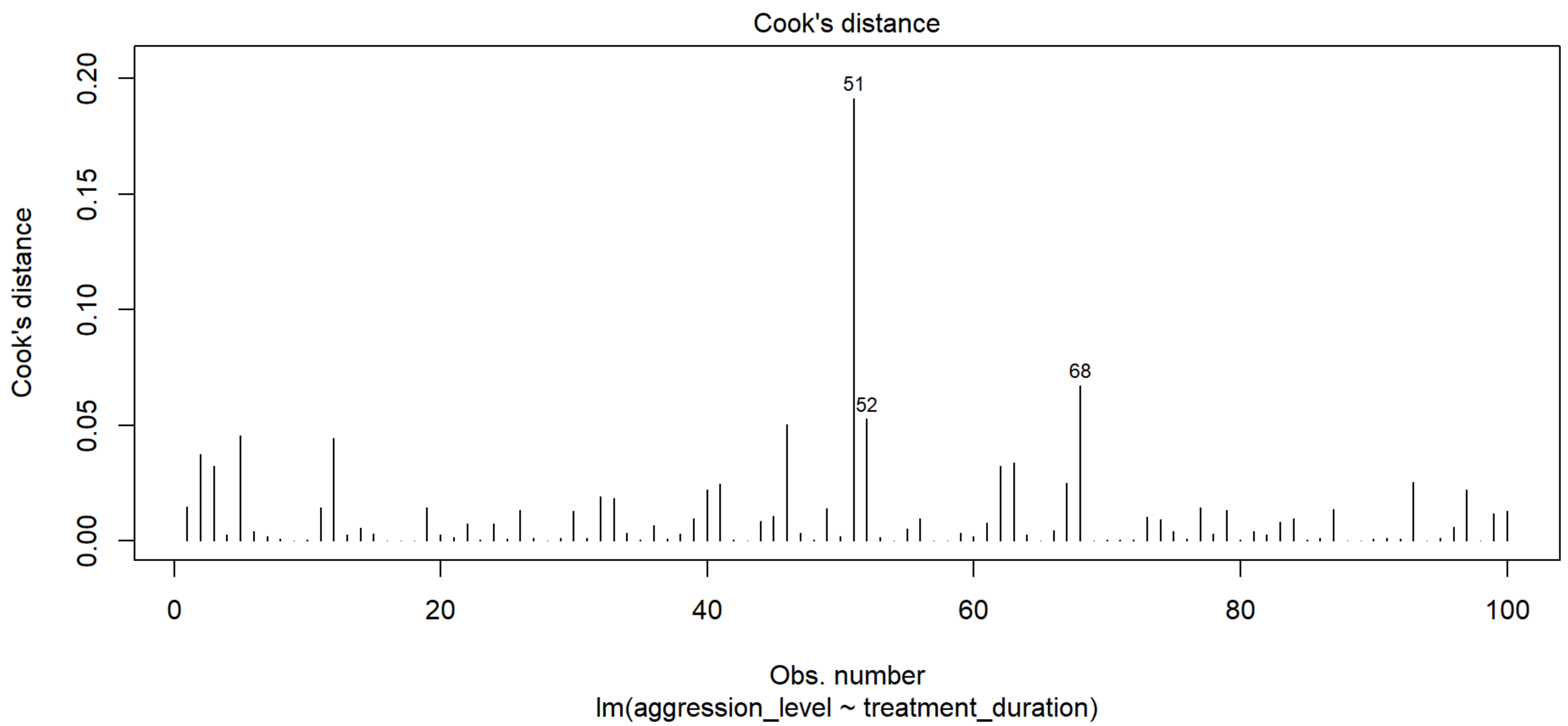
- A violation of Homogeneity of Variance would usually look like a funnel, with the data narrowing



Check assumptions: Influential cases #1

- We need to check that there are no extreme outliers - they could throw off our predictions
- We are looking for participants that have high rediduals + high leverage
  - Some guidance suggests anything higher than 1 is an influential case
  - Others suggest 4/n is the cut off point (4 divided by number of participants)

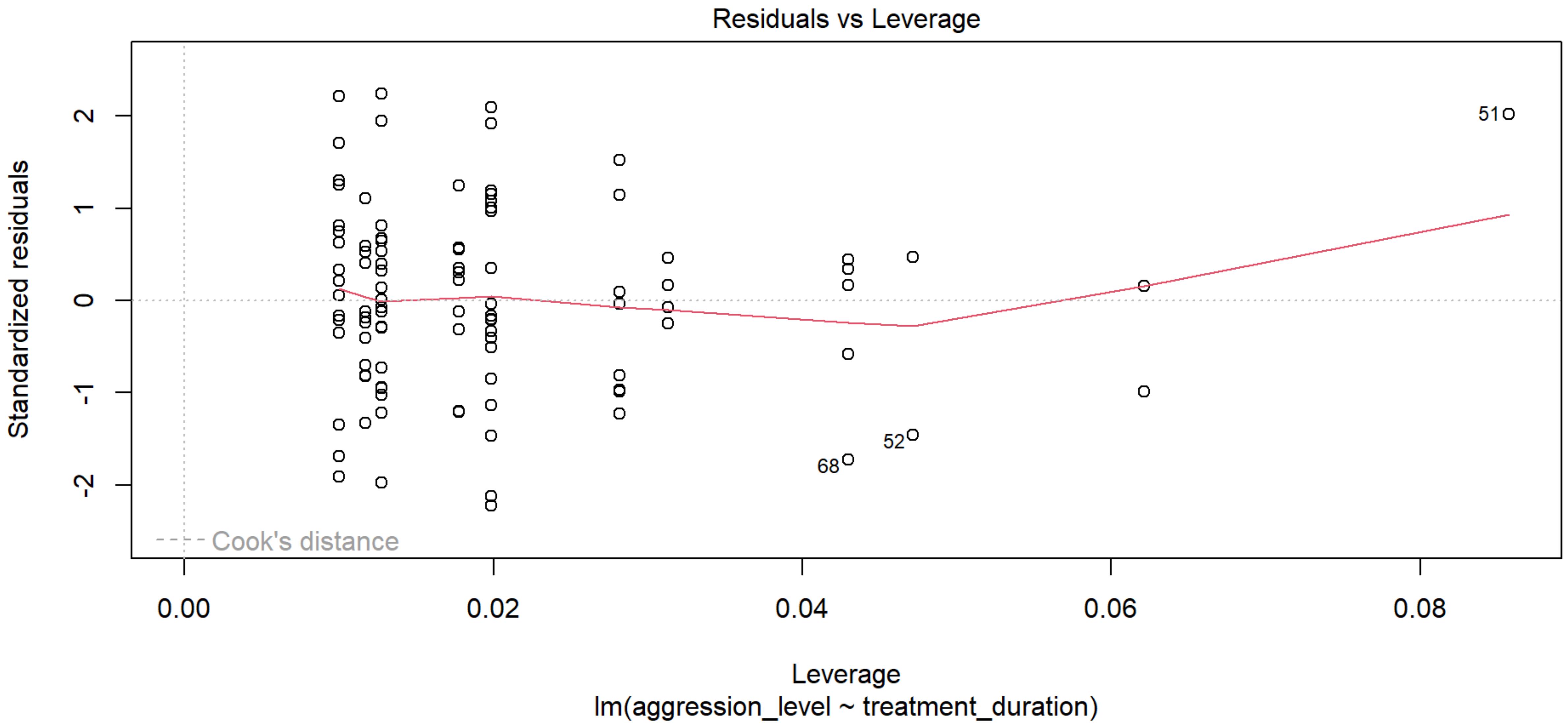
```r
plot(model1, which=4)
```



Check assumptions: Influential cases #2

- We are looking for participants that have high rediduals + high leverage
  - No cases over 1
  - Many are over 0.04 (4/n = 0.04)

```
plot(model1, which=5)
```



Check the r squared value

- r^2 = the amount of variance in the **outcome** that is explained by the **predictor(s)**
- The closer this value is to 1, the more useful our regression model is for predicting the outcome

```r
modelSummary <- summary(model1)
modelSummary
```

```
Call:
lm(formula = aggression_level ~ treatment_duration, data = regression_data)

Residuals:
    Min      1Q  Median      3Q     Max 
-3.4251 -1.1493 -0.0593  0.8814  3.4542 

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)    
(Intercept)         12.3300     0.7509   16.42  < 2e-16 ***
treatment_duration  -0.6933     0.0726   -9.55 1.15e-15 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.551 on 98 degrees of freedom
```

- The r^2 of 0.482052 means that 48% of the variance in **aggression level** is explained by **treatment duration**

Check model significance

- The model significance is displayed at the very end of the output
  - *p-value: 1.146e-15*
  - As $p < 0.05$, the model is significant

```r
modelSummary
```

```

Call:
lm(formula = aggression_level ~ treatment_duration, data = regression_data)

Residuals:
    Min      1Q  Median      3Q     Max 
-3.4251 -1.1493 -0.0593  0.8814  3.4542 

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)    
(Intercept)         12.3300     0.7509   16.42  < 2e-16 ***
treatment_duration  -0.6933     0.0726   -9.55 1.15e-15 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Check coefficient values #1

- The coefficient values are displayed in the coefficients table
- If we have more than one predictor, they are all listed here

```
modelSummary$coefficients
```

```
                     Estimate Std. Error   t value     Pr(>|t|)
(Intercept)        12.3300211 0.75087601 16.420848 6.840516e-30
treatment_duration -0.6933201 0.07259671 -9.550297 1.145898e-15
```

- The **beta coefficient** for treatment duration is in the *Estimate* column
- For every unit increase in treatment duration, aggression level decreases by 0.69

The regression equation

- The regression equation is:

Outcome = predictor value * beta coefficient + constant

- For this model, that is:

Aggression level = treatment duration * -0.69 + 12.33

```r
modelSummary$coefficients
```

```
                     Estimate Std. Error   t value     Pr(>|t|)
(Intercept)        12.3300211 0.75087601 16.420848 6.840516e-30
treatment_duration -0.6933201 0.07259671 -9.550297 1.145898e-15
```

Accounting for error in predictions

- We also know that the accuracy of predictions will be within a certain margin of error
- This is known as **standard error of the estimate** or **residual standard error**

```r
modelSummary
```

```

Call:
lm(formula = aggression_level ~ treatment_duration, data = regression_data)

Residuals:
    Min      1Q  Median      3Q     Max 
-3.4251 -1.1493 -0.0593  0.8814  3.4542 

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)    
(Intercept)         12.3300     0.7509   16.42  < 2e-16 ***
treatment_duration  -0.6933     0.0726   -9.55 1.15e-15 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.551 on 98 degrees of freedom
```

Questions?